

Tue Dec 11 16:09:58 2003

us-09-601-667c-41.fai

Page 8

LENGTH: 267 amino acids
TYPE: amino acid
STANDARDNESS: Single
TOPOLOGY: Linear
US-08-838-793D-61

Query Match
Best Local Similarity 30.7%; Score 376; DB 2; Length 267;
Best Local Similarity 39.1%; Pred. No. 3.7e-37;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

QY 9 TQGTGKXEPFRITLLADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOCKXK 66
DB 13 TQGTGKXEPFRITLLADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOCKXK 66
QY 67 TQGTGKXEPFRITLLADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOCKXK 123
DB 71 TQGTGKXEPFRITLLADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOCKXK 129
QY 124 AGH-RDQIPGLXOLIOSYAL--RPGSGTXXQARSILILQMSIAPARFPIIMEXR 179
DB 130 AGH-RDQIPGLXOLIOSYAL--RPGSGTXXQARSILILQMSIAPARFPIIMEXR 189
QY 180 OXINSKSFPLDXVMTLETSWQSGTQVQSGTDGVFNNPXRILAXGNFTLXNRYVI 239
DB 190 OXINSKSFPLDXVMTLETSWQSGTQVQSGTDGVFNNPXRILAXGNFTLXNRYVI 249
QY 240 ASIALMLFVCGERPSS 255
DB 250 ASIALMLFVCGERPSS 265

RESULT 15
US-08-838-765-1
Sequence 1, Application US/08839765
Patent No. 614631
GENERAL INFORMATION:
APPLICANT: Betelex, Marc D.
INVENTOR: Betelex, Marc D.
TITLE OF INVENTION: A System for Detecting and Isolating Compensating Ribosome Inactivation
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent release #1.0, version #1.25
CHECKSUM APPLICATION DATA: 1
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA: US 07/901,707
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/702-0153
FAX: 212/702-0153
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: Linear
NO SIGNAL TYPE: protein

US-08-838-765-1
Query Match
Best Local Similarity 30.7%; Score 376; DB 3; Length 267;
Best Local Similarity 39.1%; Pred. No. 3.7e-37;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

QY 9 TQGTGKXEPFRITLLADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOCKXK 66
DB 13 TQGTGKXEPFRITLLADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOCKXK 70
QY 67 TQGTGKXEPFRITLLADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOCKXK 123
DB 71 TQGTGKXEPFRITLLADYSSGS-FSNEIPL-LRSTIPVSDAQRVLYELTNOCKXK 129
QY 124 AGH-RDQIPGLXOLIOSYAL--RPGSGTXXQARSILILQMSIAPARFPIIMEXR 179
DB 130 AGH-RDQIPGLXOLIOSYAL--RPGSGTXXQARSILILQMSIAPARFPIIMEXR 189
QY 180 OXINSKSFPLDXVMTLETSWQSGTQVQSGTDGVFNNPXRILAXGNFTLXNRYVI 239
DB 190 OXINSKSFPLDXVMTLETSWQSGTQVQSGTDGVFNNPXRILAXGNFTLXNRYVI 249
QY 240 ASIALMLFVCGERPSS 255
DB 250 ASIALMLFVCGERPSS 265

Search completed: December 11, 2003, 14:11:38
Job time: 8.86328 secs

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Page 7

Db 13 TGAIVTSTNFIKAVRGLTGDVREHIEVLEPRVGLFIR--QRPILVLSNMAELAV 70
Cy 67 TGAIVTSTNFIKAVRGLTGDVREHIEVLEPRVGLFIR--QRPILVLSNMAELAV 123
Db 71 TGAIVTSTNFIKAVRGLTGDVREHIEVLEPRVGLFIR--QRPILVLSNMAELAV 129
Cy 124 AGH-RDQIFLIGXOLGOSVAL--KPGSTKXASILLIOMISEARFPIIMKX 179
Db 130 AGH-RDQIFLIGXOLGOSVAL--KPGSTKXASILLIOMISEARFPIIMKX 189
Cy 189 QXINSKSFLEPYXMELEFSGQOQVQVQSTDDVPMNPKXLAIXGNFTLXVAVYI 239
Db 190 TRLRNRSAPDPSVITLNSMGLSTALDSNQAFASPIQLOFRMSKPSYDVASILI 249
Cy 240 ASIAIMLFVCGSRPS 255
Db 250 PIALMRYCAPPS 265

RESULT 13
US-09-601-667c-41
Sequence 1, Application US/08646360

GENERAL INFORMATION:
APPLICANT: Bacter, Marc D.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Maltby, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 13-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McAndrews, Janet M.
REGISTRATION NUMBER: 32,518
REFERENCE/DOCKET NUMBER: 200-70, P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/470-1889
TELEFAX: 312/470-1889
TELEPHONE: 650 386-1248
TELEFAX: 650 386-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid

TOPOLOGY: linear
US-08-646-360-1
Query Match 30.7%, Score 376, DB 2, Length 267;
Best Local Similarity 39.1%, Pred. No. 3, 7e-37;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;
Cy 9 TQOTGKXFFFTLLRDPVSSGS-FSNHFL-RQSTIPVSDAQFVVELTQGXDKX 66
Db 13 TGAIVTSTNFIKAVRGLTGDVREHIEVLEPRVGLFIR--QRPILVLSNMAELAV 70
Cy 67 TGAIVTSTNFIKAVRGLTGDVREHIEVLEPRVGLFIR--QRPILVLSNMAELAV 123
Db 71 TGAIVTSTNFIKAVRGLTGDVREHIEVLEPRVGLFIR--QRPILVLSNMAELAV 129
Cy 124 AGH-RDQIFLIGXOLGOSVAL--KPGSTKXASILLIOMISEARFPIIMKX 179
Db 130 AGH-RDQIFLIGXOLGOSVAL--KPGSTKXASILLIOMISEARFPIIMKX 189
Cy 189 QXINSKSFLEPYXMELEFSGQOQVQVQSTDDVPMNPKXLAIXGNFTLXVAVYI 239
Db 190 TRLRNRSAPDPSVITLNSMGLSTALDSNQAFASPIQLOFRMSKPSYDVASILI 249
Cy 240 ASIAIMLFVCGSRPS 255
Db 250 PIALMRYCAPPS 265

RESULT 14
US-08-338-793D-61
Sequence 61, Application US/08338793D

GENERAL INFORMATION:
APPLICANT: Barth, Peter Thomas
TITLE OF INVENTION: VECTOR
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS: LARRY CISHMAN
ADDRESSER: INTELLECTUAL PROPERTY GROUP OF
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word or ASCII editors
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,793D
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842,061
FILING DATE: 26-APR-92
CLASSIFICATION: 435
APPLICATION NUMBER: 9104017.0
FILING DATE: 26-FEB-91
APPLICATION NUMBER: 9109188.4
FILING DATE: 29-APR-91
ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 6,773
REFERENCE/DOCKET NUMBER: DB/9901/215431/7GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3900
TELEFAX: 202-822-0944
TELEPHONE: 671-627 CUSH
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:

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Page 6

US-08-488-113B-1
Sequence 1, Application US/08488113B
Patent No. 5744580

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

INVENTOR: Stankovic, Gary M.

ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,113B

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McAndrews, Janet M.

REGISTRATION NUMBER: 32,918

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

REFERENCE/DOCKET NUMBER: 110220507/200-70-P3-C2A

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-488-113B-1

Query Match

Best Local Similarity 39.1%; Prod. No. 3.7e-37;

Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

DB

9 THOTGKXEPFPTLLRDVSSGS-FSNEIPL-ROSTPVSDAQFVAVLWNGGXDX 66

DB

13 TGAATVOSTTTFIRVGRGRTTADVGRSTPVLIRVGLPTN-QPTLVEASHAEISV 70

QY

67 TLAIDTNYVAVGAGOSQYLR-DARQAE-THTATGDSGLSPKSYMLRY 123

DB

71 TLAIDVAVVGVGAGNSAIFPHDQEDARITVHFT-DVONKTFAGGVNDELQ 129

QY

124 AGH-RDOIPIGICLOISVYL--RXPQSTKQASILLQWISBAAPNIMTX 179

DB

130 AGNDRNRIELANGPLEALISALVYVSTGQULPTLASFTICQITSSARFQITGEMR 189

US-08-477-484B-1
Sequence 1, Application US/08477484B
Patent No. 5756699

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

INVENTOR: Stankovic, Gary M.

ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McAndrews, Janet M.

REGISTRATION NUMBER: 32,918

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

REFERENCE/DOCKET NUMBER: 110220507/200-70-P3-C2A

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-484B-1

Query Match

Best Local Similarity 39.1%; Prod. No. 3.7e-37;

Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

DB

9 THOTGKXEPFPTLLRDVSSGS-FSNEIPL-ROSTPVSDAQFVAVLWNGGXDX 66

DB

130 AGNDRNRIELANGPLEALISALVYVSTGQULPTLASFTICQITSSARFQITGEMR 189

QY

180 QKNSKSHDPXWMLTETSGGOSTGOSTGQVNNPRLAIKXGZPTLANKY 239

DB

190 TIRNRRAPDSVITLNSWRLSTLQSNQCAFSPQLGRNRSFVSVDLSLI 249

QY

240 ASLAIMFVCGEPSS 255

DB

250 PTLNMTKCAPPS 265

RESULT 12

US-08-477-484B-1

Sequence 1, Application US/08477484B

Patent No. 5756699

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

INVENTOR: Stankovic, Gary M.

ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McAndrews, Janet M.

REGISTRATION NUMBER: 32,918

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

REFERENCE/DOCKET NUMBER: 110220507/200-70-P3-C2A

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-484B-1

Query Match

Best Local Similarity 39.1%; Prod. No. 3.7e-37;

Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

DB

9 THOTGKXEPFPTLLRDVSSGS-FSNEIPL-ROSTPVSDAQFVAVLWNGGXDX 66

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US-08-218-303-16
/ Sequence 16, Application US/08218303
/ Patent No. 5547867
/ GENERAL INFORMATION:
/ APPLICANT: KARL, Edmund A.
/ INVENTOR: KARL, Edmund A.; ROBERT C.
/ APPLICANT: Filtron 3.
/ TITLE OF INVENTION: FERMENTATION PROCESS
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cushman, Darby & Cushman
/ STREET: 1615 I Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ TELEPHONE: 202-683-5601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/218.303
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR ART REFERENCES:
/ PUBLICATION NUMBER: US 07/841,533
/ FILING DATE: 26-FEB-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kobulis, Paul N.
/ REGISTRATION NUMBER: 16,773
/ REFERENCE/DOCKET NUMBER: PMK3893/94908/NEW
/ TELEPHONE: 202-861-3000
/ TELEFAX: 202-822-0944
/ INVENTOR FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 267 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-218-303-16
Query Match 30.7%; Score 376; DB 1; Length 267;
Blast Local Similarity 39.1%; Pred. No 3.7e-37;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8
OY 9 TQCTGXXYYRITLTADYVSGS-FSNELPL-ROSTPYVDAQRFVWELTQXQX 66
DB 13 TAAATVQSYNMIAPVAGRLTGAQVDRHRIPLVIRVGLPLN--ORFLVLSNHELSV 70
OY 67 TAAIDVNXVYVAQADGOSYFLR-DAFGCAR--TILFTGTEDSSGSLPKGYSXLDLRY 123
DB 71 TLAIDVNAKVAIGIRKSNRNIETFRPNQDEBALITHEF-DVQKRYTAFAGNDITLQL 129
OY 124 AGH-ROPIPLGIXLQIDSYXL--RXPQSGTRKQASLILLOMTSEASRNFPLMKR 179
DB 130 AGNLEFNERIEGPNLEBAISLVLYSTGTOPLTAASFFICLOMISEARFQVLEBKR 189
OY 180 QXINSKSGFLPEXVYALTELTSTMGQOSTYVSHSTGVENPEXALIXKXNFVTLNXXVYI 239
DB 190 TRIRNRSAAPDSYVITLNSNMSKSLTALOESQGAASAFIOLGRNKSFGSYVDSILI 249
OY 240 ASALNTEVCGESRS 255
DB 250 FLLNMTVRCAPPS 255
RESULT 10
US-08-425-336-1
/ Patent No. 561083
/ Sequence 1, Application US/08425336

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GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
INVENTOR: Beckwith, Gary
INVENTOR: Beckwith, Gary
TITLE OF INVENTION: Compriking Ribosome-Inactivating
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Born
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: US
CONTACT NUMBER: 312/606-6402
ZIP: 60606-6402
COMPITER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1993
CLASSIFICATION: D23
PRIORITY INFORMATION:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ANTOKEY/AGENT INFORMATION:
NAME/KEY/AGENT INFORMATION:
P-346,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-1
30.7%; Score 376; DB 1; Length 267;
Best Local Similarity 33.1%; Pred. No. 376-37; Indels 12; Gaps 8
Matches 100; Conservative 43; Mismatches 101;
9 THAGTGGCTGATTTTADYVSSG--FENITPL--RGSITPDAQRFVYVETLMQGXSK 66
13 THAGVQSYNINIAVRKRLTGLDADVHEIPIYLRNVCPLPTN--CRILVETSHMELSV 70
67 TTAIVDNNVYVAAVQAGQSYFIR-DAPRGAE--TALTYGTITDRSSSLPTKGSYXDLERY 123
71 TLTLAVTNNAVVGVRGNSAPFPHDQEDABALHTLF-DVQNYTFARGSNDRLDQL 129
124 AGH-RDQIPGLTQIQSYAL--KPGGSTRKQKRSIIILIMTEEARAPNDILMKXR 179
130 AGHLEHLEHNGLEHLEHLSLVVYSGTGCPPLARSPITICQISEEARFQYICEMR 189
180 GXINSGASFLPXYXMLEETSGWGQGVQVAGSTGVGFNNPRLAIXXGNVVLANKRVI 239
190 TRIRNRRSADPSPVETLTLENMGRSLTAIDENQGAFASTPOLDRNGSGFVYDVSLII 249
240 ASATLKLFGVGRPSS 255
250 PTLAMVTRCAPPSS 265

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Thu Dec 11 16:09:58 2003

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Page 4

APPLICANT: Cartoll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Materials Comprising and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 200 First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SERIALS: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 19920619
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 57856and, Grete E.
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-901-707-1

Query Match 30.7%; Score 376; DB 1; Length 267;
Best Local Similarity 39.1%; Pred. No. 3.7e-37;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;
QY 9 THQTCGEYRFTLLADYSSGS-FENRIPPL-RGSTRIVSDAQRVLVETLNGQXSK 66
DB 13 TDAVQSYTNFIRAVGRLTADVHHEIPLNKGVLPI--GRFLVLSNHAELSY 70
QY 67 TLAIDVTKYVAVQAGDSYFR-DAPRGAE--TLFTGTDRSSLPFGSYLMEKY 123
DB 71 TLAIDVTKYVAVQAGDSYFR-DAPRGAE--TLFTGTDRSSLPFGSYLMEKY 123
QY 124 AGH-KQQLPGLXOLQSYXKL--RFGGSTRKQARSILILQWISSEARFNILMEKY 179
DB 130 AGH-KQQLPGLXOLQSYXKL--RFGGSTRKQARSILILQWISSEARFNILMEKY 189
QY 180 QXINSKSPLEPXVLELETSMQOSTVOVSTGCVFNNPRLAIXGAFVTLNVRVY 239
DB 190 TRIRNRSAPDSVITLSENMWRSLTAIOENQGFASPIQLOQRNGSFSVIVSILI 249
QY 240 ASLAIMLVQGERPS 255
DB 250 PRLAMVTRCAPEPS 265

RESULT 8
US-07-988-430-1
Sequence 1, Application US/07988430
Patent No. 5416202
GENERAL INFORMATION:
APPLICANT: Bernard, Susan L.

APPLICANT: Beller, Marc D.
APPLICANT: Marshall, Stephen F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Materials Comprising and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 200 First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SERIALS: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Grete E.
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-988-430-1

Query Match 30.7%; Score 376; DB 1; Length 267;
Best Local Similarity 39.1%; Pred. No. 3.7e-37;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;
QY 9 THQTCGEYRFTLLADYSSGS-FENRIPPL-RGSTRIVSDAQRVLVETLNGQXSK 66
DB 13 TDAVQSYTNFIRAVGRLTADVHHEIPLNKGVLPI--GRFLVLSNHAELSY 70
QY 67 TLAIDVTKYVAVQAGDSYFR-DAPRGAE--TLFTGTDRSSLPFGSYLMEKY 123
DB 71 TLAIDVTKYVAVQAGDSYFR-DAPRGAE--TLFTGTDRSSLPFGSYLMEKY 123
QY 124 AGH-KQQLPGLXOLQSYXKL--RFGGSTRKQARSILILQWISSEARFNILMEKY 179
DB 130 AGH-KQQLPGLXOLQSYXKL--RFGGSTRKQARSILILQWISSEARFNILMEKY 189
QY 180 QXINSKSPLEPXVLELETSMQOSTVOVSTGCVFNNPRLAIXGAFVTLNVRVY 239
DB 190 TRIRNRSAPDSVITLSENMWRSLTAIOENQGFASPIQLOQRNGSFSVIVSILI 249
QY 240 ASLAIMLVQGERPS 255
DB 250 PRLAMVTRCAPEPS 265

RESULT 9

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Page 2

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RESULT 2
US-08-776-059-31
Query Match
Best Local Similarity 91.3%; Pred. No. 4.3e-131;
Matches 212; Conservative 1; Mismatches 19; Indels 2; Gaps 1;
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: BAK, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1998-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1995-06-25
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 31
LENGTH: 253
ORGANISM: Viscum album

US-08-776-059-31
Query Match
Best Local Similarity 94.4%; Score 115; DB 3; Length 253;
Matches 212; Conservative 1; Mismatches 19; Indels 2; Gaps 1;
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: BAK, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1998-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1995-06-25
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 31
LENGTH: 253
ORGANISM: Viscum album

US-08-776-059-39
Query Match
Best Local Similarity 91.3%; Pred. No. 4.3e-131;
Matches 212; Conservative 1; Mismatches 19; Indels 2; Gaps 1;
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: BAK, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1998-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1995-06-25
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 39
LENGTH: 235
ORGANISM: Viscum album
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US-08-776-059-39
Query Match
Best Local Similarity 97.7%; Score 1073; DB 3; Length 235;
Matches 217; Conservative 0; Mismatches 18; Indels 2; Gaps 1;
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: BAK, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1998-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1995-06-25
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 39
LENGTH: 235
ORGANISM: Viscum album

US-09-538-873-3
Query Match
Best Local Similarity 41.9%; Pred. No. 1.9e-47;
Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;
GENERAL INFORMATION:
APPLICANT: VITEVA, EILEEN S.
APPLICANT: SHETLE, VICTOR F.
APPLICANT: SKALISHAN, JOAN K.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
FILE REFERENCE: US2003-03-90
CURRENT FILING DATE: 2000-03-30
EARLIER FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 3
LENGTH: 251
TYPE: PRT
ORGANISM: Abrys precatorius

US-09-538-873-3
Query Match
Best Local Similarity 37.7%; Score 461; DB 4; Length 251;
Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;
GENERAL INFORMATION:
APPLICANT: VITEVA, EILEEN S.
APPLICANT: SHETLE, VICTOR F.
APPLICANT: SKALISHAN, JOAN K.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
FILE REFERENCE: US2003-03-90
CURRENT FILING DATE: 2000-03-30
EARLIER FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 3
LENGTH: 251
TYPE: PRT
ORGANISM: Abrys precatorius
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us-09-601-67c-41.rapb

Db 63 LAEIAIDTGVYVGVNRSYFPDAPDAVEGLFRNTIKR--LHFGSYSLSEGR 120
Qy 125 GHRDQIPGIXOP--IQSYALRXPGSTKQASRILILIQISEAPR---NPIWR 177
Db 121 AYRETDGIEPRLGIRKLDENALIDNYKPTBIASSILVLIQWISAPRPTIENOIRN 180
Qy 178 XROXINSKSPFDXYMLEETSGQOSTQVQS-TGVFNNPKRLAIKXGFTILANR 236
Db 181 FQQRIR-----PANNISLEKNGDLSQRTSANGHSEAVLELRANRKYVTRND 234
Qy 237 XVLASLAIWLEVC 249
Db 235 QVXKRIALIKFVC 247

RESULT 12

US-10-127-890-4
Sequence 4, Application US/10127890
Publication No. US20030165196A1

GENERAL INFORMATION:
Applicant: Better, Marc D.
Studdink, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: McAndrews, Held & Malloy, Ltd.
REFERENCE/DOCKET NUMBER: 12, 918
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELE: 650 388-1248
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-127-890-4

Query Match

23.0%; Score 281; DB 12; Length 263;

Best Local Similarity 33.9%; Pred. No. 4.5e-26;
Matches 78; Conservative 44; Mismatches 88; Indels 20; Gaps 9;
Qy 13 TGKRPFTILADYVSGSPN--EIPILKOSTIPNSDAQSPULVETLNGQNDKYTA 69
Db 10 TACTIKRL--EDPKALPFSKNTYDIPLSST--ISDRFTILDLTSYAVETISVA 63
Qy 70 IDVTKXVAVAKQDOSYFLDAPGAEHTLPQTGTPRDSSEPFKSYXDLRVAQH--R 127
Db 64 IDVTVVAVAYTRDVSYFPFSSPEAVNLPKSTR--KITLPTGNTENLOT-AAKIR 120
Qy 128 DOIPIGIXOILQSYALRXPGSTKQASRILILIQISEAPRPNILMRXQKINSXS 187
Db 121 ENIDGLPALSALTTLFYNQASAPSA--LVLITQTEAKARKIRHVAQV--ATN 176
Qy 188 FLEDKYMLEETSGQOSTQV--QGSTGYPNPKRLAIKXGFTILANR 235
Db 177 FKNALISLENGSALSNGTFLAQNGQGFNNVLDLPTGRRGVTVN 226

RESULT 13

US-10-127-890-102
Sequence 102, Application US/10127890
Publication No. US20030165196A1

GENERAL INFORMATION:
Applicant: Better, Marc D.
Studdink, Gary M.
Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: McAndrews, Held & Malloy, Ltd.
REFERENCE/DOCKET NUMBER: 12, 918
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELE: 650 388-1248
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TOPOLOGY: linear

Query Match

23.0%; Score 281; DB 12; Length 263;

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us-09-601-667c-41.rapb

Page 5

	Matches	Conservative	50;	Mismatches	94;	Indels	14;	Gaps	9
QY	13	TCXKFFETILLRQYVSSGSNSNEIPILRQSTIPVSDQRFVYLVTINQGXSTALDV	72						
Db	10	TSSSGVFSINSLRKAERKLDLPRL-SLDSGS--GRALHILTNVADDTISVALDV	60						
QY	73	TNNYNYNQAGQGHTEKDA-PRQSEHYLPFQSTRQBSRLFPYGGYKDLERAYH-RDGI	130						
Db	7	INLYMISERADSTSYFBSMLATREAYVPRKDR-KYLPYRSGYRQVTRQKXENR	125						
QY	131	PLGIQQLQISQVALLRPGSGTSPKQASLLILQKIEGAPRNSNIMBRKXINSGKSPF	190						
Db	126	PLGLPALDASLITLLFYNNAS--AASALMTLLQSTSEAKRKIEQDQIGARDYK--TFIP	161						
QY	191	KXMYLEETSSQGSQSTQV--HSTQGVNPNKRLATIXKNEFVLLNRYK--VTLASLALN	246						
Db	162	SLATISLSEMSKSLSQQLQINSTRNGQSPSPVYLILNQANQVATITNADGAVSTSNALL	241						

RESULT 10
 US-10-280-6795-4
 Title: Large Scale Biology Corporation
 Pub. No. US20030050193A
 GENERAL INFORMATION
 TITLE OF INVENTION: Nonreplicating RNA Virus Transformation Vectors
 FILE REFERENCE: USBC-0109-US03
 CURRENT APPLICATION NUMBER: US/10/280,679B

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1 PRIOR APPLICATION NUMBER: 2000-04-25/57, 941
2 PRIOR FILING DATE: 2000-04-24
3 PRIOR APPLICATION NUMBER: 08/484, 341
4 PRIOR FILING DATE: 1995-06-07
5 PRIOR APPLICATION NUMBER: 07/923, 292
6 PRIOR FILING DATE: 1995-07-11
7 PRIOR APPLICATION NUMBER: 07/100, 244
8 PRIOR FILING DATE: 1990-10-22
9 PRIOR APPLICATION NUMBER: 07/641, 617
10 PRIOR FILING DATE: 1991-01-16
11 PRIOR APPLICATION NUMBER: 07/737, 899
12 PRIOR FILING DATE: 1991-07-26
13 PRIOR APPLICATION NUMBER: 07/106, 861
14 PRIOR FILING DATE: 1991-08-06
15 PRIOR APPLICATION NUMBER: 07/310, 881
16 PRIOR FILING DATE: 1989-02-17
17 PRIOR APPLICATION NUMBER: 07/160, 766
18 PRIOR FILING DATE: 1988-02-26
19 PRIOR APPLICATION NUMBER: 07/160, 771
20 PRIOR FILING DATE: 1988-02-26
21 Remaining Prior Application data removed - See File Wrapper or PALM
22 NUMBER OF SEQ ID NOS: 11
23 SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 4
;
; LENGTH: 289
;
; TYPE: PRT
;
; ORGANISM: Chinese cucumber protein alpha-trichosanthin
US-10-280-679B-4

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Query Match	24.0%	Score 294	DB 12	Length 289
Best Local Similarity	34.2%	Pred. No. 1.3e-27		
Matches 83; Conservative	49;	Mismatches 95;	Indels 14;	Gaps 9;

QY 13 TGKEYFRFTLLRDYVSSGSESNRPLRQSTIPVSDAGPVLVELTNGXDSXTAIDV 72
|::: : :||| : : : : : : : : : : : :
Db 33 TSSSGVFISNLKALPNERNKYDLPILR--SLPGS--QRALLHLTNVADRIISAIVD 89

D5 QY 73 INKYYVAYQADQSIFLRDA-PRGAEETHLPTGTTRDSSLPKSGXXDLERYAGH-RDQI 130
||:::||| ||| : ::||| :||| :||| :||| :
90 TIVYINGIRAEQDTSYFFENESATPAKTYFKDMR-KTTLPIGSNVERLOTPAAGCIRENT 148

QY 131 PLGIKOLIGVVALRKEGGSTRKOARSIILIIOMISEADEFNPIIMRXOKINSXGFLP 190
||| : : : ||| : : : ||| : : : ||| : : : |||
Db 149 PLGIAPALSAITTLPIYYNANS--AAASAMVLIOSTSEAAARKYFIFOOIGKRDKR--TFLP 204

Dy 191 DYVMELEIETSGQDSIQVC--HSTGVFNPKRLAIIXNGFVLTXNVR--VIASLATML 266
::| | ::| | :| | ::| |
Db 205 SLAISLSENSALSKOIIQIASTNGQEFLVVLINAQQRVMITTNVDAGVTSNIALL 264

RESULT 11
US-10-127-890-11
; Sequence 11, Application US/10127890
; Publication No. US2003016596A1
GENERAL INFORMATION
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.

Stunika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:

ADDRESS: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA

```
;
;      ZIP: 60661
;
;      COMPUTER READABLE FORM:
;
;      MEDIUM TYPE: Floppy disk
;
;      COMPUTER: IBM PC compatible
;
;      OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Patentin Release #1.0,
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
;

```

? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/646,360
 ? FILING DATE: 13-MAY-1996
 ? APPLICATION NUMBER: PCT/US94/0534
 ? FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 INFORMATION NUMBER: 22 010

REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
CITY: CHICAGO, ILL.

TELEBA: 650 388-1248
 INFORMATION FOR SEQ ID NO: 111:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 251 amino acids
 TYPE: amino acid
 MODIFICATIONS: 37

US-10-127-890-111

Query: mouse	23.5%	Score: 287.5	Identities: 100%
Query: human	23.5%	Score: 287.5	Identities: 100%
Best Local Similarity	34.0%	Pctid: No. 1,66-26	
Matches	86	Conservative	33
		Mismatches	113
		Indels	21
		Gaps	

Db 5 VSFSTGATATYVNFLENEKLVKLEPENGSHGIPILIRKKADDPGKA--FVLVALSNDNGQ 62

Dy 65 SATTAIDVTNXXYYVAVIQAGDQSYPRLDAERGAETHLFTGTRDRSSLEPFXXGYXDIERYA 12

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QY 240 ASLAIATLFCVCGRRSS 255
DB 285 FILLAWYRCAPPPSS 300

RESULT 7
US-09-792-793A-39
Sequence 39, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
INVENTOR: McDonald, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patent In Ver. 2.0
LENGTH: 247
SEQ ID NO 39
ORGANISM: Trichosanthea killowii
US-09-792-793A-39

Query Match 24.6%; Score 301; DB 10; Length 247;
Best Local Similarity 34.6%; Pred. No. 1.4e-28;
Matches 83; Conservative 50; Mismatches 93; Indels 14; Gaps 9;

QY 13 TGKEYFRFTLLNDYVSSGSGSENEIFLLROSTIPVSDAQRPVVLVETLWQKSDXTAIDV 72
DB 10 TSSSYGVFISNLEKALPNERKLYDIFLLR-SLFGS--QRYALHLTNVADETISVALDV 66
QY 73 TNYVVAQAGDOSTFLRDA-FRGAETHLFTGTRRSSLPEFGSYDLERYAGH-RDOI 130
DB 67 TNYVINGRAGDOSTYFENFASATEAKYKQAMR-KVTLFGSANTERLDYQAKIKRENI 125
QY 131 FLGIKQIGSVAKRFGSGTRKQARSITLLOKISPAARENFILMRKXINSQSFIP 190
DB 126 FLGIPLDLSAITTLTFYNNNS--ASALMWLIQSTSPAAKYKIEQIGKRVDK--TFLP 181
QY 191 DXYMLEETSMGQOSTQVQ--HSTDVENPEKRLAIXGNFTVLXVXK--VIASLAIWL 246
DB 182 SLATISLNSWMSALSKQIOIASITNQGSPVVLINQONRVITTVDAQVTSNIALLL 241

RESULT 8
US-10-375-209A-39
Sequence 39, Application US/10375209A
Patent No. US20030215421A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
INVENTOR: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/10/375,209A
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patent In Ver. 2.0
LENGTH: 247
SEQ ID NO 39
TYPE: PRT
ORGANISM: Trichosanthea killowii
US-10-375-209A-39

Query Match 24.6%; Score 301; DB 12; Length 247;
Best Local Similarity 34.6%; Pred. No. 1.4e-28;
Matches 83; Conservative 50; Mismatches 93; Indels 14; Gaps 9;

QY 13 TGKEYFRFTLLNDYVSSGSGSENEIFLLROSTIPVSDAQRPVVLVETLWQKSDXTAIDV 72
DB 10 TSSSYGVFISNLEKALPNERKLYDIFLLR-SLFGS--QRYALHLTNVADETISVALDV 66

QY 73 TNYVVAQAGDOSTFLRDA-FRGAETHLFTGTRRSSLPEFGSYDLERYAGH-RDOI 130
DB 67 TNYVINGRAGDOSTYFENFASATEAKYKQAMR-KVTLFGSANTERLDYQAKIKRENI 125
QY 131 FLGIKQIGSVAKRFGSGTRKQARSITLLOKISPAARENFILMRKXINSQSFIP 190
DB 126 FLGIPLDLSAITTLTFYNNNS--ASALMWLIQSTSPAAKYKIEQIGKRVDK--TFLP 181
QY 191 DXYMLEETSMGQOSTQVQ--HSTDVENPEKRLAIXGNFTVLXVXK--VIASLAIWL 246
DB 182 SLATISLNSWMSALSKQIOIASITNQGSPVVLINQONRVITTVDAQVTSNIALLL 241

RESULT 9
US-10-127-890-6
Sequence 6, Application US/10127890
Patent No. US2003016196A1
GENERAL INFORMATION:
APPLICANT: Carroll, Stephen P.
INVENTOR: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/10/127,890
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-APR-2002
CLASSIFICATION: A61K39/00 (Immunology)
PRIORITY DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 12-NOV-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: McMichael, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NOS:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPES: amino acid
TOPOLOGY: linear

Query Match 24.4%; Score 299; DB 12; Length 247;
Best Local Similarity 34.2%; Pred. No. 2.5e-28;
US-10-127-890-6

Thu Dec 11 16:09:59 2003

us-09-601-667c-41.rapb

Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;
QY 9 THQTTGKXEFREFTLLRDYVSSGS-FSNEIPLD-RQSTIPVSDAQRFVVELTNOGXSK 66
DB 13 TAGATVQSYTFRIVRGRGLTGGADVHEIPVLPNRVGLPIN--QRFILVELSNHSELV 70
QY 67 TAAIDVTNXYVAVQAGDSYFLR-DAPRGAE--THLTGTRDRSSLPFGSYKDLERY 123
DB 71 TAAIDVTNXYVAVQAGDSYFLR-DAPRGAE--THLTGTRDRSSLPFGSYKDLERY 123
QY 124 AGH-RDQIPLAGIXOLQSVVAL--RXPGSTXQASIIILIQMISEAARFPIIMEXR 179
DB 130 ANGLRNIEMELGNGLEBIAISALVYVSTGCTOLPTLARSFIIICIMISEAARFPIIMEXR 189
QY 180 QXINSXSELPDXVMLETSWQGSSTOVQHSIDGVFNPNXKALIXXGPFVTLXNVRXVI 239
DB 190 TIRYRNRASAPDSVITLNSWGRSLTAIQESNQAFASPIQLQRNRSKRSYVDVSLI 249
QY 240 ASALMLPVCGERSS 255
DB 250 PTLMLNXYKCAPPS 265

RESULT 5
US-10-127-890-1
Sequence 1, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Gardinka, Gary N.
James, James
TITLE OF INVENTION: Proteins
COMBINING: Proteins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: COMPASS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-May-1996
PUBLICATION NUMBER: US94/05348
FILING DATE: 12-May-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-May-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-Dec-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-Jun-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-Nov-1991
ATTORNEY/AGENT INFORMATION:
NAME: McAndrews, Held & Malloy, Ltd.
ADDRESS: 500 West Madison Street, 34th floor
CITY: Chicago, IL 60661
TELEPHONE: 312/707-9155
TELEFAX: 312/707-8889
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 200-70, P4
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-127-890-1
Query Match
30.7% Score 376; DB 12; Length 267;
Best Local Similarity 39.1%; Pred. No. 8, 8e-36;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

QY 9 THQTTGKXEFREFTLLRDYVSSGS-FSNEIPLD-RQSTIPVSDAQRFVVELTNOGXSK 66
DB 13 TAGATVQSYTFRIVRGRGLTGGADVHEIPVLPNRVGLPIN--QRFILVELSNHSELV 70
QY 67 TAAIDVTNXYVAVQAGDSYFLR-DAPRGAE--THLTGTRDRSSLPFGSYKDLERY 123
DB 71 TAAIDVTNXYVAVQAGDSYFLR-DAPRGAE--THLTGTRDRSSLPFGSYKDLERY 123
QY 124 AGH-RDQIPLAGIXOLQSVVAL--RXPGSTXQASIIILIQMISEAARFPIIMEXR 179
DB 130 ANGLRNIEMELGNGLEBIAISALVYVSTGCTOLPTLARSFIIICIMISEAARFPIIMEXR 189
QY 180 QXINSXSELPDXVMLETSWQGSSTOVQHSIDGVFNPNXKALIXXGPFVTLXNVRXVI 239
DB 190 TIRYRNRASAPDSVITLNSWGRSLTAIQESNQAFASPIQLQRNRSKRSYVDVSLI 249
QY 240 ASALMLPVCGERSS 255
DB 250 PTLMLNXYKCAPPS 265

RESULT 6
US-10-083-336A-1
Sequence 1, Application US/10083336A
Publication No. US2003018165A1
GENERAL INFORMATION:
APPLICANT: Oison, Mark A
APPLICANT: Willard, Charles B
APPLICANT: Byrme, Michael P
APPLICANT: Hammecker, Robert W
TITLE OF INVENTION: Proteins and Methods of Making and Using Thereof
CURRENT APPLICATION NUMBER: US/10/083,336A
FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentia Ver. 2.1
SEQ ID NO: 1
LENGTH: 576
TYPE: PRT
ORGANISM: Rictinus communis
Query Match
30.7% Score 376; DB 12; Length 576;
Best Local Similarity 39.1%; Pred. No. 2, 5e-37;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;
QY 9 THQTTGKXEFREFTLLRDYVSSGS-FSNEIPLD-RQSTIPVSDAQRFVVELTNOGXSK 66
DB 48 TAGATVQSYTFRIVRGRGLTGGADVHEIPVLPNRVGLPIN--QRFILVELSNHSELV 105
QY 67 TAAIDVTNXYVAVQAGDSYFLR-DAPRGAE--THLTGTRDRSSLPFGSYKDLERY 123
DB 106 TAAIDVTNXYVAVQAGDSYFLR-DAPRGAE--THLTGTRDRSSLPFGSYKDLERY 123
QY 124 AGH-RDQIPLAGIXOLQSVVAL--RXPGSTXQASIIILIQMISEAARFPIIMEXR 179
DB 165 ANGLRNIEMELGNGLEBIAISALVYVSTGCTOLPTLARSFIIICIMISEAARFPIIMEXR 224
QY 180 QXINSXSELPDXVMLETSWQGSSTOVQHSIDGVFNPNXKALIXXGPFVTLXNVRXVI 239
DB 225 TIRYRNRASAPDSVITLNSWGRSLTAIQESNQAFASPIQLQRNRSKRSYVDVSLI 264

QY 121 ERYAHRDQIPGLIGKQILOSVALRXPGRSTKXQARSTILLIOMISEARPNILMRXQ 180
DB 119 ERYAHRDQIPGLIGKQILOSVALRXPGRSTKXQARSTILLIOMISEARPNILMRXQ 178
QY 181 XINSKSPFLPDYVYMLRSTWQOQSTVOGSHSTGVFNNPRLAIXGNFTLVANEXYIA 240
DB 179 YINSASFLPDYVYMLRSTWQOQSTVOGSHSTGVFNNPRLAIXGNFTLVANEXYIA 238
QY 241 SLAIVLFCGERP 254
DB 239 SLAIVLFCGERP 252

RESULT 2
US-09-347-064-2
Sequence 2, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Beck, Jürgen
APPLICANT: Schmauder, Arno
APPLICANT: Schmauder, Arno
TITLE OF INVENTION: Ribosome-inactivating Proteins Based on
TITLE OF INVENTION: Ribosome-inactivating Proteins of the mistletoe Viscum
TITLE OF INVENTION: album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 252
LENGTH: 252
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-2

Query Match 94.1%; Score 1151; DB 9; Length 252;
Best Local Similarity 91.3%; Pred. No. 2,2e-133;
Matches 231; Conservative 1; Mismatches 19; Indels 2; Gaps 1;
QY 1 YERIALRHTQTCXKRFRTLLADYVSSGFSNFIPLRQSTIPVSDAQRVLTWQXDA 60
DB 2 YERIALRHTQTCXKRFRTLLADYVSSGFSNFIPLRQSTIPVSDAQRVLTWQXDA 61
QY 61 QGKDSKTAIDVYVYVAYVADDSYFLRDPAGATHTLFTGTTRSSSLPFGSYXDL 120
DB 62 QGKDSKTAIDVYVYVAYVADDSYFLRDPAGATHTLFTGTTRSSSLPFGSYXDL 119
QY 121 ERYAHRDQIPGLIGKQILOSVALRXPGRSTKXQARSTILLIOMISEARPNILMRXQ 180
DB 119 ERYAHRDQIPGLIGKQILOSVALRXPGRSTKXQARSTILLIOMISEARPNILMRXQ 178
QY 181 XINSKSPFLPDYVYMLRSTWQOQSTVOGSHSTGVFNNPRLAIXGNFTLVANEXYIA 240
DB 179 YINSASFLPDYVYMLRSTWQOQSTVOGSHSTGVFNNPRLAIXGNFTLVANEXYIA 238
QY 241 SLAIVLFCGERP 254
DB 239 SLAIVLFCGERP 252

RESULT 3
US-10-282-935-3
Sequence 3, Application US/10282935
Publication No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETTE, VICTOR F.
APPLICANT: SMALISHAW, JOAN
APPLICANT: BALUNA, ROXANA G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: USID:88405
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-03-30
EARLIER APPLICATION NUMBER: 2000-03-30
PRIOR APPLICATION NUMBER: 2000-03-30
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 237
LENGTH: 251
TYPE: PRT
ORGANISM: Abrus precatorius
US-10-282-935-3

Query Match 37.7%; Score 461; DB 12; Length 251;
Best Local Similarity 41.9%; Pred. No. 2.7e-48;
Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;
QY 9 THQTCXKRFRTLLADYVSSGFSNFIPLRQSTIPVSDAQRVLTWQXDA 68
DB 9 THQTCXKRFRTLLADYVSSGFSNFIPLRQSTIPVSDAQRVLTWQXDA 67
QY 69 AIDVYVYVAYVADDSYFLRDPAGATHTLFTGTTRSSSLPFGSYXDLERYACH R 127
DB 67 GIDVYVYVAYVADDSYFLRDPAGATHTLFTGTTRSSSLPFGSYXDLERYACH R 124
QY 128 QGKDSKTAIDVYVYVAYVADDSYFLRDPAGATHTLFTGTTRSSSLPFGSYXDL 187
DB 125 QGKDSKTAIDVYVYVAYVADDSYFLRDPAGATHTLFTGTTRSSSLPFGSYXDL 184
QY 188 QGKDSKTAIDVYVYVAYVADDSYFLRDPAGATHTLFTGTTRSSSLPFGSYXDL 237
DB 185 QGKDSKTAIDVYVYVAYVADDSYFLRDPAGATHTLFTGTTRSSSLPFGSYXDL 234
QY 238 -VISAIVLFCGERP 249
DB 235 -VISAIVLFCGERP 247

RESULT 4
US-10-282-935-1
Sequence 1, Application US/10282935
Publication No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETTE, VICTOR F.
APPLICANT: SMALISHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: USID:88405
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 2000-03-30
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 237
LENGTH: 251
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-10-282-935-1

Query Match 30.7%; Score 376; DB 12; Length 267;
Best Local Similarity 39.1%; Pred. No. 8.8e-38;

Thu Dec 11 16:09:58 2003

us-09-601-667c-41.rag

Page 12

DZ	N-PSDB; AAIV51343.
XX	Nucleic acid encoding fusion protein containing mistletoe lectin A
PT	Protein chain - useful for treatment of proliferative and autoimmune
XX	diseases, allergies and tumours
XX	Disclousre; Fig 11a; 115pp; German.
XX	This sequence encodes a variant mistletoe lectin A-chain, rMLA. This
CC	sequence can be used in the construction of a fusion protein which
CC	comprises an effector module that is cytotoxic intracellularly, a
CC	processing module covalently bonded to the effector module and
CC	containing a protease recognition sequence, and a binding module
CC	covalently bonded to the processing module, able to bind specifically to
CC	proteins involved in the transmembrane internalisation of the fusion
CC	protein. Such a fusion protein can be used for treating disorders
CC	involving proliferation and/or elevated activation of cells, especially
CC	autoimmune disease, allergy and tumours. The proteins can be administered
CC	e.g. by injection or topically but especially by intravenous injection,
CC	at 1 ng to 500 nm g/kg/day, or for ex vivo use at 1 pg to 500 ng/ml.
CC	Fusion proteins can develop toxic activity in a wide range of target
CC	cells. The processing module prevents extracellular dissociation, and
CC	fusion proteins based on mistletoe lectin A-chain are far more active
CC	than those based on ricin and do have the associated problems of
CC	non-specific toxicity. The protein may be expressed in a non-mammalian
CC	form such as in the blood where the mistletoe lectin B-chain is used,
CC	it actively assists in translocation of the ML A-chain from the
CC	endoplasmic reticulum to the cytoplasm.
XX	
XQ	Sequence 252 AA;
Query Match	94.4%; Score 1155; DB 19; Length 252;
Best Local Similarity	91.3%; Pred. No. 6,6e-132;
Matches 232; Conservative 1; Mismatches 19; Indels 2; Gaps 1	
OY	1 YEELATLRTMTCCKXPRFTLLIDPYSSGSFNEPLMGSTPPSGDPGFWVLTNN 60
Db	1 YERILRLMTQTTEETPEFTILLIDVYSSGSFNEPLMGSTTPVDAGPFLVLTNN 60
OY	61 QGDKSDTALDVTKNYAVAYADQDSYELEDAFGALHTLFGTGRDSELPFYGSXYDL 120
Db	61 QGGDSYTLADVTLVYAAYADQDSYELEDAFGRAHTLFTGIT--RSSDFPNFSYEDL 118
OY	121 ERYAHARDPIGLGIKLOLSYALKARPGSTTXNALSILLIIONTSAPNFETIPRQ 180
Db	119 ERFAHARDPIGLAIOLNSYALKARPGSTTRPSGSTSILLIIIONTSAPNFETIPRMO 178
OY	181 XINSQSLEPDYMYALELISNGSQSVQVSITDGVFPNNXSLALXAGNFTLVANXVIA 240
Db	179 YINSQSFLPDYVMLEISNGSQSVQVSITDGVFNPFILALIPGNFVLTVNRDIVA 238
OY	241 SLIAMT.PVCGERS 254
Db	239 SLIAMT.VFCGRRS 252

Search completed: December 11, 2003, 14:07:49
Job time : 26.2959 secs

FT Misc-difference 224
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 FT Misc-difference 225
 FT /label= Pro, Thr
 FT Misc-difference 233
 FT /label= Thr, Ser
 FT Misc-difference 236
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 FT /label= Asn, Ser
 FT Misc-difference 290
 FT /label= Cys, Arg
 FT Misc-difference 325
 FT /label= Gly, Asn
 FT Misc-difference 366
 FT /label= Gly, Asp
 FT Misc-difference 425
 FT /label= Gly, Gln
 FT Misc-difference 435
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 FT Misc-difference 439
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 FT Misc-difference 442
 FT /label= Gly, none
 FT Misc-difference 443
 FT /label= Arg, Lys
 FT Misc-difference 466
 FT /label= Cys, Ser, Val
 FT Misc-difference 480
 FT /label= Ala, Gly
 FT Misc-difference 481
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 FT Misc-difference 483
 FT /label= Ser, Gly
 FT Misc-difference 484
 FT /label= Gly, Ser
 FT Misc-difference 493
 FT /label= Gly, Tyr
 FT Misc-difference 500
 FT /label= Asn, Ser, Thr, Lys
 FT Misc-difference 501
 FT /label= Ser, Gly
 FT Misc-difference 502
 FT /label= Leu, Pro
 FT Misc-difference 503
 FT /label= Ala, Met
 FT Misc-difference 504
 FT /label= Met, Val
 FT Misc-difference 533
 FT /label= Pro, Phe
 DE19804210-A1.
 12-NUC-1999.
 03-FEB-1998; 98DE-1004210.
 03-FEB-1998; 98DE-1004210.
 (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 Morris P, Stiefel T, Voelker W, Welters P;
 WPI; 1999-44535/38.
 Preparation of mistletoe lectins in heterologous systems.
 Particularly for use as anticancer agents and immunostimulants
 Claim 40; Page 37-38; 78PP; German.
 This invention describes a novel mistletoe lectin (I) and its fragments
 which have antitumour and immunostimulatory activity. The A-chain (MLA)
 of the mistletoe lectin binds to, and inactivates, the 28S subunit of

CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, are used as adjuvants of the
 CC (immunisation, treatment, or prophylaxis) of bacterial or viral
 CC (immunisation, treatment, or prophylaxis) of bacterial or viral
 CC mistletoe lectin and its individual chains. In many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a consensus sequence of the mistletoe lectin described in the
 CC specification.
 XX Sequence 533 AA;
 SQ
 Query Match 95.1% Score 1162.5; DB 20; Length 533;
 Query 1 YERLRLKVTHTGKXEPFRTLLPDDVSSGSFNSNIPRLQSTIPVSAQRFLVLELTN 60
 Db 1 YERLRLKVTHTGKXEPFRTLLPDDVSSGSFNSNIPRLQSTIPVSAQRFLVLELTN 60
 Qy 61 QXKXSTAAIDVTNXYVAAYQAGQSYFLRDAFRGAEHTLFTGTRDRSSLPFGSYXDL 120
 Db 61 QXKXSTAAIDVTNXYVAAYQAGQSYFLRDAFRGAEHTLFTGTRDRSSLPFGSYXDL 119
 Qy 121 ERNAGRDITFLGKILQICVYALFAPGSTRVQARSTILITOMISARRPPIIMRRQ 180
 Db 120 ERNAGRDITFLGKILQICVYALFAPGSTRVQARSTILITOMISARRPPIIMRRQ 179
 Qy 181 XINSKXSPDPXVMELETSWQSGTGVHSDGVNPNPKRLAIXXNFTVLKXVAXVIA 240
 Db 180 XINSKXSPDPXVMELETSWQSGTGVHSDGVNPNPKRLAIXXNFTVLKXVAXVIA 239
 Qy 241 SLATMLFVCGRPSRS 256
 Db 240 SLATMLFVCGRPSRS 255
 RESCUT 15
 ID AM64661 standard; Protein; 252 AA.
 AC AM64661;
 DT 23-OCT-1998 (first entry)
 DE Mistletoe rMLA variant protein.
 KW Lectin A-chain; mistletoe; rMLA; fusion protein; effector; cytotoxic;
 KW intercalin; processing module; protease recognition; targeting module;
 KW internalisation; treatment; disorder; cell proliferation; evaluation;
 KW autoimmune disease; allergy; tumour; ricin; translocation; se.
 CS Viscum album.
 FH Key Location/Qualifiers
 FT Protein 1..252
 FT /note="partial"
 FN W09829540-A2.
 PD 09-JUL-1998.
 PX 02-JUN-1998; 98NO-EP00009.
 RX 02-JUN-1997; 97EP-0100012.
 PA (BRAI-) BRAIN BIOTECHNOLOGY RES & INNOVATION NE.
 PI Eck J, Schmidt A, Zinke H;
 WPI; 1998-388122/33.

[illegible]

Dd			180 XINSAKSEFPXWMAELETSMQCSOTVOSTDGVGNPFRLATIXGPNFVLNNAVIA 239
Oy	241	SLAIPLPVGGRPS6S 256 	
Dd	240	SLAIPFGCGRPS6S 255 	
ID	AAZ2573	standard; protein; 533 AA.	
Xx	AAY25973;		
Xc	AAZ25973;		
Dt	18-OCT-1999	(first entry)	
Xk	MiscJctoe	Iactin protein consensus sequence 2.	
Kw	Riboprecipitate	antitumor; immunostimulant; A-chain; MAb; immunity; response; T-cell activation; immune response; T-cell growth; treatment; cancer; cytotoxicity; antigen; isoform. Lymphocyte-producing macrophages; uncontrolled cell growth; tumor	
Km	cancer; cytotoxicity; antigen; isoform.		
Xl	Viscum album.		
Os	Viscum album.		
Xv	Key	Location/Qualifiers	
Ff	Misc-difference 15	/label= Asp, Glu	
Ff	Misc-difference 13	/label= Gly, Gln	
Ff	Misc-difference 66	/label= Ile, Val	
Ff	Misc-difference 75	/label= Leu, Ala	
Ff	Misc-difference 107	/label= Ser, Thr	
Ff	Misc-difference 113	/label= Asn, Thr	
Ff	Misc-difference 134	/label= Pro, Thr	
Ff	Misc-difference 141	/label= Asp, Glu	
Ff	Misc-difference 145	/label= Ser, Thr	
Ff	Misc-difference 152	/label= Phe, Tyr	
Ff	Misc-difference 170	/label= Ala, Tyr	
Ff	Misc-difference 180	/label= Tyr, Asp	
Ff	Misc-difference 191	/label= Ala, Glu	
Ff	Misc-difference 219	/label= Val, Met	
Ff	Misc-difference 225	/label= Ile, Phe	
Ff	Misc-difference 233	/label= Pro, Thr	
Ff	Misc-difference 236	/label= Thr, Ser	
Ff	Misc-difference 287	/label= Asp, Ser	
Ff	Misc-difference 325	/label= Asn, Ser	
Ff	Misc-difference 364	/label= Cys, Arg	
Ff	Misc-difference 364	/label= Gly, Asn	
Ff	Misc-difference 364	/label= Gly, Asp	

FT Misc-difference 236
FT /label= Asp, Ser
FN DE19804210-A1.
XX
XX 12-AUG-1999.
PD
XX 03-FEB-1998; 98DE-1004210.
XX
XX 03-FEB-1998; 98DE-1004210.
PR
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Walters P;
XX WPI; 1999-44535/38.
DR
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 41, Page 39; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MLA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of the
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen production of
XX (tumour-associated, bacterial or viral). The method of the present invention
XX involves the production of recombinant A-chain fragments of different isoforms
XX and on a large scale at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a consensus sequence of the mistletoe lectin A chain (MLA)
XX described in the invention.
SQ Sequence 255 AA;

Query Match 95.1%; Score 1162.5; DS 20; Length 255;
Best Local Similarity 99.2%; Pred. No. 8.2e-133;
Matches 254; Conservative 1; Indels 1; Gaps 1;

QY 1 YERIRATVTOGTTGKVEYFRTILADRYSSGSPSEIPIILQSTIVSDQKRVVALIN 60
Db 1 YERIRATVTOGTTGKVEYFRTILADRYSSGSPSEIPIILQSTIVSDQKRVVALIN 60
QY 61 QGXSXTALIDVNNYVAQKQSGYFLADPARAGETHLPTGTDDSSLPKQSYXL 120
Db 61 QGXSXTALIDVNNYVAQKQSGYFLADPARAGETHLPTGTDDSSLPKQSYXL 120
QY 61 QGXSXTALIDVNNYVAQKQSGYFLADPARAGETHLPTGTDDSSLPKQSYXL 119
Db 61 QGXSXTALIDVNNYVAQKQSGYFLADPARAGETHLPTGTDDSSLPKQSYXL 119
QY 121 BRVAGRDQIPGIXQLIGSVVALKPGGSTRQKASIIILQITSEAFNFIIMEXQ 180
Db 121 BRVAGRDQIPGIXQLIGSVVALKPGGSTRQKASIIILQITSEAFNFIIMEXQ 180
QY 120 BRVAGRDQIPGIXQLIGSVVALKPGGSTRQKASIIILQITSEAFNFIIMEXQ 179
Db 120 BRVAGRDQIPGIXQLIGSVVALKPGGSTRQKASIIILQITSEAFNFIIMEXQ 179
QY 181 XINGKSLPDXMELFETSWQSGSTQVSTIDGVFNNPRLAIXGKPVTLXNVRVIA 239
Db 181 XINGKSLPDXMELFETSWQSGSTQVSTIDGVFNNPRLAIXGKPVTLXNVRVIA 239
QY 241 SLATMLFVCGRRPSSS 256
Db 241 SLATMLFVCGRRPSSS 256
QY 240 SLATMLFVCGRRPSSS 255
Db 240 SLATMLFVCGRRPSSS 255

RESIDT 12
AAV25970
AD AAV25970 standard; protein; 533 AA.
XX
XX AAV25970;
AC
XX
DT 18-OCT-1999 (first entry)
XX
DE Mistletoe lectin protein consensus sequence 1.

XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MLA; immunity;
KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform.
XX
XX Viscum album.
XX
FH Key Location/Qualifiers
FH
FH Misc-difference 15
FT /label= Asp, Glu
FT
FT Misc-difference 63
FT /label= Gly, Glu
FT
FT Misc-difference 66
FT /label= Ile, Val
FT
FT Misc-difference 75
FT /label= Leu, Ala
FT
FT Misc-difference 100
FT /label= Asp, Arg or none
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FT /label= Asp, Thr
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FT Misc-difference 117
FT /label= Pro, Thr
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FT Misc-difference 141
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FT Misc-difference 145
FT /label= Phe, Tyr
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FT /label= Thr, Ala
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FT /label= Tyr, Asp
FT
FT Misc-difference 185
FT /label= Ala, Glu
FT
FT Misc-difference 191
FT /label= Val, Met
FT
FT Misc-difference 219
FT /label= Ile, Phe
FT
FT Misc-difference 220
FT /label= Pro, Ser
FT
FT Misc-difference 225
FT /label= Pro, Thr
FT
FT Misc-difference 232
FT /label= Thr, Ser
FT
FT Misc-difference 236
FT /label= Asp, Ser
FT
FT Misc-difference 287
FT /label= Asn, Ser
FT
FT Misc-difference 290
FT /label= Cys, Arg
FT
FT Misc-difference 325
FT /label= Gly, Asn
FT
FT Misc-difference 364
FT /label= Gly, Asp
FT
FT Misc-difference 426
FT /label= Gly, Glu
FT
FT Misc-difference 435
FT /label= Val, Asp
FT
FT Misc-difference 438
FT /label= Glu, Lys
FT
FT Misc-difference 442
FT /label= Gly or none
FT
FT Misc-difference 443
FT /label= Arg, Lys
FT
FT Misc-difference 464
FT /label= Cys, Ser, Val
FT
FT Misc-difference 480
FT /label= Ala, Gly
FT
FT Misc-difference 481
FT /label= Gly, Ala

FT Misc-difference 117 /label= Pro, Thr
FT Misc-difference 134 /label= Asp, Gln
FT Misc-difference 141 /label= Ser, Thr
FT Misc-difference 145 /label= Phe, Tyr
FT Misc-difference 152 /label= Thr, Ala
FT Misc-difference 177 /label= Ala, Tyr
FT Misc-difference 180 /label= Tyr, Asp
FT Misc-difference 185 /label= Ala, Gln
FT Misc-difference 191 /label= Val, Met
FT Misc-difference 218 /label= Ile, Phe
FT Misc-difference 224 /label= Phe, Ser
FT Misc-difference 225 /label= Pro, Thr
FT Misc-difference 232 /label= Thr, Ser
FT Misc-difference 236 /label= Asp, Ser
XX DE3904210-A1.
XX
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DB-1004210.
XX
XX 03-FEB-1998; 98DB-1004210.
XX
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX
XX Morris P, Sclafel T, Voelter W, Welters P;
XX WPI: 1999-445335/38.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 5, Page 30; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MAA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosome, a cytotoxic form of (I) activate T-cell and (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a consensus sequence of the mistletoe lectin A chain (MAA)
XX described in the invention.
XX
XX Sequence 255 AA:
XX
XX Query Match 95.1%; Score 1162.5; DB 20; Length 255;
XX Best Local Similarity 99.2%; Pred. No. 8.2e-133;
XX Matches 254; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 61 QXDSXIAIDVTNNXYVAVYAGAGDSYFLADAPGAETHLFTGTRDRSLPFXGSYXD 120
DB 61 QXDSXIAIDVTNNXYVAVYAGAGDSYFLADAPGAETHLFTGTR-XSLPFXGSYXD 119
QY 121 ERYAGRDQIPLGIXOLIGSYALRXPGSTRXQARSILILIQMISAAENPTLWXEQ 180
DB 120 ERYAGRDQIPLGIXOLIGSYALRXPGSTRXQARSILILIQMISAAENPTLWXEQ 179
QY 181 XINSXGFLPDXVWLEFTSGQSTQVGHSTQVGHSTQVGHSTQVGHSTQVGHSTQVGHST 240
DB 180 XINSXGFLPDXVWLEFTSGQSTQVGHSTQVGHSTQVGHSTQVGHSTQVGHSTQVGHST 239
QY 241 SLALMLFVCGSRPSS 256
DB 240 SLALMLFVCGSRPSS 255
XX
XX RESULT 11
XX AN25977
XX AN25977 standard: protein: 255 AA.
XX
XX AN25977:
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin A chain MAA consensus protein sequence 3.
XX
XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MAA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform.
XX
XX Viscum album.
XX
XX Location/Qualifiers
XX FT Key
XX FT Misc-difference 15 /label= Asp, Gln
XX FT Misc-difference 63 /label= Gly, Gln
XX FT Misc-difference 66 /label= Ile, Val
XX FT Misc-difference 107 /label= Leu, Ala
XX FT Misc-difference 113 /label= Asp, none
XX FT Misc-difference 117 /label= Asn, Thr
XX FT Misc-difference 117 /label= Pro, Thr
XX FT Misc-difference 134 /label= Asp, Gln
XX FT Misc-difference 141 /label= Ser, Thr
XX FT Misc-difference 145 /label= Phe, Tyr
XX FT Misc-difference 152 /label= Thr, Ala
XX FT Misc-difference 177 /label= Ala, Tyr
XX FT Misc-difference 180 /label= Tyr, Asp
XX FT Misc-difference 185 /label= Ala, Gln
XX FT Misc-difference 191 /label= Val, Met
XX FT Misc-difference 218 /label= Ile, Phe
XX FT Misc-difference 224 /label= Phe, Ser
XX FT Misc-difference 225 /label= Pro, Ser
XX FT Misc-difference 232 /label= Pro, Thr
XX FT Misc-difference 236 /label= Thr, Ser

ID AM10021 standard; Protein; 564 AA.
XX
AC AM10021;
XX
KW 18-DEC-1997 (first entry)
XX
DE Prepro mistletoe lectin.
XX
KW Mistletoe; lectin; cytotoxic; A chain; B chain; dimer.
XX
OS Viscum album.
XX
PN EP751221-A1.
XX
PD 02-JAN-1997.
XX
PR 26-JUN-1995; 95EP-0109949.
XX
PR 26-JUN-1995; 95EP-0109949.
XX
PI (MADU) MADUS KOEHLN AG.
XX
PI Baur A, Eck J, Lentzen H, Zinke H;
XX
DR WPI; 1997-054678/06.
DR N-PSDB; AAT70473.
XX
FT Nucleic acid encoding pre-pro form of mistletoe lectin - for
XX therapeutic or diagnostic use
XX
ES Claim 12; Fig 4C; 30pp; German.
XX
CC Mistletoe lectin is a cytotoxic agent that has been used for tumour
CC therapy. It can be used in immunotoxic and medicaments. Nucleic
CC acid fragments can be used in diagnostic methods. Mistletoe lectin
CC (AAT70473) comprises an A chain (AAT70474) and a B chain (AAT70475).
XX
SQ Sequence 564 AA;
Query Match 95.3%; Score 1165; DB 18; Length 564;
Best Local Similarity 91.8%; Pred. No. 1.2e-132;
Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;
OY 1 YERLRATVHTQTKEXEYFRFTLLRDYVSSGSFSENEIFLLRQSTIPVSDAQRFLVLELN 60
DB 34 YERLRATVHTQTKEXEYFRFTLLRDYVSSGSFSENEIFLLRQSTIPVSDAQRFLVLELN 93
OY 61 QGDSXTALADVNNVYVAAGDSYFLRDAPRGAETHLFTGTTRDSLSLPRKQSYDL 120
DB 94 QGDSXTALADVNNVYVAAGDSYFLRDAPRGAETHLFTGTTRDSLSLPRKQSYDL 151
OY 121 ERVAGHDQIPGIGDQISVYALRPFQGSSTRQASILLIOMISAPRFPILMRKQ 180
DB 152 ERVAGHDQIPGIGDQISVYALRPFQGSSTRQASILLIOMISAPRFPILMRKQ 211
OY 181 XINGKSFLEPDYMLLETSMGQSTQVGHSTQVFNPKALIXXGNFTLXNEXVIA 240
DB 212 YINGKSFLEPDYMLLETSMGQSTQVGHSTQVFNPKALIXXGNFTLXNEXVIA 271
OY 241 SLATMLFVCGERSSS 256
DB 272 SLATMLFVCGERSSS 287

DE Mistletoe lectin prepro-protein.
XX
KW Mistletoe; lectin; M; transgenic plant; glycosylation;
XX dimer; immunotoxin; large-scale production; diagnosis; therapeutic;
XX cancer.
XX
OS Viscum album.
XX
PN EP84388-A1.
XX
PD 16-DEC-1998.
XX
PR 26-JUN-1995; 98EP-0105660.
XX
PR 26-JUN-1995; 95EP-0109949.
XX
PR 26-JUN-1995; 98EP-0105660.
XX
PI (MADU) MADUS KOEHLN AG.
XX
PI Baur A, Eck J, Lentzen H, Zinke H;
XX
DR WPI; 1999-026582/03.
DR N-PSDB; AAV74182.
XX
FT New transgenic plant expressing mistletoe lectin - useful for
XX producing recombinant lectin in e.g. cancer diagnosis and therapy
XX
ES Claim 1a; Fig 4c; 30pp; German.
XX
CC This invention describes a novel transgenic plant transformed with a
CC vector capable of encoding a mistletoe (Viscum album) lectin
CC also describes a polypeptide produced by a plant where the polypeptide
CC exhibits at least one enzymatic modification other than the glycosylation
CC that occurs in Viscum album or the polypeptide is a fusion protein, a
CC mistletoe lectin polypeptide dimer and an immunotoxin comprising a
CC polypeptide or the polypeptide dimer. The plants are used for large-scale
CC production of mistletoe lectin for diagnostic or therapeutic purposes
CC (e.g. in cancer therapy). This sequence represents the mistletoe lectin
CC (updated on 20-MAR-2003 to correct PF field).
XX
SQ Sequence 564 AA;
Query Match 95.3%; Score 1165; DB 20; Length 564;
Best Local Similarity 91.8%; Pred. No. 1.2e-132;
Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;
OY 1 YERLRATVHTQTKEXEYFRFTLLRDYVSSGSFSENEIFLLRQSTIPVSDAQRFLVLELN 60
DB 34 YERLRATVHTQTKEXEYFRFTLLRDYVSSGSFSENEIFLLRQSTIPVSDAQRFLVLELN 93
OY 61 QGDSXTALADVNNVYVAAGDSYFLRDAPRGAETHLFTGTTRDSLSLPRKQSYDL 120
DB 94 QGDSXTALADVNNVYVAAGDSYFLRDAPRGAETHLFTGTTRDSLSLPRKQSYDL 151
OY 121 ERVAGHDQIPGIGDQISVYALRPFQGSSTRQASILLIOMISAPRFPILMRKQ 180
DB 152 ERVAGHDQIPGIGDQISVYALRPFQGSSTRQASILLIOMISAPRFPILMRKQ 211
OY 181 XINGKSFLEPDYMLLETSMGQSTQVGHSTQVFNPKALIXXGNFTLXNEXVIA 240
DB 212 YINGKSFLEPDYMLLETSMGQSTQVGHSTQVFNPKALIXXGNFTLXNEXVIA 271
OY 241 SLATMLFVCGERSSS 256
DB 272 SLATMLFVCGERSSS 287

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Page 4

KM		Iymphokine-producing macrophage; uncontrolled cell growth; treatment;
XN		cancer; cytotoxicity; antigen; isoform; lectin I.
OS	Viscum album.	
PX	DEI9604210-AL.	
PN	12-AUG-1998.	
PF	03-FEB-1998;	98DE-1004210.
XX	03-FEB-1998;	98DE-1004210.
PR	(BIOG-) BIOGEN ARNEIMITTEL GMBH.	
PA	Morris P., Stefefel T., Voelter W., Welters P:	
PI	WPI: 1999-445315/78.	
DZ	N-PDBJ; AA209103.	
PT	Preparation of mulsitoeo lectins in heterologous systems,	
FY	particularly for use as anticancer agents and immunostimulants	
XX	Claime Y.; Fig IB; 78pp; German.	
CC	This invention describes a novel mulsitoeo lectin (I) and its fragments	
CC	which are capable of inducing immunostimulatory activity, the A-chain (MAA)	
CC	of the mulsitoeo lectin binds to CD activate T-cell and induces	
CC	fibroses. Non-cytotoxic forms of (I) activate T-cell and	
CC	Iymphokine-producing macrophages, so stimulate immunity. (I) and its	
CC	fragments are used to treat uncontroled cell growth (particulary of	
CC	cancers) and if they lack cytotoxicity, to increase the strength of che	
CC	immune response, particularly to a co-administered antigen	
CC	(tumour-associated, bacterial or viral). The method allows production of	
CC	mulsitoeo lactein, and its individual chains, in many different hosts	
CC	and on a large scale, at any time, from plant-derived products such	
CC	as rice bran leghemoglobin, which can be purified by chromatography	
CC	to represent a mulsitoeo lectin I protein fragment..	
XX	Sequence 531 AA:	
QV	Query Match	95.3%; Score 1165; DB 20; Length 531:
Bd	Best Local Similarity	91.8% ; Freq. No. 1,le-132;
Matches 255;	Conservative	0; Mismatches 19; Indels 2; Gaps 1
Db	1 YEARNRRTMTGGCTCKEPEFTTIDPYYSSGSFSEIRPLATSGTPSPDAGFYVELTN 60 1 YEARNRHTQTGTBEFFTTILNRYSYGSSFMEIELAQSTIPSDAGSFYVELTN 60	
Oy	61 QGDKSTPALADIVKYVVYAQAQGVSFLDDAPRCALTLEFCGRDSLSFPFGSYLXL 120 61 OGGBSIFLAIDVMNVVAOQBQSFLDDAPRALTLTGFI--RSLSLFNGSVPL 118	
Db	121 ERYAGRHOETPGIGIXOLIOSVALKKPGSGTRXONSRLIILOMSIEARFNPLIAEXKO 180 119 ERASRGROETPLDIIDIQSQSLNSGNFRSGSRGSKGLAKNLAAKNAPTLYANRXVDA 178	
Oy	181 KINSGARGPOELPDIDQLALETSNQSNQVGSTGYRNPKXKLALAXNKAFLLANRWXYA 240 179 VINSGAESLPDYVMLEETSNGQOSTGVGSTLDGFVNRPDLAIAPPNGVTLTNNRDVIA 238	
Oy	241 SLATALPVCGERRPSIS 256	
Db	239 SLATMLVCGERISS 254	
RESULT 6		
ID	AAY55982	
AC	AAY55982 standard; Protein: 532 AA.	
XX	AAY55982;	
DT	18-OCT-1999 (first entry)	

XX		Mistletoe lectin I (variant) protein fragment.
DX		
KX		Mistletoe lectin; antitumor; immunostimulant; A-chain; IL6; immunity;
LX		Ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
MX		Lymphokine-producing macrophage; uncontrolled cell growth; treatment;
NX		Cancer; cytotoxicity; antigen; isoform; lectin I.
OX		
OS	Viscum album.	
PX		
PM	DE19804210-AL.	
PN	12-AUG-1999.	
PP		
PR	03-FEB-1998:	980E-1004210.
PS		
PT	03-FEB-1998:	980E-1004210.
PA	(BIOSYN ARZNEIMITTEL GMBH.	
PI	Morris P, Stiefel T, Voelter W,	welters P;
PL	WPI, 1999-465335/38.	
PM	N-ESB; AT20310C.	
PN		
PT	particularily for use as anticancer agents and immunostimulants	
PS	Disclosure; Fig 4b; 78pp; German.	
XX		This invention describes a novel mistletoe lectin (I) and its fragments
CC		which have antitumor and immunostimulant activity. The A-chain (MLA)
CC		of the mistletoe cytotoxic forms of (I) activate T-cell and thus
CC		lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC		fragments are used to treat uncontrolled cell growth (particularly
CC		cancers) and if they lack cytotoxicity, to increase the strength of the
CC		immune response, particularly to a co-administered antigen
CC		(tumor-associated, bacterial or viral). The method allows production of
CC		mistolee lectin, and its individual chains, in many different vectors
CC		and on a large scale, at any time of the year. Resistant plants free
CC		from toxins present in natural mistletoe can be selected. This sequence
CC		represents a fragment of a mistletoe lectin I protein variant.
XX		
SQ	Sequence 532 AA:	
	Query Match	95.3%; Score 1165; DB 20; Length 532;
	Best Local Similarity	91.8%; Pred. No. 1,1e-132;
	Matches 235; Conservative	0; Mismatches 19; Indels 2; Gaps 1
QY	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
DB	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
QY	61 GDNKSXTALDNTKKVMVVAAGSGSYFLDPAPGATLEFTGRDRSDSLPFXKSYDL	120
DB	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
QY	61 GGDSHTALDVTNLYVVAAGSGSYFLDPAPRATHLETGT--RSSLPFNSYDPL	118
DB	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
QY	121 ERYVNGRIQPLPICIXIOLISYVALRPGGTTRGXARSLILIONISEAKNFILMAHQ	180
DB	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
QY	119 ENYVGSRQLPYGLIDQLSELSNGSGSRTGCGDFGNFKSLALAXXGSPVLXNVRYIA	240
DB	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
QY	179 YINGASFLDPVYMLESMSGSGSYGVGSTLDGVFNFRIFALIPGPFVLTANRVDA	238
DB	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
	1 YERLRVTHQTGKXEYFFITLLRDVSSGSFSNEFLMIOSTLPIFGDQRFUENRN	60
QY	241 SLAIIMEFYCGRRSS 256	
DB	239 SLAIIMEFYCGRRSS 254	
RESULT 7		
AAHI0021		

XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welters P;
XX WPI; 1999-44535/38.
XX N-PSDB; AA209104.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Disclosure; Fig 2B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (WLA)
XX of the mistletoe lectin binds to and inactivates the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate immunity. (I) and its
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumor-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of the mistletoe lectin A1 protein.
XX Sequence 254 AA;
XX
XX Query Match 95.3%; Score 1165; DB 20; Length 254;
XX Best Local Similarity 91.8%; Pred. No. 4e-133;
XX Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;
XX
QY 1 YERLRARVTHQTGXKXFFRFTLLADYVSSGSFSNEIPILRGSTTPVSDAQRFLVVELTN 60
DB 1 YERLRARVTHQTGXKXFFRFTLLADYVSSGSFSNEIPILRGSTTPVSDAQRFLVVELTN 60
QY 61 QGXDXKTAIDVTNNXYVAQAQGSFTLRARAGATHLFTGTRDSGLPEPKGSYDL 120
DB 61 QGXDXKTAIDVTNNXYVAQAQGSFTLRARAGATHLFTGTRDSGLPEPKGSYDL 120
QY 121 ERYAGHRDQIPLAGIXQLIGSYVALXPGSGSTRXQASILLIOMISARFNPILRRXQ 180
DB 121 ERYAGHRDQIPLAGIXQLIGSYVALXPGSGSTRXQASILLIOMISARFNPILRRXQ 180
QY 119 ERYAGHRDQIPLAGIDILIGSYVALXPGSGSTRXQASILLIOMISARFNPILRRXQ 178
DB 119 ERYAGHRDQIPLAGIDILIGSYVALXPGSGSTRXQASILLIOMISARFNPILRRXQ 178
QY 181 XINSKGFPLDPXYMLELSTWQGSSTGVQSTGVFNNPKXLAIXKGNPVLTXNXXVYA 240
DB 179 YINSKGFPLDPXYMLELSTWQGSSTGVQSTGVFNNPKXLAIXKGNPVLTXNXXVYA 238
QY 241 SLAIWLPVQGRPS 256
DB 239 SLAIWLPVQGRPS 254

RESULT 4
AAZ5983
ID AAZ5983 standard; Protein; 254 AA.
XX
XX AAZ5983;
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin A1 (variant) protein fragment.

XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin A1.
XX
XX Viscum album.
XX

PN DEL9804210-A1.
XX 12-AUG-1999.
PD 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX Morris P, Stiefel T, Voelter W, Welters P;
XX WPI; 1999-44535/38.
XX N-PSDB; AA209107.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Disclosure; Fig 5B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (WLA)
XX of the mistletoe lectin binds to and inactivates the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate immunity. (I) and its
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumor-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin A1 protein variant.
XX Sequence 254 AA;
XX
XX Query Match 95.3%; Score 1165; DB 20; Length 254;
XX Best Local Similarity 91.8%; Pred. No. 4e-133;
XX Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;
XX
QY 1 YERLRARVTHQTGXKXFFRFTLLADYVSSGSFSNEIPILRGSTTPVSDAQRFLVVELTN 60
DB 1 YERLRARVTHQTGXKXFFRFTLLADYVSSGSFSNEIPILRGSTTPVSDAQRFLVVELTN 60
QY 61 QGXDXKTAIDVTNNXYVAQAQGSFTLRARAGATHLFTGTRDSGLPEPKGSYDL 120
DB 61 QGXDXKTAIDVTNNXYVAQAQGSFTLRARAGATHLFTGTRDSGLPEPKGSYDL 120
QY 121 ERYAGHRDQIPLAGIXQLIGSYVALXPGSGSTRXQASILLIOMISARFNPILRRXQ 180
DB 121 ERYAGHRDQIPLAGIXQLIGSYVALXPGSGSTRXQASILLIOMISARFNPILRRXQ 180
QY 119 ERYAGHRDQIPLAGIDILIGSYVALXPGSGSTRXQASILLIOMISARFNPILRRXQ 178
DB 119 ERYAGHRDQIPLAGIDILIGSYVALXPGSGSTRXQASILLIOMISARFNPILRRXQ 178
QY 181 XINSKGFPLDPXYMLELSTWQGSSTGVQSTGVFNNPKXLAIXKGNPVLTXNXXVYA 240
DB 179 YINSKGFPLDPXYMLELSTWQGSSTGVQSTGVFNNPKXLAIXKGNPVLTXNXXVYA 238
QY 241 SLAIWLPVQGRPS 256
DB 239 SLAIWLPVQGRPS 254

RESULT 5
AAZ5979
ID AAZ5979 standard; Protein; 531 AA.
XX
XX AAZ5979;
XX
XX 18-OCT-1999 (first entry)
XX
XX Mistletoe lectin I protein fragment.

XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX

PT Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 PS Claim 8; Fig 3B; 78pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to, and activates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of the mistletoe lectin A2 protein.
 XX
 SQ Sequence 256 AA;
 SO Query Match 97.6%; Score 1194; DB 20; Length 256;
 SO Best Local Similarity 92.6%; Freq. No. 1.2e-136;
 SO Matches 237; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1 YERLRVHTQTCXEPFRITLARDVSSGSPNRPILRGSTIPVSDAQRFLVELTN 60
 DB 1 YERLRVHTQTCXEPFRITLARDVSSGSPNRPILRGSTIPVSDAQRFLVELTN 60
 QY 61 QGQDSITPAIDVMAVVAOAGDSYFLRDPAGAEHLFTGTRRSSLPEFGSYDYL 120
 DB 61 QGQDSITPAIDVMAVVAOAGDSYFLRDPAGAEHLFTGTRRSSLPEFGSYDYL 120
 QY 121 ERVAGHRQIPLGIGIOLIOSVAFRRPGSSTAPAKRSIIILQMSBAARFPIIMRQ 180
 DB 121 ERVAGHRQIPLGIGIOLIOSVAFRRPGSSTAPAKRSIIILQMSBAARFPIIMRQ 180
 QY 181 XINSGKSPFLPDXYMLELSTWQSGTOVQSHSTDVGNPNFRALISTGNFVLSNRSVYA 240
 DB 181 XINSGKSPFLPDXYMLELSTWQSGTOVQSHSTDVGNPNFRALISTGNFVLSNRSVYA 240
 QY 241 SLAIMLFCGERPSS 256
 DB 241 SLAIMLFCGERPSS 256
 RESULT 2
 AAY25984
 ID AAY25984 standard; Protein; 256 AA.
 AC AAY25984;
 XX
 DT 18-OCT-1999 (first entry)
 XX
 DE Mistletoe lectin A2 (variant) protein fragment.
 XX
 KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin A2.
 XX
 OS Viscum album.
 KM DE19804210-A1.
 XX
 DM 12-AUG-1999.
 XX
 PF 03-FEB-1998; 98DE-1004210.
 XX
 PR 03-FEB-1998; 98DE-1004210.
 XX
 PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX

PI Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI; 1999-44535/38.
 DR N-PSDB; AAY29108.
 XX
 CC Preparation of mistletoe lectins in heterologous systems,
 CC particularly for use as anticancer agents and immunostimulants
 PS Disclosure; Fig 6B; 78pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin A2 protein variant.
 XX
 SQ Sequence 256 AA;
 SO Query Match 97.6%; Score 1194; DB 20; Length 256;
 SO Best Local Similarity 92.6%; Freq. No. 1.2e-136;
 SO Matches 237; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1 YERLRVHTQTCXEPFRITLARDVSSGSPNRPILRGSTIPVSDAQRFLVELTN 60
 DB 1 YERLRVHTQTCXEPFRITLARDVSSGSPNRPILRGSTIPVSDAQRFLVELTN 60
 QY 61 QGQDSITPAIDVMAVVAOAGDSYFLRDPAGAEHLFTGTRRSSLPEFGSYDYL 120
 DB 61 QGQDSITPAIDVMAVVAOAGDSYFLRDPAGAEHLFTGTRRSSLPEFGSYDYL 120
 QY 121 ERVAGHRQIPLGIGIOLIOSVAFRRPGSSTAPAKRSIIILQMSBAARFPIIMRQ 180
 DB 121 ERVAGHRQIPLGIGIOLIOSVAFRRPGSSTAPAKRSIIILQMSBAARFPIIMRQ 180
 QY 181 XINSGKSPFLPDXYMLELSTWQSGTOVQSHSTDVGNPNFRALISTGNFVLSNRSVYA 240
 DB 181 XINSGKSPFLPDXYMLELSTWQSGTOVQSHSTDVGNPNFRALISTGNFVLSNRSVYA 240
 QY 241 SLAIMLFCGERPSS 256
 DB 241 SLAIMLFCGERPSS 256
 RESULT 2
 AAY25980
 ID AAY25980 standard; Protein; 254 AA.
 AC AAY25980;
 XX
 DT 18-OCT-1999 (first entry)
 XX
 DE Mistletoe lectin A1 protein fragment.
 XX
 KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin A1.
 XX
 OS Viscum album.
 KM DE19804210-A1.
 XX
 DM 12-AUG-1999.
 XX
 PF 03-FEB-1998; 98DE-1004210.
 XX

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us-09-601-667c-41.frag

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 25.2959 Seconds
(without alignments)
1606.345 Million cell updates/sec

Title: US-09-601-667C-41

Sequence: 123
1 TBRRLATVHTQTTCKEYFRF.....XTNLAIMEFVCGSPSS 256

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 9

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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21:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT*
22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT*
23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1194	97.6	256	AAV25981	Mistletoe lectin A
2	1194	97.6	256	AAV25984	Mistletoe lectin A
3	1165	95.3	254	AAV25980	Mistletoe lectin A
4	1165	95.3	254	AAV25983	Mistletoe lectin A
5	1165	95.3	531	AAV25979	Mistletoe lectin I
6	1165	95.3	532	AAV25982	Mistletoe lectin I
7	1165	95.3	564	AAV10021	Prepro mistletoe I
8	1165	95.3	564	AAV90127	Mistletoe lectin P
9	1162.5	95.1	255	AAV25971	Mistletoe lectin A

10	1162.5	95.1	255	AAV25974	Mistletoe lectin A
11	1162.5	95.1	255	AAV25977	Mistletoe lectin A
12	1162.2	95.1	253	AAV25970	Mistletoe lectin P
13	1162.2	95.1	253	AAV25973	Mistletoe lectin P
14	1162.5	95.1	533	AAV25976	Mistletoe lectin P
15	1155	94.4	253	AAV64661	Mistletoe rRNA var
16	1155	94.4	253	AAV10022	Prepro mistletoe I
17	1155	94.4	253	AAV90125	Mistletoe Mt A-cha
18	1151	94.1	252	AAV64659	Mistletoe rRNA pro
19	1129	92.3	551	ABR79450	Galactose-recogins
20	1094	89.5	254	ABR47090	A-chain isoform fo
21	1073	87.7	254	ABR47091	A-chain isoform fo
22	989	80.9	256	ABR47092	A-chain isoform fo
23	597	48.8	174	ABR47097	Korean mistletoe I
24	562	37.8	250	ABR47097	Nitro acid sequence
25	453.2	37.1	250	ABR47097	ABR47097
26	453.2	36.4	250	ABR47097	ABR47097
27	447	36.4	252	ABR81976	Recombinant abrin
28	444	36.3	253	ABR81977	Recombinant abrin
29	438	35.8	253	ABR81978	Recombinant abrin
30	376	30.7	267	ABR30722	Ricin A from pici1
31	376	30.7	267	ABR37290	Ricin A-chain (RA
32	376	30.7	267	ABR63902	Ricin A-chain (RA
33	376	30.7	267	ABR12855	Amino acid sequenc
34	376	30.7	332	AAV70097	Ricin A. Sequence
35	376	30.7	332	AAV70097	Sequence of Ricin
36	376	30.7	332	AAV70097	Ricin A encoded by
37	376	30.7	583	ABP90079	Ricin D. Ricinus
38	376	30.7	583	ABP90079	Modified cactor be
39	376	30.7	574	ABP94793	DNA sequence of r1
40	376	30.7	574	ABP94793	Sequence of Ricin
41	376	30.7	576	AAV70326	Castorbean ricin.
42	376	30.7	576	AAV25787	Castor bean ricin
43	376	30.7	576	AAV55892	Ricinus communis r
44	376	30.7	576	AAV78592	Ricinus communis r
45	376	30.7	576	AAV78301	Castor bean prepro

ALIGNMENTS

RESULT 1		
ID	AAV25981	standard: Protein: 256 AA.
AAV25981		
XX	AAV25981;	
XX	18-OCT-1999	(first entry)
XX		
DE	Mistletoe lectin A2 protein fragment.	
XX		
XX	Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity; ribopzyme 28S subunit; non-cytotoxic; T-cell activation; immune response; lymphocyte-producing macrophage; uncontrolled cell growth; treatment; cancer; cytotoxicity; antigen; isoform; lectin A2.	
XX		
OS	Viscum album.	
XX		
FN	DE19904210-A1.	
XX		
ED	12-AUG-1999.	
XX		
XX	03-FEB-1998;	98DB-1004210.
XX		
FR	03-FEB-1998;	98DB-1004210.
XX		
PA	(BIOS-) BIOSYN ARZNEIMITTEL GMBH.	
XX		
PI	Morris P, Stiefel T, Voelter W, Welters P,	
XX		
DR	WPI; 1999-445335/38.	
DR	N-PSDB; AA209105.	
XX		

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Page 8

QY 9 THQTVGKXEFRTLLRDPYSSGSPSNRIPILRQ-STIPVSDAORPVVWELTNQXDS-X 66
Db 8 TKKATKTSYTOPIELAKQALASGEHPHGIYWERSTVP--DSKEFLIVELSNWADSPV 65
QY 67 TAAIDVTNXYVAVQAKDQSYFLR-DAPRGAETHLFTGTRDSSLPKXSYKLERVAG 125
Db 66 TLAVDVINAVVAKRISQSEFTLEKEDDPALNHLPTI--KVTTFSSSTDLRGVAG 123
QY 126 -HRDCPIGIXQLIGVAAEKPG-GSTXQASGIIIIQISEAAFPDILAKKXKXIN 183
Db 124 ERREIILGMDLENAISALWISNNOORALARSLIVIQWVAEVAFRFLRYRVGSGIS 183
QY 184 SXSEFLPDXYMLETSWGOQSTOVQHSTD-GVFNFPKALIXXGNFVTLXNVF-XVIA 241
Db 184 RAEWFRPDPMLSLKMKWALSNVAVQSQGVSSPVELRSISNKKPVYGVSDRVISG 243
QY 242 LAIMLFVC--GERPS 255
Db 244 LAIMLFICRSTNASS 259

Search completed: December 11, 2003, 14:01:07
Job time : 20.7321 secs

RT genes encoding cinnamomin proteins and study of their expression
RT submitted (JUN-2001) to the EMBL/GenBank/DBJ databases
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AY039802; AAK82459.1; -
DR InterPro: IPR000772; R1cin_B_lectin.
DR InterPro: IPR001574; R1P.
DR Pfam: PF00652; R1cin_B_lectin; 6.
DR PRINTS: PF00652; R1P; 1.
DR SMART: SMO0458; R1cin_B_lectin.
DR PROSITE: PS00231; R1cin_B_lectin; 2.
DR PROSITE: PS00231; R1cin_B_lectin; 2.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
SQ SEQUENCE 580 AA; 64265 MW; 3784289ECCECF CRC64;
Query Match 35.0%; Score 428.5; DB 10; Length 580;
Best Local Similarity 43.8%; Pred. No. 2,2e-39;
Matches 112; Conservative 36; Mismatches 95; Indels 13; Gaps 10;
DB 9 TQCTCKEYRPTFLADYVSSGSFSEMERPIAQ-STIPSAQRFVLTETNOGKEXT 67
QY 9 TQCTCKEYRPTFLADYVSSGSFSEMERPIAQ-STIPSAQRFVLTETNOGKEXT 67
DB 40 TQATKSTYQTEFLALDQGLASDEPRGIFPMDSYTP--DSKPIVLSLMAADSPV 97
QY 68 A-AIDVTKYVVAQADQSYFLRDPAGAEHLFTGTRRSLSLFPYGYDLERYAG 125
DB 98 ALADVTNAYVVAQADQSYFLRDPAGAEHLFTGTRRSLSLFPYGYDLERYAG 155
QY 126 H-RDQIPGLXQLQISYALRKPQ-GSTYKQARSLILQISLSEARFNPILMKXKXIN 183
DB 156 ELREKILLMDPELNNISALMTSNINQALANGLVITQMAKAVYFETIRVBSIT 215
QY 184 SGKSLFDYKMLSEFSGQSTQVQSTND-GPNPYPKALIXGNFTVLNAYR-XVTA 241
DB 216 RAEFRDPAMSLNNMNSLGNVQSGVSSFPYELASISNKKYVVSQSRVLSG 275
QY 242 LAIMLFCV--GEPSS 255
DB 276 LAIMLFCRSSDRSS 291
RESULT 14
ID 006076 PRELIMINARY; PRT; 528 AA.
AC 006076;
DT 01-NOV-1996 (Trembl) 01. Created
DT 01-NOV-1996 (Trembl) 01. Last sequence update
DT 01-MAR-2003 (Trembl) 23. Last annotation update
DE Abtin-d (BC 3.2.2.22) (tRNA N-glycosidase) (fragment).
OS Abtin precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Euphorbia; Fabales; Fabaceae; Papilionoideae; Abraceae; Abtinus.
NCBI_TaxID=3816;
RN 11
RX SEQUENCE FROM N.A.
RX MEDLINE=3912798; PubMed=842113;
RX 11-11-1996 (Trembl) 01. Created
RT "Primary structure of three distinct isoforms determined by cDNA
RT sequencing; conservation and significance.";
RL J. Mol. Biol. 229:263-267 (1993).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: M98346; AAK32626.1; -
DR HSP; P1140; IABR.
DR InterPro: IPR000772; R1cin_B_lectin.
DR InterPro: IPR001574; R1P.
DR Pfam: PF00652; R1cin_B_lectin; 6.

DR Pfam: PF00652; R1P; 1.
DR SMART: SMO0458; R1cin_B_lectin.
DR PROSITE: PS00231; R1cin_B_lectin; 2.
DR PROSITE: PS00231; SHIGA_R1cin; 1.
KW Hydrolase; Toxin.
FT NON_TER 1 1
FT NON_TER 528 528
SQ SEQUENCE 528 AA; 58870 MW; 62ED42F8EPEBES0B CRC64;
Query Match 34.8%; Score 426; DB 10; Length 528;
Best Local Similarity 42.4%; Pred. No. 3.0e-38;
Matches 109; Conservative 36; Mismatches 98; Indels 6; Gaps 5;
DB 9 TQCTCKEYRPTFLADYVSSGSFSEMERPIAQ-STIPSAQRFVLTETNOGKEXT 66
QY 9 TQCTCKEYRPTFLADYVSSGSFSEMERPIAQ-STIPSAQRFVLTETNOGKEXT 66
DB 69 AIDVTKYVVAQADQSYFLRDPAGAEHLFTGTRRSLSLFPYGYDLERYAG-R 127
QY 67 GIDVTNAYVVAQADQSYFLRDPAGAEHLFTGTRRSLSLFPYGYDLERYAG-R 124
DB 128 DQIPGLXQLQISYALRKPQ-GSTYKQARSLILQISLSEARFNPILMKXKXIN 187
QY 125 ELREKILLMDPELNNISALMTSNINQALANGLVITQMAKAVYFETIRVBSIT 215
DB 188 FLPDYKMLSEFSGQSTQVQSTND-GPNPYPKALIXGNFTVLNAYR-XVTA 246
QY 185 FQDPBAMSLNNMNSLGNVQSGVSSFPYELASISNKKYVVSQSRVLSG 275
DB 247 FVC 249
DB 245 FVC 247
RESULT 15
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AC 009722;
DT 01-MAR-2001 (Trembl) 16. Created
DT 01-MAR-2001 (Trembl) 16. Last sequence update
DT 01-OCT-2002 (Trembl) 22. Last annotation update
DE Type II ribosome-inactivating protein cinnamomin (BC 3.2.2.22) (tRNA
DE N-glycosidase) (fragment).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI_TaxID=11429;
RN 11
RX SEQUENCE FROM N.A.
RX Xie L, Liu W -Y, Wang F -D;
RT "Molecular cloning of cinnamomin A', B-chain and the expression,
RT purification, characterization and mutagenesis of the A'-Chain.";
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF259548; AAF68978.2; -
DR HSP; P02879; ZAM.
DR InterPro: IPR000772; R1cin_B_lectin.
DR InterPro: IPR001574; R1P.
DR Pfam: PF00652; R1cin_B_lectin; 5.
DR PRINTS: PF00652; SHIGA_R1cin.
DR SMART: SMO0458; R1cin_B_lectin; 2.
DR PROSITE: PS00231; R1cin_B_lectin; 2.
KW Hydrolase; Toxin.
FT NON_TER 1 1
SQ SEQUENCE 549 AA; 60648 MW; 02607E607CA450 CRC64;
Query Match 34.3%; Score 419.5; DB 10; Length 549;
Best Local Similarity 43.4%; Pred. No. 2.1e-38;
Matches 111; Conservative 38; Mismatches 94; Indels 13; Gaps 10;

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Page 6

DT 01-NOV-1998 (7EMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (7EMBLrel. 19, Last annotation update)
 DE Abirin-B (RRNA N-glycosidase) (SC 3.2.2.22) (Fragment).
 DN Abirin-B, precursor (Indian licorice) (Crab's eye).
 NR Abirin-B, precursor (Indian licorice) (Crab's eye).
 OC Bacteriophages; Viridiplantae; Streptophyta; Tracheophytes;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucucids 1; Fabales; Fabaceae; Papilionoideae; Abraceae; Abrus;
 OC NCBI_TaxID=3816;
 RN [1]
 RN SEQUENCE FROM N.A.
 RN TISSUE:LEAF
 RX PubMed=201129. PubMed=151600.
 RX PubMed=201129. PubMed=151600.
 RT "Direct molecular cloning and expression of two distinct abir-
 A chains".
 RL J. Biol. Chem. 266:6648-6652(1991).
 CC -1. FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS BY REMOVING ADENINE FROM INITIATION OF 60S RIBOSOMAL
 CC SUBUNITS BY REMOVING ADENINE FROM INITIATION 4,524 OF 26 S RRNA.
 CC -1. FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
 CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
 CC PRECEDES ENDOCYTOSIS.
 CC -1. CATALYTIC ACTIVITY: ENDOCHONDRIALYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1. SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC -1. COMPOSITION: 2 CHAINS, 28S RRNA, 28S RRNA, 28S RRNA, 28S RRNA
 CC -1. SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
 CC PROTEINS. BELONGS TO TYPE 2 RIP.
 DR EMBL: X54873; CAA38554.1; -.
 DR HSSP; P11410; IABR.
 DR Interpro; IPR001574; RIP.
 DR Pfam; PF001036; RIBACTIN.
 DR PROSITE; PS00275; SHIGA_RICIN_1.
 DR HydroLase; GlycoLase; Toxin; Repeat; Glycoprotein; Lectin.
 FT CHAIN 1 232
 FT NON_TER 252 232
 SEQUENCE 252 AA; 28309 MW; B8FC946B95285DE CRC64;

[illegible]

PT	01-MAR-2003 (TREMBL:23, Last annotation update)
DE	Type 2 ribosome-inactivating protein cinnamomum III precursor
OS	(NC 3.2.2.22) (rRNA N-glycosylase).
DE	Cinnamomum camphora (camphor tree).
CC	Bakayev; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC	Spermatophyta; Magnoliophyta; Nudicales; Lauraceae; Cinnamomum.
PK	NCBI_TaxId=13429;
RP	SEQUENCE FROM N.A.
RA	Yang Q., Gong Z.Z., Liu W.Y.;
RT	"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT	genes encoding cinnamomum proteins and study of their expression
RT	patterns";
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBD databases.
CC	-1- CATALYTIC ACTIVITY: ENDORIBOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC	SPECIFIC ADENOSINE ON THE 28S RRNA.
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR	EMBL: AY039803; AKK32460.1;
DR	Interpro: IPR000172; Ricin_B_lectin.
DR	Interpro: IPR000551; Ricin_B_lectin; 6.
DR	Pfam: PF00161; RIP: I_lectin; 6.
DR	PRINTS: PR00366; SHGARIQIN.
DR	SMART: SM00456; RCIN; 2.
DR	PROSITE: PS50231; RICIN_B_LECTIN; 2.
DR	Hydrolase; Signal; Toxin.
FT	DOMAIN
FT	STANDARD
FT	CHAIN
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOMUM III
FT	SEQUENCE
FT	580 AA; 64421 NM; 940D0701E7B556 CEC64;
FT	33
FT	580
FT	1
FT	32
FT	POTENTIAL.
FT	TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT	CINNAMOM

QY	9	THQTGAEFFRITLLROYVSSGSFNEILLRP-STTPSDAKQFVLTVELTNGXDS-X-66	
Dh	40	TKAKKSTVGTGIEALFAKQLASGEPPGICPMWRKSTVP-DSEKFLVEILSNAPDSV	97
QY	67	TAADITNNVYVAYONGQSYFIR-DAPGAEHTLFTGTTRDSSLEPPGICYXLERFNG	135
QY	126	-HHQITLITXIALGSDYALFXEG-GSTQSPRSTILLIOMISEAPAPNPLMXKXQXN	183
Dh	98	TLAVVTAIVTAIVTAVTQFSEEDPDPRNENLPPDI-XKTFPGSGSYDLDERAG	155
Dh	156	EREHILLIOMPLLNKNIISALMISNLNQALASLILVIVQWAEVAFRIEYVESST	215
QY	184	SGKSELPDYXMLEETPSNGQSGVQSTND-GVNNPKRLAIKXNPFLLXNR-XVIA	241
Dh	216	RAIMRPDPAPMLSTENKMSALSNAAVOOSNGGVSPVELLSISNKQVYGVSDRVIG	275
QY	242	LAIMFVC-GERPSS	255
Dh	276	LAIMFLICSTGRASS	291
RESULT 13			
Q94BM4		PRELININART; FRT; 580 AA.	
Q94BM4			
AC	094BM4	(TREMBL) 19, (Cleaved)	
DT	01-DEC-2001	(TREMBL) 19, (last sequence update)	
DT	01-DEC-2001	(TREMBL) 23, (last annotation update)	
DT	01-MAR-2003	(TREMBL) 23, (last annotation update)	
DE	Type 2, ribosome-inactivating protein cinnamon ii precursor		
DE	(EC 3.2.2.22) (cRN N-glycosylase).		
OS	Cinnamon camphor (Camphor tree).		
OC	Bakayocra, Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.		
OX	NCBI_TaxId=13429;		
NP	(1)		
NP	SEQUENCE FROM N.A.		
RT	Yang Q., Gong Z.Z., Liu W.Y.;		
RT	Molecular cloning of three type 2 RIP (ribosome-inactivating protein)		

QY 9 TQTTGKXEFRTLLADYVSSGSFSENEILROSTIPVSDARFVVELTNGQDXNTA 68
DB 9 TEGATSGSYKQPIEAKRERL-RGGLIHDIIVLPDPT-TLQENNRITIVELNSDTESEV 66
QY 69 AIDVTKXVYVAYKQKQSYFLDAPRAGETLFTGTTPRSGSLPRGQYDLEPRACH-R 127
DB 67 GIDVTNAYVAYVAYRAGTGYFLDAPRAGETLFTGT--DQSLPFGYGVGLERNAHQSR 124
QY 128 DQIPGLIGXOLISVAXLXPGSGSTRQKARSILILQWISFAARFNPILMXRXOXINSGX 187
DB 125 QQIPGLIGXOLISVAXLXPGSGSTRQKARSILILQWISFAARFNPILMXRXOXINSGX 184
QY 188 FLDPXVMELETSWGQSTQVQSHSTDGVFNPNKRLAIXGNFVTLANVX----- 237
DB 185 FQPDAAKISLENNWNLISRGVQSGVQDTFFNQ-----VTLNINRNPVYDLSLH 234
QY 238 -VINSTAINTLFC 249
DB 235 PTAVATLMLTFC 247

RESULT 9
Q96237
ID Q96237 PRELIMINARY; FRT; 251 AA.

AC Q96237, 1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PCNNAc-1-E164A/R167L protein (EC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment)
OS Abrys precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrys.
NCBI TaxID=3816;
OX NCBI TaxID=3816;
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE=9756; PubMed=8307038;
RA Chih-hung H. Lee M.C. Chen J.K.
RT "Cloning and expression of three abrys r-chains and their mutants
derived by site-specific mutagenesis in Escherichia coli.";
RT Eur. J. Biochem. 219:83-87(1994).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; X76722; CA54140.1; -
DR HSSP; P11440; IABR.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR HYDROLASE; toxin.
FT NON TER 1 1
FT NON TER 251 251
SQ SEQUENCE 251 AA; 28055 MW; 6f64755C3DBA97E CRC64;

Query Match 37.6%; Score 460; DB 10; Length 251;
Best Local Similarity 41.9%; Pred. No. 1.9e-43;

Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;

QY 9 TQTTGKXEFRTLLADYVSSGSFSENEILROSTIPVSDARFVVELTNGQDXNTA 68
DB 9 TEGATSGSYKQPIEAKRERL-RGGLIHDIIVLPDPT-TLQENNRITIVELNSDTESEV 66
QY 69 AIDVTKXVYVAYKQKQSYFLDAPRAGETLFTGTTPRSGSLPRGQYDLEPRACH-R 127
DB 67 GIDVTNAYVAYVAYRAGTGYFLDAPRAGETLFTGT--DQSLPFGYGVGLERNAHQSR 124
QY 128 DQIPGLIGXOLISVAXLXPGSGSTRQKARSILILQWISFAARFNPILMXRXOXINSGX 187
DB 125 QQIPGLIGXOLISVAXLXPGSGSTRQKARSILILQWISFAARFNPILMXRXOXINSGX 184
QY 188 FLDPXVMELETSWGQSTQVQSHSTDGVFNPNKRLAIXGNFVTLANVX----- 237

DB 185 FQPDAAKISLENNWNLISRGVQSGVQDTFFNQ-----VTLNINRNPVYDLSLH 234
QY 238 -VINSTAINTLFC 249
DB 235 PTAVATLMLTFC 247

RESULT 10

Q96235
ID Q96235 PRELIMINARY; FRT; 251 AA.

AC Q96235, 1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PCNNAc-1-E164A/R167L protein (EC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment)
OS Abrys precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrys.
NCBI TaxID=3816;
OX NCBI TaxID=3816;
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE=94139756; PubMed=8307038;
RA Chih-hung H. Lee M.C. Chen J.K. Chen J.Y.
RT "Cloning and expression of three abrys r-chains and their mutants
derived by site-specific mutagenesis in Escherichia coli.";
RT Eur. J. Biochem. 219:83-87(1994).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; X76644; CA54092.1; -
DR HSSP; P11440; IABR.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR HYDROLASE; toxin.
FT NON TER 1 1
FT NON TER 251 251
SQ SEQUENCE 251 AA; 27997 MW; 3B6031839A9B7E CRC64;

Query Match 37.1%; Score 454; DB 10; Length 251;
Best Local Similarity 41.5%; Pred. No. 9.1e-43;

Matches 105; Conservative 34; Mismatches 88; Indels 26; Gaps 6;

QY 9 TQTTGKXEFRTLLADYVSSGSFSENEILROSTIPVSDARFVVELTNGQDXNTA 68
DB 9 TEGATSGSYKQPIEAKRERL-RGGLIHDIIVLPDPT-TLQENNRITIVELNSDTESEV 66
QY 69 AIDVTKXVYVAYKQKQSYFLDAPRAGETLFTGTTPRSGSLPRGQYDLEPRACH-R 127
DB 67 GIDVTNAYVAYVAYRAGTGYFLDAPRAGETLFTGT--DQSLPFGYGVGLERNAHQSR 124
QY 128 DQIPGLIGXOLISVAXLXPGSGSTRQKARSILILQWISFAARFNPILMXRXOXINSGX 187
DB 125 QQIPGLIGXOLISVAXLXPGSGSTRQKARSILILQWISFAARFNPILMXRXOXINSGX 184
QY 188 FLDPXVMELETSWGQSTQVQSHSTDGVFNPNKRLAIXGNFVTLANVX----- 237
DB 185 FQPDAAKISLENNWNLISRGVQSGVQDTFFNQ-----VTLNINRNPVYDLSLH 234
QY 238 -VINSTAINTLFC 249
DB 235 PTAVATLMLTFC 247
RESULT 11
ID Q98760 PRELIMINARY; FRT; 252 AA.
AC Q98760, 1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DE Lectin chain A isoform 1 (EC 3.2.2.22) (rRNA N-glycosidase)
DS MEDLINE-2156752; PubMed-11710524;
OS Viscum album subsp. coloratum
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxId=159976;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-2156752; PubMed-11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RY Do M.-S., Song S.K.;
RN "cDNA cloning and sequence analysis of the lectin genes of the Korean mistletoe (Viscum album coloratum).";
RT Mol. Cells 12:215-220(2001).
RL [2]
RP SEQUENCE FROM N.A.
RX Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF069244; JMW6532.1.;
DR DDB: J017001394; R1P.
DR PIR: P00396; SHIGARICIN.
DR PRINTS: PR00396; SHIGARICIN.
KW Hydrolase; Toxin.
FT NON TER 1 1
FT TER 254 254
SQ SEQUENCE 254 AA; 28446 MW; 6DB5C3B18FAFE0 CRC64;
Query Match 89.5%; Score 1094; DB 10; Length 254;
Best Local Similarity 85.5%; Pred. No. 5.2e-115;
Matches 219; Conservative 8; Mismatches 27; Indels 2; Gaps 1;
QY 1 YERRLRVHTGTCGEXRPRITLIDRVYSGSFNRIPLRGSTIPYSDAPRFLVETN 60
DB 1 YERRLRVHTGTCGEXRPRITLIDRVYSGSFNRIPLRGSTIPYSDAPRFLVETN 60
QY 61 QGKDSXTALIDVTNXYVAVOAGDSYFLDAPRGAETHLFTGTRDSSLPFGSYXDL 120
DB 61 QGKDSXTALIDVTNXYVAVOAGDSYFLDAPRGAETHLFTGTRDSSLPFGSYXDL 120
QY 61 QGDSITLALDVTNLVYVAVOAGDSYFLDAPRGAETHLFTGTRDSSLPFGSYXDL 118
DB 61 QGDSITLALDVTNLVYVAVOAGDSYFLDAPRGAETHLFTGTRDSSLPFGSYXDL 118
QY 121 ERYAGRDQIPGIXQLIGVYALEKPGSTGXQASILLICMSEAAFNPLWEXQ 180
DB 121 ERYAGRDQIPGIXQLIGVYALEKPGSTGXQASILLICMSEAAFNPLWEXQ 180
QY 119 ERYAGRDQIPGIXQLIGVYALEKPGSTGXQASILLICMSEAAFNPLWEXQ 178
DB 119 ERYAGRDQIPGIXQLIGVYALEKPGSTGXQASILLICMSEAAFNPLWEXQ 178
QY 181 XINGKASIPKXVLETSWQGSQSTOVGHSTGVFNPKALIXGNFTLXNRYA 240
DB 181 XINGKASIPKXVLETSWQGSQSTOVGHSTGVFNPKALIXGNFTLXNRYA 240
QY 179 YISSGSPFLPDYTLQLETSWQGSQSTOVGHSTGVFNPKALIXGNFTLXNRYA 238
DB 179 YISSGSPFLPDYTLQLETSWQGSQSTOVGHSTGVFNPKALIXGNFTLXNRYA 238
QY 241 SLAINLFCVCEPRSSS 256
DB 241 SLAINLFCVCEPRSSS 256
QY 239 SLAINLFCVCEPRSSS 254
DB 239 SLAINLFCVCEPRSSS 254
RESULT 5
QBLK04 PRELIMINARY; PRT; 249 AA.
ID QBLK04
DT 01-OCT-2002 (TRENBERG) 22, Created!
DT 01-OCT-2002 (TRENBERG) 22, Last sequence update!
DT 01-MAR-2003 (TRENBERG) 23, Last annotation update!
DE Lectin chain A isoform 2 (EC 3.2.2.22) (rRNA N-glycosidase)
OS Viscum album subsp. coloratum
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxId=159976;
RN [1]
RP SEQUENCE FROM N.A.
RX Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RY Do M.-S., Song S.K.;
RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF069244; JMW6532.1.;
DR DDB: J017001394; R1P.
DR PIR: P00396; SHIGARICIN.
DR PRINTS: PR00396; SHIGARICIN.
KW Hydrolase; Toxin.
FT NON TER 1 1
FT TER 249 249
SQ SEQUENCE 249 AA; 27821 MW; 3C5870F83BDBA5 CRC64;

EX MEDLINE-2156752; PubMed-11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RY Do M.-S., Song S.K.;
RN "cDNA cloning and sequence analysis of the lectin genes of the Korean mistletoe (Viscum album coloratum).";
RT Mol. Cells 12:215-220(2001).
RL [2]
RP SEQUENCE FROM N.A.
RX Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF069244; JMW6532.1.;
DR DDB: J017001394; R1P.
DR PIR: P00396; SHIGARICIN.
DR PRINTS: PR00396; SHIGARICIN.
KW Hydrolase; Toxin.
FT NON TER 1 1
FT TER 249 249
SQ SEQUENCE 249 AA; 27821 MW; 3C5870F83BDBA5 CRC64;
Query Match 86.2%; Score 1054; DB 10; Length 249;
Best Local Similarity 83.9%; Pred. No. 1.6e-110;
Matches 209; Conservative 13; Mismatches 25; Indels 2; Gaps 1;
QY 1 YERRLRVHTGTCGEXRPRITLIDRVYSGSFNRIPLRGSTIPYSDAPRFLVETN 60
DB 1 YERRLRVHTGTCGEXRPRITLIDRVYSGSFNRIPLRGSTIPYSDAPRFLVETN 60
QY 61 QGKDSXTALIDVTNXYVAVOAGDSYFLDAPRGAETHLFTGTRDSSLPFGSYXDL 120
DB 61 QGKDSXTALIDVTNXYVAVOAGDSYFLDAPRGAETHLFTGTRDSSLPFGSYXDL 120
QY 61 QGDSITLALDVTNLVYVAVOAGDSYFLDAPRGAETHLFTGTRDSSLPFGSYXDL 118
DB 61 QGDSITLALDVTNLVYVAVOAGDSYFLDAPRGAETHLFTGTRDSSLPFGSYXDL 118
QY 121 ERYAGRDQIPGIXQLIGVYALEKPGSTGXQASILLICMSEAAFNPLWEXQ 180
DB 121 ERYAGRDQIPGIXQLIGVYALEKPGSTGXQASILLICMSEAAFNPLWEXQ 180
QY 119 ERYAGRDQIPGIXQLIGVYALEKPGSTGXQASILLICMSEAAFNPLWEXQ 178
DB 119 ERYAGRDQIPGIXQLIGVYALEKPGSTGXQASILLICMSEAAFNPLWEXQ 178
QY 179 YISSGSPFLPDYTLQLETSWQGSQSTOVGHSTGVFNPKALIXGNFTLXNRYA 238
DB 179 YISSGSPFLPDYTLQLETSWQGSQSTOVGHSTGVFNPKALIXGNFTLXNRYA 238
QY 241 SLAINLFCV 249
DB 241 SLAINLFCV 249
QY 239 SLAINLFCV 247
DB 239 SLAINLFCV 247
RESULT 6
QBLK04 PRELIMINARY; PRT; 251 AA.
ID QBLK04
DT 01-OCT-2002 (TRENBERG) 22, Created!
DT 01-OCT-2002 (TRENBERG) 22, Last sequence update!
DT 01-MAR-2003 (TRENBERG) 23, Last annotation update!
DE Lectin chain A isoform 3 (EC 3.2.2.22) (rRNA N-glycosidase)
OS Viscum album subsp. coloratum
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxId=159976;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-2156752; PubMed-11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RY Do M.-S., Song S.K.;
RN "cDNA cloning and sequence analysis of the lectin genes of the Korean mistletoe (Viscum album coloratum).";
RT Mol. Cells 12:215-220(2001).
RL [2]
RP SEQUENCE FROM N.A.
RX Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RY Do M.-S., Song S.K.;
RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF069244; JMW6532.1.;
DR DDB: J017001394; R1P.
DR PIR: P00396; SHIGARICIN.
DR PRINTS: PR00396; SHIGARICIN.
KW Hydrolase; Toxin.
FT NON TER 1 1
FT TER 251 251
SQ SEQUENCE 251 AA; 28446 MW; 6DB5C3B18FAFE0 CRC64;

Matches 231: Conservative 3; Mismatches 20; Indels 2; Gaps 1;

QY 1 YERLRLRVTHQTQXKYEFRITLLRDYVSSGSPSNELPILROSTIIPVSDAQRFVLVELTN 60
DB 1 YERLRLRVTHQTQXKYEFRITLLRDYVSSGSPSNELPILROSTIIPVSDAQRFVLVELTN 60

QY 61 QGKDSKTAIDVTNXYVVAQAGQSYFLDAPRGAETHLPTGTDDSSLPKSGSYXDL 120
DB 61 QGKDSKTAIDVTNXYVVAQAGQSYFLDAPRGAETHLPTGTDDSSLPKSGSYXDL 120

QY 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQAKRSILILQWISBAARPNILMKXQ 180
DB 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQAKRSILILQWISBAARPNILMKXQ 180

QY 119 ERYAGRRDQIPLGIDGLICSVTALRPPGQNTQKRSILILQWISBAARPNILMKXQ 178
DB 119 ERYAGRRDQIPLGIDGLICSVTALRPPGQNTQKRSILILQWISBAARPNILMKXQ 178

QY 181 XINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 240
DB 181 XINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 240

QY 179 YINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 238
DB 179 YINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 238

QY 241 SLAINLFCGRSPSS 256
DB 241 SLAINLFCGRSPSS 256

QY 239 SLAINLFCGRSPSS 254
DB 239 SLAINLFCGRSPSS 254

RESULT 2

Q8W243 PRELIMINARY; PRT; 565 AA.

AC Q8W243: 2002 (Trembl). 20. Created.

DT 01-MAR-2002 (Trembl). 20. Last sequence update.

RT 01-OCT-2002 (Trembl). 20. Last sequence update.

RU VCA Isoform 2 (EC 3.2.2.22) (rRNA N-glycosylase).

CC Viscum album subsp. coloratum.

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Santalales; Viscaceae; Viscum.

OX NCBI_TaxID=159976;

RN [1]

RP SEQUENCE FROM N.A.

RA Park W.-B., Liu S.;

RT Cloning of Viscum album subsp. coloratum (Korean mistletoe)."

RT Biochem. Biophys. Res. Commun. 0 Genbank/DBJ databases.

RU Submitted (FBI-2002) to the EMBL/Genbank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

DR EMBL: AF669961; AL040417.1; "

DR InterPro: IPR000772; Ricin_B_lectin.

DR InterPro: IPR001574; RIP.

DR Pfam: PF00652; Ricin_B_lectin; 6.

DR Pfam: PF00161; RIP; 1.

DR PRINTS: PR00396; SHIGACIN.

DR SMART: SM00458; RICIN; 2. LECTIN; 2.

DR PROSITE: PS00231; RICIN_B_LECTIN; 2.

DR HYDROLASE; Signal; Toxin.

KA 223 POTENTIAL.

FT CHAIN 23 VCA ALPHA CHAIN.

FT CHAIN 309 565 VCA BETA CHAIN.

SO SEQUENCE 565 AA; 62401 MW; 591E394DM05F11 CRC64;

Query Match

Best Local Similarity 91.3%; Score 116; DB 10; Length 565;

Matches 224; Conservative 4; Mismatches 26; Indels 2; Gaps 1;

QY 1 YERLRLRVTHQTQXKYEFRITLLRDYVSSGSPSNELPILROSTIIPVSDAQRFVLVELTN 60
DB 1 YERLRLRVTHQTQXKYEFRITLLRDYVSSGSPSNELPILROSTIIPVSDAQRFVLVELTN 60

QY 61 QGKDSKTAIDVTNXYVVAQAGQSYFLDAPRGAETHLPTGTDDSSLPKSGSYXDL 120
DB 61 QGKDSKTAIDVTNXYVVAQAGQSYFLDAPRGAETHLPTGTDDSSLPKSGSYXDL 120

QY 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQAKRSILILQWISBAARPNILMKXQ 180
DB 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQAKRSILILQWISBAARPNILMKXQ 180

QY 119 ERYAGRRDQIPLGIDGLICSVTALRPPGQNTQKRSILILQWISBAARPNILMKXQ 178
DB 119 ERYAGRRDQIPLGIDGLICSVTALRPPGQNTQKRSILILQWISBAARPNILMKXQ 178

QY 181 XINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 240
DB 181 XINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 240

QY 179 YINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 238
DB 179 YINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 238

QY 241 SLAINLFCGRSPSS 256
DB 241 SLAINLFCGRSPSS 256

QY 239 SLAINLFCGRSPSS 254
DB 239 SLAINLFCGRSPSS 254

QY 181 XINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 240
DB 181 XINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 240

QY 212 YINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 271
DB 212 YINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 271

QY 241 SLAINLFCGRSPSS 256
DB 241 SLAINLFCGRSPSS 256

QY 272 SLAINLFCGRSPSS 287
DB 272 SLAINLFCGRSPSS 287

RESULT 3

Q8RXH7 PRELIMINARY; PRT; 249 AA.

AC Q8RXH7: 2002 (Trembl). 21. Created.

DT 01-JUN-2002 (Trembl). 21. Last sequence update.

RT 01-OCT-2002 (Trembl). 21. Last sequence update.

RU Viscum album (European mistletoe).

CC Viscum album (European mistletoe).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Santalales; Viscaceae; Viscum.

OX NCBI_TaxID=3972;

RN [1]

RP SEQUENCE FROM N.A.

RA Tisserand N., Grinyan A., Singh T.P.;

RT Viscum album (Indian) mRNA for Mistletoe Lectin Chain A, Isoform 2."

RT Submitted (FBI-2002) to the EMBL/Genbank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.

CC EMBL: AY081148; AL07005.1; "

DR InterPro: IPR001574; RIP.

DR Pfam: PF00161; RIP; 1.

DR HYDROLASE; Toxin.

FT NON-TER 249

FT NON-TER 249

SO SEQUENCE 249 AA; 27944 MW; 69FAFB7309A833 CRC64;

Query Match 91.0%; Score 113; DB 10; Length 249;

Best Local Similarity 88.8%; Pred. No. 3; 6e-117;

Matches 223; Conservative 3; Mismatches 23; Indels 2; Gaps 1;

QY 1 YERLRLRVTHQTQXKYEFRITLLRDYVSSGSPSNELPILROSTIIPVSDAQRFVLVELTN 60
DB 1 YERLRLRVTHQTQXKYEFRITLLRDYVSSGSPSNELPILROSTIIPVSDAQRFVLVELTN 60

QY 61 QGKDSKTAIDVTNXYVVAQAGQSYFLDAPRGAETHLPTGTDDSSLPKSGSYXDL 120
DB 61 QGKDSKTAIDVTNXYVVAQAGQSYFLDAPRGAETHLPTGTDDSSLPKSGSYXDL 120

QY 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQAKRSILILQWISBAARPNILMKXQ 180
DB 121 ERYAGRRDQIPLGIXOLGOSVALLKPKGSTRQAKRSILILQWISBAARPNILMKXQ 180

QY 119 ERYAGRRDQIPLGIDGLICSVTALRPPGQNTQKRSILILQWISBAARPNILMKXQ 178
DB 119 ERYAGRRDQIPLGIDGLICSVTALRPPGQNTQKRSILILQWISBAARPNILMKXQ 178

QY 181 XINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 240
DB 181 XINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 240

QY 179 YINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 238
DB 179 YINSGXSLPDXYMLELSTWQSQSTVOVSHSTGVPNNPKRLAIXXNPFVTLNXYRVA 238

QY 241 SLAINLFCGRSPSS 251
DB 241 SLAINLFCGRSPSS 251

QY 239 SLAINLFCGRSPSS 249
DB 239 SLAINLFCGRSPSS 249

RESULT 4

Q8LXK6 PRELIMINARY; PRT; 254 AA.

AC Q8LXK6: 2002 (Trembl). 22. Created.

DT 01-OCT-2002 (Trembl). 22. Last sequence update.

RT 01-MAR-2003 (Trembl). 23. Last annotation update.

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OK protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 19,7321 seconds
(without alignments)
3347,915 Million cell updates/sec

Title: US-09-601-667C-41

Score: 152
Sequence: 1 YERARLRYHOTGKRYFR.....XTASALMLFVCGEPSSS 256

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Minimum Match 10%

Database: Listing first 45 summaries

1: sp.archaea:*

2: sp.bacteria:*

3: sp.fungi:*

4: sp.human:*

5: sp.invertebrate:*

6: sp.mammal:*

7: sp.muc:*

8: sp.outgroup:*

9: sp.outgroup:*

10: sp.plant:*

11: sp.virus:*

12: sp.virus:*

13: sp.vertibrate:*

14: sp.unclassified:*

15: sp.virus:*

16: sp.bacteriapi:*

17: sp.archaeapi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1147	93.8	531	10	Q8RXH6	Q8RXH6 viscum albu
2	1116	91.3	565	10	Q8W243	Q8W243 viscum albu
3	1113	91.0	249	10	Q8RXH7	Q8RXH7 viscum albu
4	1024	82.5	248	10	Q8LXOC	Q8LXOC viscum albu
5	977	79.9	251	10	Q8LXOC	Q8LXOC viscum albu
6	977	79.9	251	10	Q8LXOC	Q8LXOC viscum albu
7	467	38.2	252	10	Q8R761	Q8R761 abrus prec
8	461	37.7	251	10	Q8G237	Q8G237 abrus prec
9	460	37.6	251	10	Q8G237	Q8G237 abrus prec
10	454	37.1	251	10	Q8G235	Q8G235 abrus prec
11	443	36.2	252	10	Q8R760	Q8R760 abrus prec
12	428.5	35.0	580	10	Q94BW3	Q94BW3 cinnaomum
13	428.5	35.0	580	10	Q94BW4	Q94BW4 cinnaomum
14	425	34.8	528	10	Q8G076	Q8G076 abrus prec
15	419.5	34.3	549	10	Q8FV22	Q8FV22 cinnaomum
16	418.5	34.2	551	10	Q94BW5	Q94BW5 cinnaomum

17	380	31.1	547	10	Q9W6E9	Q9W6E9 abrus prec
18	374	30.6	570	10	Q41358	Q41358 sambucus ni
19	370	30.3	541	10	Q41174	Q41174 ricinus com
20	367.0	30.0	540	10	Q24115	Q24115 sambucus ni
21	367.0	29.9	540	10	Q24115	Q24115 sambucus ni
22	362.5	29.6	565	10	Q04071	Q04071 sambucus ni
23	361	29.5	592	10	Q8W287	Q8W287 iris hollan
24	356	29.1	573	10	Q8W288	Q8W288 iris hollan
25	350.5	28.7	563	10	Q04367	Q04367 sambucus ni
26	347	28.4	566	10	Q04072	Q04072 sambucus ni
27	345	28.2	569	10	Q93543	Q93543 sambucus ni
28	339	27.6	563	10	Q94582	Q94582 sambucus ni
29	338	27.5	563	10	Q94582	Q94582 sambucus ni
30	334.5	27.4	564	10	Q94582	Q94582 sambucus ni
31	327	26.7	564	10	Q94582	Q94582 sambucus ni
32	327	26.7	564	10	Q94582	Q94582 sambucus ni
33	286	24.2	247	10	Q91R83	Q91R83 trichosan
34	286	24.2	270	10	Q8GV09	Q8GV09 trichosan
35	296	24.2	277	10	Q8GV09	Q8GV09 trichosan
36	296	24.2	289	10	Q41216	Q41216 trichosan
37	294	24.0	277	10	Q8GV11	Q8GV11 trichosan
38	289.5	23.7	300	10	Q04357	Q04357 iris hollan
39	289	23.6	275	10	Q8H1Y4	Q8H1Y4 gynosetema
40	288	23.5	277	10	Q8H1Y5	Q8H1Y5 gynosetema
41	288	23.5	603	10	Q9W653	Q9W653 gynosetema
42	286.5	23.4	277	10	Q8GV10	Q8GV10 gynosetema
43	286.5	23.4	300	10	Q94356	Q94356 iris hollan
44	286.5	23.4	300	10	Q94356	Q94356 iris hollan
45	276.5	22.6	298	10	Q04358	Q04358 iris hollan

ALIGNMENTS

RESULT 1

Q8RXH6 PRELIMINARY: FFT, 531 AA.

AC Q8RXH6: 2002 (TRENBERG, 21, Last sequence update)

DT 01-JUN-2002 (TRENBERG, 21, Last sequence update)

DT 01-MAR-2003 (TRENBERG, 23, Last annotation update)

DE Lactin chain A isoform 1 (EC 3.2.2.22) (TRNA N-glycosylase)

DE (Fragment)

OS Viscum album (European mistletoe)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;

OC Santalales; Viscaceae; Viscum.

NCBI_TaxID=3972;

NCBI_TaxID=3972;

NCBI_TaxID=3972;

NCBI_TaxID=3972;

NCBI_TaxID=3972;

NCBI_TaxID=3972;

NCBI_TaxID=3972;

NCBI_TaxID=3972;

NCBI_TaxID=3972;

NCBI_TaxID=3972;

NCBI_TaxID=3972;

NCBI_TaxID=3972;

Query Match 93.8%; Score 1147; DB 10; Length 531;
Best Local Similarity 90.2%; Pred. No. 1.5e-120;

Thu Dec 11 16:10:00 2003

us-09-601-667c-41.rsp

CC EMBL: AB045560; BAB19677.1; -.
DR HSP; P16094; IARC.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGRICIN.
DR PROSITE: PS00275; SHIGA RICIN; 1.
KV Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
toxin; Signal.
FT SIGNAL. 1 21
FT CDS. 22 286
FT ACT SITE 185 185
FT CARBOHYD 103 103
FT CARBOHYD 110 110
FT CARBOHYD 252 252
SQ SEQUENCE 286 AA; 31771 MW; 4EPD4966E04DA1 CRC64;
Query Match 21.94; Score 267.5; DB 1; Length 286;
Best Local Similarity 31.64; Pred. No. 4.8e-22;
Matches 75; Conservative 45; Mismatches 102; Indels 15; Gaps 8;
DB 17 YRRTLLRDVSSGSFSENPILRGSTPYSDQREYVELTQGXSTAAIDVTKY 76
40 YKRTLSRNALPNAGIYNIPLVPS--ISGSRYLMDQSNVEGNTTAAVDVTVNY 96
QY 77 VVAYQAGDSYFLDA-PRGAEHLFGFTEDRSSLPKXSYDLERYA-GHDDQIFLG 134
DB 97 IMGILVNGTSYFNETDAQAKFVQGY--KSITLPYSGNYQLQSVAREHDSIFLG 154
QY 135 XQLQSYXALRPGSGSTPYQANSILILQMTSEARFNPILMRKXINS-GKSPLEPKY 193
DB 155 MALDQALSTLY--YDSKSPYAFVLVLTQTAEMARKYI--EQQLIDRSVSKYPLA 209
QY 194 KSELETSGQOSTQV--HSDGVNPPRLAIXKNTYTLANRYVIAISALMLFV 248
DB 210 AISEENWELSKQIQIKSNNGQFQPKIINDKGIQILEVNVSSIVVTNIMLL 266

Search completed: December 11, 2003, 14:09:10
Job time : 5.48263 secs

QY 73 TNYVYVAVQAGDQSYFLRDPAPGAEHTLFTGTTRDRSSLPFVGSYXDLERYAG-HRDQIP 131
 DB 86 TNYVYVAVRDAVSYFELTPAPKFLIPGTVYK-LPFGSKYDKQSYVGRDQITE 143
 QY 132 LQIXQIQSGVAKLRPGSGTRKQKRSILILQWISKAAPNFIIMKXKQIKNGKSLFD 191
 DB 144 LQIPALSSAIIIMVY--YDQSTAAALVLIQCTAPKARKYIKQYSHISS--NYEIN 199
 QY 192 XYMLEPETSNGQOSTOVQ--SRDPVNNPKELAKXGNFYTLXAVXK--VYASLAINL 246
 DB 200 QAVISLENKMGALSROIQIANRTGQGFENVELYNDQTRSVTTSAGVYKRIILL 259
 QY 247 F 247
 DB 260 Y 260

RESULT 14
 RIPC_GELMU
 ID_RIPC_GELMU STANDARD; PRT; 316 AA.
 AC P3186;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein gelonin precursor (rRNA N-glycosidase)
 DB (EC 3.2.2.22).
 GN GEL.
 OS Gelonium multiflorum (Baphorbaceae himalaica).
 CC Ribosome-inactivating protein (RIP) family; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliopsida; Eudicotyledons; Rosidae;
 CC euroside I; Malpighiales; Baphorbaceae; Gelonium.
 OK NCBI_TaxID:3979;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94085781; PubMed=7916721;
 RA Nolan P.A., Garrison D.A., Better M.,
 RT "Cloning and expression of a gene encoding gelonin, a ribosome-
 RT inactivating protein from Gelonium multiflorum."
 RL Int. J. Pept. Protein Res. 33:263-267(1989).
 RN [3]
 RP SEQUENCE OF 47-93.
 RC TISSUE=Seed;
 RX MEDLINE=8932691; PubMed=2753596;
 RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stille F., Scia M.,
 RT "N-terminal sequence of some ribosome-inactivating proteins."
 RL Int. J. Pept. Protein Res. 33:263-267(1989).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RX MEDLINE=9533189; PubMed=7608911;
 RA Kuman K.V., Nair B., Sackymamthy P., Misquith S., Suroja A.,
 RT "X-ray structure of gelonin at 1.8-A resolution."
 RL J. Mol. Biol. 250:368-380(1995).
 CC -|- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -|- SUBUNIT: Homodimer.
 CC -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC
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 CC EMBL: L12243; AAA16312.1; -
 CC PIR: J70753; J70753.
 CC DR HSSE; P09989; IMR.
 CC InterPro: IPR001574; RIP.

DR PFAM: PRO0161; RIP; 1.
 DR PRINTS: PRO0396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; FALSE NEG.
 DR Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
 KW glycoprotein.
 FT SIGNAL 1 26
 FT PROPE 27 26
 FT PROPE 27 26
 FT PROPE 28 316
 FT DISULFID 90 96
 FT CARBOHYD 235 235
 FT ACT SITE 212 212
 FT CONFLICT 90 90 C -> K (IN REF. 2).
 FT CONFLICT 93 93 P -> D (IN REF. 2).
 SO SEQUENCE 316 AA; 35418 MW; 1252FE710901B85 CRC64;
 Query Match 22.4%; Score 273.5; DB 1; Length 316;
 Best local similarity 33.3%; Pred. No. 1,26-22;
 Matches 87; Conservative 33; Mismatches 110; Indels 31; Gaps 7;
 QY 9 THQTGKEVREFTLADVUSGSSNSU-----PLFQSTIPVSDQFVL 55
 DB 42 TSKTGLDVSFKGATITVYVNLHRAVLAEPGNSHGIDPLRKKC--DPGKCFVL 99
 QY 56 VELTRQKQSDXTAIDVNNVYVAVQAGDQSYFLRDPAPGAEHTLFTGTTRDRSSLPFXG 115
 DB 100 VALSDNQGLAETADVTSVYVGVYVQVANSYFKAAPALYGLFKVITKTR-LHFGG 157
 QY 116 SYXDLERYAGHDQIPILGIXDL--IGSVAKLRPGSGTRKQKRSILILQWISKAAPN 171
 DB 158 STPSLSEKRYKERTDQERFLAQIKQIDBNALDNKRTLSLILVLYQVSDAKRT 217
 QY 172 ---NIIIMKRXQXINSQXFLPDXMTLEFTSGQOSTOVQHS--TDVFNPKRLAIXXG 227
 DB 218 FENQIRNPFQRIK-----PANNTISLENKMGKLSFQITSGANWFESEVLEERANG 271
 QY 228 NFVTLANRYVYASLAINMFV 248
 DB 272 KKYVTAVDQVETALKEV 292

RESULT 15
 RIPC_CUCFI
 ID_RIPC_CUCFI STANDARD; PRT; 286 AA.
 AC Q9PRX4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
 DB (EC 3.2.2.22).
 OS Cucumis figetis.
 CC Cucurbitales; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliopsida; Eudicotyledons; Core eudicots; Rosidae;
 CC euroside I; Malpighiales; Cucurbitaceae; Cucumis.
 OK NCBI_TaxID:131071;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada T., Ohki S.T., Osaki T.,
 RT "Cloning and analysis of a cDNA coding a putative ribosome-
 RT inactivating protein from Cucumis figetis."
 RL Plant Biotechnol. 17:337-340(2000).
 CC -|- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -|- SUBUNIT: Homodimer.
 CC -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC
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CC eucosids I; Cucurbitales; Cucurbitaceae; Momordica.
OC NCBI_Taxid=3672;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=seed;
RX MEDLINE=9128081; PubMed=1408771;
RZ Molecular biological and preliminary structural analysis of
RT "momordin II, a ribosome inactivating protein from Momordica
RL balsamina, is homologous to other plant proteins".
RL Molec Acids Res. 20:4662-4663(1992).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
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CC -----
DR ENEM, 211175; CAAB166.1; .
DR ER; S2560; S2560;
DR IPRODPO; IPROD1574; RIP.
DR PRNMS; PPO0396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
KV 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 286
FT FT
FT ACT SITE 181 B' SIMILARITY
SQ SEQUENCE 266 AA, 32031 MW, 3689FPRIAE62986 CC64;

Query Match 23.0%; Score 281; DI 1; Length 286;
Best Local Similarity 33.9%; Pred. No. 1.5e-23;
Matches 78; Conservative 44; Mismatches 88; Indels 20; Gaps 9;

QY 13 TKCYPRFITLADVYSGSGPSN--EIPLRQSTIPEVDNQPFVLVEETNGGXNTA 69
DY DK TKCYTRTF--EDPRAFLPSHFHYDTPLHLSIT--ISDSRFILDLTLSDAYSTAVSHA 86
QY 70 IDPMNVVAAYAKOGQSPPIAPBAQRATHEFGCTGTSSAPFKSYXCDLRYANW-R 127
DY 87 IDVMNVVVAAVRDDVPKSPFAVNIILFGR-KTLPTPTGNTELQT-NALKR 143
QY 148 DDPFGIXGLIQSVVALXPKGSRTKQASILLTIOWISAPARENIIMXKQIKNSXS 187
DY 144 ENIDGIGPLMSAITLTFFLYNAQSPA--LVLLQTTLPAPARKXIRERVAKYV-ATN 199
QY 168 FLPPDXLMLETSWGQSTGV--GHSTGGVFNNPYALAIKGFVTLANV 235
DY 200 FEFNALIISLENQMSLSNDIIFLAQKGQSNRPFDLPFRTERPGVNV 249

RESULT 12
ID RIP1_BRADI STANDARD; FRU, 290 AA.
AC P313193; Q9S913;
DI RIP1_BRADI
DR 01-OCT-1993 (Rel. 27, Created)
DR 16-OCT-2001 (Rel. 40, Last sequence update)
DR 28-FEB-2003 (Rel. 41, Last annotation update)
DR (RefSeq) 3-DEC-2002 (RefSeq) 3-DEC-2002 (RefSeq)
DR BRYONIA dioica (Red bryonia).
DR Eukaryotes; Viridiplantae; streptophyta; Embryophyta; Tracheophytes;
OC Spermatophyta; Magnoliophyta; eucoicladomads; core eucoicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Bryonia.
OC NCBI_Taxid=3672;
RN [1]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC TISSUE=leaf;
RX MEDLINE=9128081; PubMed=9115986;
RZ Molecular biological and preliminary structural analysis of
RT "momordin II, a ribosome inactivating protein from the plant
RL Balsaminia dioica".
RL Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
RN [1]
RP SEQUENCE OF 24-66.
RC TISSUE=seed;
RX MEDLINE=8932691; PubMed=2753596;
RZ Molecular biological and preliminary structural analysis of
RT "bryodin bryodin I, a ribosome-inactivating protein from the plant
RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
RN [1]
RP SEQUENCE OF 24-43.
RC TISSUE=seed;
RX MEDLINE=95151812; PubMed=7849072;
RZ Molecular biological and preliminary structural analysis of
RT "bryodin bryodin I, a ribosome-inactivating protein from the plant
RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
RN [1]
RP SEQUENCE OF 24-43.
RC TISSUE=seed;
RX MEDLINE=95151812; PubMed=7849072;
RZ Molecular biological and preliminary structural analysis of
RT "bryodin bryodin I, a ribosome-inactivating protein from the plant
RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
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RX MEDLINE=95151812; PubMed=7849072;
RZ Molecular biological and preliminary structural analysis of
RT "bryodin bryodin I, a ribosome-inactivating protein from the plant
RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
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RZ Molecular biological and preliminary structural analysis of
RT "bryodin bryodin I, a ribosome-inactivating protein from the plant
RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
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RX MEDLINE=95151812; PubMed=7849072;
RZ Molecular biological and preliminary structural analysis of
RT "bryodin bryodin I, a ribosome-inactivating protein from the plant
RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
RN [1]
RP SEQUENCE OF 24-43.
RC TISSUE=seed;
RX MEDLINE=95151812; PubMed=7849072;
RZ Molecular biological and preliminary structural analysis of
RT "bryodin bryodin I, a ribosome-inactivating protein from the plant
RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
RN [1]
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RZ Molecular biological and preliminary structural analysis of
RT "bryodin bryodin I, a ribosome-inactivating protein from the plant
RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
RN [1]
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RX MEDLINE=95151812; PubMed=7849072;
RZ Molecular biological and preliminary structural analysis of
RT "bryodin bryodin I, a ribosome-inactivating protein from the plant
RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
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CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
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RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
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RT "bryodin bryodin I, a ribosome-inactivating protein from the plant
RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
RN [1]
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RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
RN [1]
RP SEQUENCE OF 24-43.
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RX MEDLINE=95151812; PubMed=7849072;
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RT "bryodin bryodin I, a ribosome-inactivating protein from the plant
RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
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RN [1]
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RL Balsaminia dioica".
RN [1]
RP Biochemistry 36:3095-3103(1997).
CC (2)
CC SEQUENCE FROM N.A.
CC Sigall C.B.;
RT cloning and expression of a gene encoding bryodin I from Bryonia
RT dioica." and expression of a gene encoding bryodin I from Bryonia
RN [1]
RP SEQUENCE OF 24-43.
RC TISSUE

FT HELIX 109 114
 FT TURN 115 117
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 FT STRAND 124 127
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Query Match
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 Matches 83; Conservative 50; Mismatches 93; Indels 14; Gaps 9;

QY 13 TCXEFPRFTLLADYVSSGSFSENEIFLAKOGTIPVSDAGRFVVELTPOCKDXKTAALIV 72
 DB 33 TSSYGVFISNLRKALPHEKXYDIFLR-SLPGS--CRYALHLTNVADETISVALIV 89
 QY 73 TNYVVAOAGDQSYFLRDA-FRGAETHLFTGTDRSSLPFGSYXDLERYAGH-RDQI 130
 DB 90 TNYVINGVAGDTSYFPMESKATEAKVYFDMAR-KVLPISNTERLQPAAGKINENI 148
 QY 131 FLGIXOLIOSYALAKXPGOSTXQNSITLITONSPARENPILMRKQINSXSELP 190
 DB 149 FLGIPALDSATITLTPYNNAS--ASALMVLIQSTSEAKVYFEEQIGKVDK--TFEP 204
 QY 191 DXYWLELTSGQOSTVO--HSTDGVNPNPKALIXGNFTLXNVX--VIASLAINI 246
 DB 205 SLATISLNSMALSKOIQTASTNNGEFPVVLINQKQKQVITTVADGVTSIALLL 264

RESULT 10
 RIPS-TXIKI
 ID RIPS-TXIKI STANDARD; PRT: 289 AA.
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein karasurin precursor (rRNA
 DE N-glycosidase) (EC 3.2.2.22)
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC eucotyledons I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=3677;
 RX MEDLINE=9735652; PubMed=9212998;
 RP SEQUENCE FROM N.A.
 RP TISSUE=Root tuber;
 RA Minkami H., Iida K., Kondo T., Ogihara Y.;
 RT "Cloning and bacterial expression of a gene encoding ribosome-
 inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
 kirilowii var. japonica."

RL Biol. Pharm. Bull. 20:711-713(1997).
 RN [2]
 RP SEQUENCE OF 24-270. PubMed=1914000;
 RX MEDLINE=92005921; PubMed=1914000;
 RA TOKOKAWA S., TAKEEDA T., KATO T., MAKIYASHI K., OGIHARA Y.;
 RT "The complete amino acid sequence of an abortifacient protein,
 karasurin-A, from Trichosanthes kirilowii var. japonica."
 RL Chem. Pharm. Bull. 39:1244-1249(1991).
 CC -1- FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC
 CC 60S RIBOSOMAL SUBUNIT.
 CC -1- CATALYTIC ACTIVITY: Endonucleolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.

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CC EMBL; AB000666; BAA21786.1;
 DR PIR; JCS606; JCS606.
 DR PIR; J00393; J00393.
 DR HSSP; P09989; IAKU.
 DR INTERPRO; IPR00035; RIP.
 DR PROSITE; PS00150; RIP.
 DR PRINTS; PR00196; SHIGARICIN.
 DR PROSITE; PS00275; SHIGARICIN.
 DR Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
 KW Toxin; Signal.

FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 270 KARASURIN-C.
 FT CHAIN 24 270 KARASURIN-A.
 FT PROPEP 271 289 REMOVED IN NATURE FORM.
 FT ACT SITE 183 183 51 SIMILARITY.
 SQ SEQUENCE 289 AA; 31704 MW; 883D35242867B26 CRC64;

Query Match
 Basic Local Similarity 35.4%; Score 300; DB 1; Length 289;
 Matches 85; Conservative 46; Mismatches 95; Indels 14; Gaps 9;

QY 13 TCXEFPRFTLLADYVSSGSFSENEIFLAKOGTIPVSDAGRFVVELTPOCKDXKTAALIV 72
 DB 33 TSSYGVFISNLRKALPHEKXYDIFLR-STLPGS--CRYALHLTNVADETISVALIV 89
 QY 73 TNYVVAOAGDQSYFLRDA-FRGAETHLFTGTDRSSLPFGSYXDLERYAGH-RDQI 130
 DB 90 TNYVINGVAGDTSYFPMESKATEAKVYFDMAR-KVLPISNTERLQPAAGKINENI 148
 QY 131 FLGIXOLIOSYALAKXPGOSTXQNSITLITONSPARENPILMRKQINSXSELP 190
 DB 149 FLGIPALDSATITLTPYNNAS--ASALMVLIQSTSEAKVYFEEQIGKVDK--TFEP 204
 QY 191 DXYWLELTSGQOSTVO--HSTDGVNPNPKALIXGNFTLXNVX--VIASLAINI 246
 DB 205 SLATISLNSMALSKOIQTASTNNGEFPVVLINQKQKQVITTVADGVTSIALLL 264

RESULT 11
 RIPS-TXIKI
 ID RIPS-TXIKI STANDARD; PRT: 286 AA.
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribosome-inactivating protein momordin II precursor (rRNA
 DE N-glycosidase) (EC 3.2.2.22)
 OS Momordica balsamina (Bitter melon).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC

Best Local Similarity 36.6%; Fred. No. 1.6e-29;
Matches 89; Conservative 37; Mismatches 99; Indels 18; Gaps 9;

QY 13 TGEKFRPTLTADYSSGS--FSNEIPILKQSTTFVSDMORFVLTENCKQKXTALD 71
Db 32 TQATFTYINLNTYVIGTFRVYDIPVLRNAGLA--RQVLTINNGESYVALD 88
QY 72 YLXXVYVYAGDQSYFLADAPRGAETHLPTFTEDSLSPKSGYXDLERVAGH--RDQ 129
Db 89 VVNVYVYVYRANVYFLADASTFANNVLPAGINVR--LPVGNVGLSTAGIRSEN 146
QY 130 ILGIKXLIQSYVAL--KXPQGSTKQARSLILQWISSEARPNFIMEXQKXNGSX 187
Db 147 IELGPEELISANNFHNHFGTSV--PRAFTYIQTVESEARPKYIKQVSE--NVGTX 201
QY 188 FLDPXYLLELSNQGQSYQV--HSTQGFNNEXKLTXGNFTLXNVR--VLSLAI 244
Db 202 KEDPAPFLSQNNMOSLSQDILQVTRQGRARFVETFTVNTFTVNVSPVQKIDL 261
QY 245 MLP 247
Db 262 LLY 264

RESULT 9
RPT TRKI STANDARD; PRT; 289 AA.
AC 60938; 1988 (Rel. 10, Created)
DT 01-NOV-1996 (Rel. 16, Last annotation update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribosome-inactivating protein alpha-trichosanthin precursor
DE (tRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).
OS Trichosanthin Kirilowii (Mongolian snake-gourd).
OC Bukariota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
NCBI TaxID=3677;
RX 11
RP SEQUENCE FROM N.A.
RA SHAW P.C., YUNG M.H., ZHU R.H., HO W.K.K., NG T.B., YEUNG H.W.;
RQ MEDLINE=9115657; PubMed=1993291.
RT Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
RL "Cloning of trichosanthin cDNA and its expression in *Escherichia coli*."; Gene 97:267-272 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Maximowicz; TISSUE=Leaf;
RX MEDLINE=9025790; PubMed=2341400;
RA CHOW T., FELDMAN R.A., LOWETT M., PLATAK M.;
RT Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
RL U. Biol. Chem. 265:8670-8674 (1990).
RN [3]
RP SEQUENCE OF 24-270.
RC STRAIN=Maximowicz; TISSUE=Tuberous root;
RX MEDLINE=9025789; PubMed=2341399;
RA COLLINS E.J., ROBERTUS J.D., LOPESTI M., STONE K.L., WILLIAMS K.R.,
RT "Primary amino acid sequence of alpha-trichosanthin and molecular
RL models for abrin A-chain and alpha-trichosanthin."; J. Biol. Chem. 265:8665-8669 (1990).
RN [4]
RP SEQUENCE OF 24-270.
RC TISSUE=Tuberous root;
RA WANG Y., QIAN R.O., GU Z.W., JIN S.W., ZHANG L.O., XIA Z.X.,
RT "Scientific evaluation of Tian Hua Fan (THF): history, chemistry and
RL application."; Pure Appl. Chem. 58:789-798 (1996).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
RX MEDLINE=94344957; PubMed=8066085;
RA ZHOU F., FU Z., CHEN M., LIN Y., PAN K.;
RT "Structure of trichosanthin at 1.88-A resolution."; Proteins 19:14-15 (1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RA HUANG O., LIU S., FANG Y., JIN S., WANG Y.;
RT "Studies on crystal structures, active-centre geometry and
RL dequating mechanism of two ribosome-inactivating proteins."; Biochem. J. 309:285-298 (1995).
CC -1- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
CC CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
CC INACTIVATES ENDOCYTIC 60S RIBOSOMAL SUBUNTS.
CC -1- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- ENZYME CLASSIFICATION: EC 3.2.2.22
CC -1- ENZYME: RIBOSOME-INACTIVATING PROTEIN FAMILY.
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DR EMBL: M4458; AAA1207.1; -
DR PIR: J00564; A1272.
DR PDB: 1MRK; 07-FEB-95.
DR PDB: 1TOS; 10-JUL-95.
DR PDB: 1I4G; 28-JAN-03.
DR PDB: 1QD2; 24-APR-00.
DR InterPro: IPR001574; RFP.
DR Pfam: PF00161; RFP.1.
DR PRINTS: PF00396; SHOGKICIN.
DR PROSITE: PS00273; SHOGKICIN.1.
DR Trichosanthin is a protein that inhibits protein synthesis inhibitor; hydrolase;
DR Trichosanthin is a protein that inhibits protein synthesis inhibitor; hydrolase;
DR Trichosanthin is a protein that inhibits protein synthesis inhibitor; hydrolase;
FT CHAIN 24 270
FT PROPEP 271 289
FT ACT_SITE 183 183
FT CONFLICT 57 60
FT CONFLICT 82 84
FT CONFLICT 87 87
FT CONFLICT 92 92
FT CONFLICT 102 104
FT CONFLICT 105 106
FT CONFLICT 125 126
FT CONFLICT 231 231
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FT CONFLICT 246 246
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FT TURN 25 28
FT TURN 30 31
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FT TURN 47 47
FT TURN 50 54
FT TURN 52 56
FT TURN 56 66
FT TURN 66 69
FT TURN 70 76
FT TURN 78 79
FT TURN 82 82
FT TURN 89 92
FT TURN 93 99
FT TURN 100 101
FT TURN 102 105

Thu Dec 11 16:10:00 2003

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RA MEDLINE=65374222; PubMed=8705133; Monzingo A.F., Pascal J.M.,
 RA Day P.O., Ernst S.R., Frankel A.B.,
 RA Molinari-Vincent M.C., Robertus U.D.,
 RA "Pure and activity of an active site substitution of ricin A
 RA chain".
 RL Biochemistry 35:11098-1103 (1996).
 RL [13]
 RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS) OF A-CHAIN.
 RP MEDLINE=97240820; PubMed=9085280;
 RA Yan Y., Hollis T., Swint M., Day P., Monzingo A.F., Milne G.W.,
 RA Robertus U.D.,
 RA "Structure-based identification of a ricin inhibitor".
 RA U. Mol. Biol. 266:1043-1049 (1997).
 RL MEDLINE=93165632; PubMed=1287657;
 RL MEDLINE=93165632; PubMed=1287657;
 RL Kin Y., Robertus U.D.,
 RA "Analysis of several key active site residues of ricin A chain by
 RA mutagenesis and X-ray crystallography".
 RL Protein Eng. 5:775-779 (1992).
 CC -1- FUNCTION: Ricin is highly toxic to animal cells and to a lesser
 CC extent to plant cells. The A chain is responsible for of 608
 CC protein synthesis through the catalytic residues that removes a
 CC specific adenine residue from an exposed loop of 28S ribosomal
 CC RNA. As this loop is involved in the binding of elongation
 CC factors, the modified ribosomes are unable to support protein
 CC synthesis. The A chain can inactivate a few thousand ribosomes
 CC per minute, thus inactivating them faster than the cell can make
 CC new ones. A single A-chain molecule can therefore kill an animal
 CC cell. The B chain binds to cell receptors and facilitates the
 CC entry into the cell of the A chain; B chains are also responsible
 CC for cell agglutination (lectin activity). It binds to beta-D-
 CC galactopyranoside moieties and hydrolysis of the N-glycosidic bond at one
 CC -1- specific adenosine on the 28S rRNA.
 CC -1- SUGAR: Disulfide-linked dimer of A and B chains.
 CC -1- DOMAIN: The B chain is composed of two domains, each domain
 CC consists of 3 homologous subdomains (alpha, beta, gamma).
 CC -1- PM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 271.
 CC MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS A RIBOSOME INACTIVATING DOMAIN.
 CC -1- WITH THE SEQUENCE TRANSLATED FROM DNM (REF.1, REF.2 AND REF.3).
 CC -1- DATABASE: NMR-protein SpotLight.
 CC NOTE- Issue 31 of expasy.org/spotlight/articles/spl1031.html".
 CC
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 CC
 DR EMBL: X03179; CA226939.1; -
 DR EMBL: X52908; CA337095.1; -
 DR EMBL: X02388; CA226939.1; -
 DR EMBL: A12892; CA010058.1; -
 DR PIR: A24041; R1CSD.
 DR PDB: 2AA1; 3I-VAN-94.
 DR PDB: 1AB9; 3I-OAN-94.
 DR PDB: 1F85; 3I-OCT-93.
 DR PDB: 11F7; 1I-VAN-98.
 DR PDB: 11F7; 1I-VAN-98.
 DR PDB: 1R7C; 3I-OCT-93.
 DR PDB: 10B5; 16-JUN-97.
 DR PDB: 10B7; 16-JUN-97.
 DR PDB: 1AB5; 02-SEP-95.

[illegible]

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FT DOMAIN 272 399 RICIN B-TYPE LECTIN 1.
FT DOMAIN 402 526 RICIN B-TYPE LECTIN 2.
FT REPEAT 282 324 1-ALPHA.
FT REPEAT 325 364 1-BETA.
FT REPEAT 368 400 2-ALPHA.
FT REPEAT 413 448 2-BETA.
FT REPEAT 452 486 2-GAMMA.
FT REPEAT 494 527 2-DELTA.
FT ACT SITE 163 163
FT DISULFID 246 268 INTERCHAIN (BY SIMILARITY).
FT DISULFID 285 304 BY SIMILARITY.
FT DISULFID 328 345 BY SIMILARITY.
FT DISULFID 416 425 BY SIMILARITY.
FT DISULFID 455 472 BY SIMILARITY.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
FT CARBOHYD 110 110 N-LINKED (GLUCNA. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLUCNA. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLUCNA. . .) (POTENTIAL).
FT CONFLICT 291 291 D -> N (IN REF. 2).
FT CONFLICT 350 351 AE -> PO (IN REF. 2).
FT CONFLICT 378 378 S -> N (IN REF. 2).
FT CONFLICT 426 426 L -> M (IN REF. 2).
FT CONFLICT 428 428 Y -> D (IN REF. 2).
FT CONFLICT 431 431 N -> S (IN REF. 2).
FT CONFLICT 484 484 R -> K (IN REF. 2).
FT CONFLICT 491 491 H -> S (IN REF. 2).
FT CONFLICT 493 493 R -> G (IN REF. 2).
FT CONFLICT 503 503 R -> Q (IN REF. 2).
FT CONFLICT 513 513 H -> W (IN REF. 2).
FT CONFLICT 516 516 H -> T (IN REF. 2).
SQ SEQUENCE 527 AA; 59114 MW; 3253A490C9494A CRC64;
Query Match 33.1%; Score 404.5; DB 1; Length 527;
Best Local Similarity 41.2%; Pred. No. 7,1e-37;
Matches 100; Conservative 38; Mismatches 98; Indels 7; Gaps 6;
QY 9 THQTKXIRPFTLLADYVSSGSPFNEILPQSTIPSDAQFVLYELNKGDSXIA 68
DB 9 TKGATQSGVQKTEFKRQRL-NGGLHGHVPLVDPT-TLQSRNRYISVELNSNDTSIEA 66
QY 69 AIDVTXVYVAVYQAGDQSYFADAPRGAETLFTGTFRDSELPFGSGYKDERACH-R 127
DB 67 GIVSNAYVAVYAGNRSYFLADAFISARFLPTGT--QVSYLFFNGSYIDLERLAQCR 124
QY 128 DQPLGIXQILQGVYALKKPKGSTRQKRSILLQWISPAARFNIIMKRXQINSXS 187
DB 125 QQPLGALQALPAISFLQSG-GRDQSIKALIVIIQWASBARFRISRVGVSRTNIA 183
QY 188 FLEPXYMELSTWQSGQVQVHSTGCPFNKPKALIKKXFTYLLAV-XVYIAALIM 246
DB 184 RPPDAMISLNNWNLNLSGVQVQDPTFRNATLISYNNQVTVVSLTHQSVYALIM 243
QY 247 FVC 249
DB 244 FVC 246
RESULT 5
R101 RICINCOO STANDARD; PRT; 576 AA.
X1 128279; Q02890; Bel. 01; Created)
X2 218717; 1986 (Bel. 01; last sequence update)
DT 11-NOV-1987 (Bel. 05; last annotation update)
DE Ricin precursor (Contains: Ricin A chain (rRNA N-glycosylase)
DE (EC 3.2.2.22); Ricin B chain).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids I; Malpighiales; Euphorbiaceae; Ricinus.

OX NCBI_TaxID=3988;
RP SEQUENCE FROM N.A.
RX MEDLINE=86067214; PubMed=2999712;
RA Hailing K.C., Hailing A.C., Murray E.E., Ladin B.F., Houston L.L.,
R1 "Genomic cloning and characterization of a ricin gene from Ricinus
R2 communis.";
R3 Nucleic Acids Res. 13:8019-8033(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92163016; PubMed=1371405;
RA Tregear J.W., Roberts L.W.;
R1 "The lectin gene family of Ricinus communis: cloning of a functional
R2 ricin gene and three lectin pseudogenes.";
R3 Plant Mol. Biol. 18:515-525(1992).
RN [3]
RP SEQUENCE OF 12-576 FROM N.A.
RX MEDLINE=8517472; PubMed=1338723;
RA Lamb A., Roberts L.W., Lord J.W.;
R1 "Nucleotide sequence of cloned cDNA coding for preproricin.";
R2 Eur. J. Biochem. 148:265-270(1985).
RN [4]
RP SEQUENCE OF 36-302.
RX Yoshitake S., Funatsu G., Funatsu M.;
R1 "Isolation and sequences of peptic peptides, and the complete
R2 sequence of the chain of ricin-D.";
R3 Agric. Biol. Chem. 42:1267-1274(1978).
RN [5]
RP SEQUENCE OF 315-576.
RX Funatsu G., Kimura M., Funatsu M.;
R1 "Primary structure of Ala chain of ricin D.";
R2 Agric. Biol. Chem. 43:2221-2224(1979).
RN [6]
RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
RX MEDLINE=90344223; PubMed=1368317;
RA Kimura Y., Kusonoki H., Tada M., Takagi S., Funatsu G.;
R1 "Structural analyses of sugar chains from ricin A-chain variant.";
R2 Agric. Biol. Chem. 54:157-162(1990).
RN [7]
RP MEDLINE=21480122; PubMed=11595634;
RX Olanes S., Kozlov J.V.;
R1 "Ricin.";
R2 Toxicol. 39:1723-1728(2001).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=91655983; PubMed=3588397;
RA Morfitt W., Vallatfranca U.E., Konings A.F., Ernst S.R., Katzin B.,
R1 Ruedenber E., Xuong N.H., Hamlin R., Roberts U.D.;
R2 "The three-dimensional structure of ricin at 2.8 A.";
R3 J. Biol. Chem. 262:5598-5603(1987).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=91352004; PubMed=1881881;
RA Katzin B.J., Collins E.J., Roberts J.D.;
R1 "Structure of ricin A-chain at 2.5 A.";
R2 Proteins 10:251-259(1991).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
RX MEDLINE=91352005; PubMed=1881882;
RA Ruedenber E., Roberts U.D.;
R1 "Structure of ricin B-chain at 2.5-A resolution.";
R2 Proteins 10:260-269(1991).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=95082010; PubMed=7990130;
RA Weston S.A., Tucker A.D., Thatcher D.R., Derdyshe D.J.;
R1 "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.";
R2 J. Mol. Biol. 244:410-422(1994).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.

CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUPERFAMILY.
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC -----
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 CC -----
 CC EMBL: X55667; CA39202.1; -.
 CC PIR: S16022; S16022.
 CC HSRF: P11140; 1ABR.
 CC InterPro: IPR000772; Ricin_B_lectin.
 CC InterPro: IPR001574; Ricin_B_lectin; 6.
 CC Pfam: PF00622; Ricin_B_lectin.
 CC PRINTS: PR00396; SHIGARICIN.
 CC SMART: SM00458; RICIN. 2.
 CC PROSITE: PS00231; RICIN B LECTIN. 2.
 CC PROSITE: PS00275; SHIGA RICIN. 1.
 CC DR Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 CC Glycoprotein; Lectin; Signal; Pyroglutamate carboxylic acid.
 CC KW SIGNAL 1 34
 CC FT CHAIN 1 35 285
 CC FT PEPTIDE 286 295
 CC FT CHAIN 296 562
 CC FT DOMAIN 303 339
 CC FT DOMAIN 340 437
 CC FT REPEAT 317 359
 CC FT REPEAT 360 400
 CC FT REPEAT 403 435
 CC FT REPEAT 448 483
 CC FT REPEAT 487 526
 CC FT REPEAT 529 562
 CC FT ACT_SITE 198 198
 CC FT DISULFID 281 303
 CC FT DISULFID 320 339
 CC FT DISULFID 340 359
 CC FT DISULFID 453 460
 CC FT DISULFID 490 507
 CC FT MOD_RES 35 35
 CC FT CARBOHYD 234 234
 CC FT CARBOHYD 395 395
 CC FT CARBOHYD 435 435
 CC SQ SEQUENCE 562 AA; 62817 MW; 1P0DBCT7BA6278 CRC64;
 CC
 CC Query Match 34.8%; Score 126; DB 1; Length 562;
 CC Best Local Similarity 42.4%; Seed No. 32e-398; Indels 6; Gaps 5;
 CC Matches 105; Conservative 36; Mismatches 98;
 CC
 CC 9 TQGTGKVEYFPTILLADYVSGSGSSEPELROSTIVSDQRFVYALNQGQDXTA 68
 CC 43 TEATNSQSYKOFIFILRQRL-TGLIHDIPLVLPDPPT-TVEENRRIYVLENSERSSEIEV 100
 CC
 CC 69 AIDVNNYVAVVQKQKQSYFLADPARGATLHFTGTIDSSSIPKQSYXDLERVAGH-8 127
 CC 101 GIDVNNYVAVVQKQKQSYFLADPARGATLHFTGTIDSSSIPKQSYXDLERVAGH-8 158
 CC 128 DQPIGIXQGLQSYVXALXKQSGSTKQAKSILILQMSLAPRPILWRKXQINSKX3 187
 CC 159 ERIISLGLQALHAIISFLSAGNSDEKATIVILQMSLAPRPILWRKXQINSKX3 218
 CC
 CC 188 FLPEKYMLELFTSWCOOSTQVQSTVDVNNPKHLAIKXNPFVLYLNV-RVYLISLAIM 246
 CC 219 FQEDPAALSLIENWMDLISGQVQSVQDTFFNNVLSINQPPVVDLSHPFVAVLALML 278
 CC
 CC 247 FVC 249

Db 279 FVC 281
 |||
 RESULT 4
 ABRS ABRS STANDARD; PRT: 527 AA.
 ID 06077; E81374;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Abirin-B precursor [Contains: Abirin-B A chain (rRNA N-glycosidase)
 DE (EC 3.2.2.22); Abirin-B chain]
 OS Abrus precatorius (Indian licorice) (Crab's eye)
 CC Eukaryote; Vitellin/plantae; Streptophyta; Tracheophyta;
 CC Spermatophytes; Angiosperms; Rosales; Rosaceae; Rubiaceae; Papilionaceae; Abreace; Abrus
 CC [NCBI TaxID=5816]
 CC [1]_taxid=5816;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=9112798; PubMed=8421313;
 RA Hung C.-H., Lee M.-C., Lee T.-C., Lin Y.-Y.;
 RT "Primary structure of three distinct isabirins determined by cDNA
 RL sequencing. Conservation and significance.";
 RL J. Mol. Biol. 229:263-267 (1993).
 RN [2]
 RP SEQUENCE OF 260-527.
 RA MEDLINE=93169023; PubMed=7763422;
 RA Kimura M., Sumitawa T., Funatsu G.;
 RT "Type complete amino acid sequences of the B-chains of abirin-B and
 RL abirin-B, toxic proteins from the seeds of Abrus precatorius.";
 RL Biosci. Biotechnol. Biochem. 57:166-169 (1993).
 CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
 CC ABRIN-A IS MORE TOXIC THAN RICIN.
 CC -1- FUNCTION: THE B CHAIN IS A CARBOXY-PEPTIDASE SPECIFIC LECTIN THAT
 CC BINDS TO THE N-TERMINAL SECTION OF ABRIN TO THE CELL MEMBRANE THAT
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S RNA.
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUPERFAMILY.
 CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: M98345; AAA3625.1; -.
 CC PIR: S32430; S32430.
 CC HSRF: P11140; 1ABR.
 CC InterPro: IPR000772; Ricin_B_lectin.
 CC InterPro: IPR001574; Ricin_B_lectin; 6.
 CC Pfam: PF00622; Ricin_B_lectin.
 CC PRINTS: PR00396; SHIGARICIN.
 CC SMART: SM00458; RICIN. 2.
 CC PROSITE: PS00231; RICIN B LECTIN. 2.
 CC PROSITE: PS00275; SHIGA RICIN. 1.
 CC DR Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 CC Glycoprotein; Lectin; Pyroglutamate carboxylic acid.
 CC KW CHAIN 1 250
 CC FT PEPTIDE 251 260
 CC FT CHAIN 261 527
 CC ABRIN-B A CHAIN.
 CC ABRIN-B B CHAIN.

	FT	STRAND	424	428	
	FT	TORN	432	433	
	FT	HELIAX	435	437	
	FT	STRAND	439	441	
	FT	TORN	443	444	
	FT	STRAND	445	446	
	FT	TORN	449	450	
	FT	STRAND	452	453	
	FT	TORN	454	455	
	FT	STRAND	457	472	
	FT	TORN	474	475	
	FT	HELIAX	478	480	
	FT	STRAND	483	484	
	FT	TORN	486	487	
	FT	STRAND	490	492	
	FT	TORN	493	496	
	FT	STRAND	495	501	

Query Match 38.2% Score 467; DB 1; Length 528;
Best Local Similarity 42.3%; Pctd: No, 8.4e-44;
Matches 107; Conservative 34; Mismatches 86; Indels 26; Gaps 6

Oy	9	THQYGEVPEPTILRLDYSSGSSNSNEPLLRQSTFVPSPADRPFLVELTMOGXDSXTA	68
Db	9	TEBASQSYKGFIFALRRER-RGLIHDPVLDPPT-QLGRNRYYSSTPSISIV	66
Oy	69	AIDVTNNYYANQAGDGYTLRLDAFRCAETHLFTGTDDSSLPFGXSIYDLERYGH-R	127
Db	67	GIVPKNAYWAKYSLXALXGSGTSFXQASGLIILOMSLEAPRFPYLWRKXIXGS	187
Oy	128	DOEFGXOLOSXYALKXGSGTSFXQASGLIILOMSLEAPRFPYLWRKXIXGS	187
Db	67	GIVPKNAYWAKYSLXALXGSGTSFXQASGLIILOMSLEAPRFPYLWRKXIXGS	187
Oy	125	QQPPIGIALHNGISPFSGSDNDEMRATLVIIVIMVAENAFYISNRVAVIOTGYA	184
Db	108	FELPKVMELEFSWGOSTGVGHSTGDVENNPXKLIXGNPFVLYXNVXX	237
Oy	185	FGPDAMISLEEMNDINDSRGVESYQTFEPNQ-----VLTINREPVTVDSLIR	234
Db	238	VASTIAITMENC	249
Oy	235	PVVNIAMLMETVC	247

RESULT 3

ID	ABRC	ABRRP	STANDARD	FRT	562 AA.
AC	E28550:				
DT	01-DIC-1992 (Rel. 24, Created)				
DR	01-DIC-1992 (Rel. 24, Last sequence update)				
DT	26-FEB-2003 (Rel. 41, Last annotation update)				
DE	Abrin'-c precursor [combains: Abrin'-c A chain (tRNA N-glycosidase) (EC 3.2.2.22); Abrin'-c B chain)].				
D5	Abrus precatorius (Indian licorice) (Crab's eye).				
OC	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
CC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurostis I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.				
NB	NCBI_TaxId=3816;				
RN	(1) SEQUENCE FROM N.A.				
TX	TRINITY-CLUST				
RX	MEDLINE=9126657; PubMed=2050149;				
CC	Wood X.A., Lord J.M., Wawrzyniak E.J., Platak M.;				
RT	"Preproabrin: genomic cloning, characterisation and the expression of				
RL	the A-chain in Escherichia coli."				
CC	Eur. J. Biochem. 198;723-732(1991).				
-1-	FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN				
CC	SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL				
CC	SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE				
CC	B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE				
CC	BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.				
-1-	NOTE: THIS ENTRY REPRESENTS ONE OF THE 186 UNITS				
CC	SPECIFIC ADONISIN ON THE 186 UNITS				
-1-	STANDUIT: DISULPHIDE-LINKED DIMER OF A AND B CHAINS				

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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 4.3929 Seconds
(without alignments)
2736.539 Million cell updates/sec

Title: US-09-601-667C-41

Perfect score: 1223
Sequence: 1 YERLRRLRYHTGTTGKVFRR.....XVTLASLAIHLFVCGEPPSS 256

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Displaying first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1165	95.3	254	1	MIA VISAL
2	467	38.2	528	1	ABR2_ABR2
3	426	34.8	562	1	ABR2_ABR2
4	404.5	33.1	527	1	ABR2_ABR2
5	376	30.7	576	1	RICI_RICCO
6	370.5	30.3	564	1	AGGL_RICCO
7	339	27.7	563	1	NIGB_SAMI
8	326	26.7	282	1	RIP2_BERDI
9	307	24.6	289	1	RIP2_BERDI
10	289	24.6	289	1	RIP2_BERDI
11	289	24.6	289	1	RIP2_BERDI
12	278.5	22.8	290	1	RIP1_BRYDI
13	276.5	22.4	316	1	RIP2_GELDI
14	273.5	22.4	316	1	RIP2_GELDI
15	267.5	21.9	286	1	RIP1_CUCFI
16	243.5	20.7	277	1	RIP1_MOMCH
17	244.5	20.0	286	1	RIP1_MOMCH
18	239.5	19.6	250	1	RIP1_LUEFY
19	233.5	19.1	278	1	RIP1_MIRNA
20	191.5	15.7	261	1	RIP1_MIRNA
21	184	15.8	333	1	RIP1_MIRNA
22	184	15.8	333	1	RIP1_MIRNA
23	168	13.7	253	1	RIP1_SAPOR
24	166	13.6	253	1	RIP1_SAPOR
25	162	13.2	299	1	RIP1_SAPOR
26	157	12.8	292	1	RIP1_SAPOR
27	138.5	11.3	310	1	RIP2_PHYLAC
28	131	10.7	293	1	RIP2_PHYLAC
29	127	10.4	236	1	RIP1_DIACH
30	126	9.8	280	1	RIP1_HORVU
31	111.5	9.1	315	1	SLRA_BH13
32	111.5	9.1	315	1	SLRA_BH13
33	110	9.0	280	1	RIP2_HORVU

Result No.	Score	Match	Length	DB ID	Description
34	106	8.7	219	1	SLRA_BH13
35	99.5	8.1	580	1	SLRA_BH13
36	76	6.2	879	1	YMG5_YMG5
37	76	6.2	879	1	YMG5_YMG5
38	73.5	6.0	243	1	RIP1_RH10
39	73.5	6.0	927	1	TR2N_AGRVI
40	73	6.0	755	1	YPP3_CAEEL
41	72	5.9	574	1	YPP3_CAEEL
42	72	5.9	781	1	SPI_MOUSE
43	72	5.9	788	1	SPI_MOUSE
44	71.5	5.8	157	1	RIP2_SAPOR
45	71.5	5.8	611	1	ADAS_DICTDI

ALIGNMENTS

RESULT 1

ID MIA VISAL STANDARD; PRT: 254 AA.

AC P81446; 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE Beta-galactoside specific lectin I A chain (MIA) (ML-1 A) (RNA N-

glycosidase) (EC 3.2.2.22)

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

CC Santalales; Santalaceae; Viscum.

CX NCBI_TaxID=3972;

NP [1]

RP SEQUENCE.

RC MEDLINE=9714581; PubMed=8980141;

RA Soier W.H., Soeys S., Schwammon C., Wilhelm S., Stiefel T.,

RB Voelter W.;

RT PDB complete amino acid sequence of the A chain of mistletoe lectin I.;

RS FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN

SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL

SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE

B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY

INTO THE CELL OF THE A CHAIN; B CHAINS ARE ALSO RESPONSIBLE FOR

CELL AGGLUTINATION (LECTIN ACTIVITY)

CC SPECIFIC ADENOSINE ON THE 28S RNA.

CC -1- SUBUNIT disulfide-linked dimer of A and B chains.

CC -1- SUBUNIT disulfide-linked dimer of A and B chains.

CC -1- SUBUNIT disulfide-linked dimer of A and B chains.

CC -1- SUBUNIT disulfide-linked dimer of A and B chains.

CC -1- SUBUNIT disulfide-linked dimer of A and B chains.

CC -1- SUBUNIT disulfide-linked dimer of A and B chains.

CC -1- SUBUNIT disulfide-linked dimer of A and B chains.

CC -1- SUBUNIT disulfide-linked dimer of A and B chains.

Thu Dec 11 16:09:59 2003

us-09-601-667c-41.rpt

Page 8

Db 144 ENIDIGLPLSSAITTLEFYMAQAPSA--LIVLIQTREARPFKIEHVAKYV--ATN 199
QY 186 FLBDXYMLBLETWGOOSTOY--OHSIDYFNNPXLAIXXGNFTLXNV 235
Db 200 KPNLAIISLENQMSALSQIFLAONQCKFNNFVDIKPTGERFOVTNV 249

Search completed: December 11, 2003, 13:55:48
Job time : 8.95724 secs

Thu Dec 11 16:09:59 2003

us-09-601-667c-41.rpt

Page 7

QY 131 EGIKXKLIQSVALRPGSGSTRKQARSILLIOWISAKRNPPIIMRKQKINSGLFP 190
DB 126 PGLPRLADSLSTLTFTNNNS--ASALMVLQSTSSAKRFEEQGRGVX--TEFP 181
QY 151 DAYVLEIETNSGQOSTQV--HSIDGVFNNPKRLAIKXGNFTLVXEX--VIASLAWL 246
DB 182 SLATISLSSMSALSKRIQIDASTNNGQEFPPVYINACHQSVITVMDAGVTSINLL 241

Result 13
JCS606
Karasurin C - Trichosanthin Kiriowii var. japonica
N/contans: Karasurin A
C/species: trichosanthin Kiriowii var. japonica
C/revision: trichosanthin revision 23-Sep-1997 #ext change 19-Jul-2002
Claccession: JCS606; JCS503
R1:Mitaku, H.; Iida, K.; Kondo, T.; Ogihara, Y.
Biol. Pharm. Bull. 20, 711-713, 1997
A1:Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating protein
/Reference number: JCS606; PMID:9735552; PMID:1212598

A.residues: 1-269 <M>
A.cross-references: DDBJ|AB000666; MID|92329630; PIDD|BA21766.1; FID|G2328631
R.xondo, T., Mutakiri, H., Takeida, T., Ogihara, Y.
E.coli strain: M11-19, 1485+1489, 1996
A.refseq accession number: U00096
A.reference number: C5C052; NCBI|91108948; MID|9551163
A.accession: JCS0033
A.status: preliminary
A.molecule type: protein
A.residues: 22-270 <N>
A.comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, abortifacient, and embryocidal activities.
C.superfamily: rRNA N-glycosidase rRNA N-glycoside-inactivating proteins which catalyze cleavage of 2'-O-methylguanosine
F.22-270/Product: karasinin C status predicted <MC>
F.27-266/Domains: rRNA N-glycosidase homology <RN>

Query Match 24.5%; Score 300; DB 2; Length 289;
Best Local Similarity 35.4%; Pred. No. 5,3e-25;
Matches 85; Conservative 46; Mismatches 95; Indels 14; Gaps 9

QY	13	TKXYRPFITLADYVSSGSPNIEPIILROSTIPYNAQOEYUWNNQKXSTAYD	72
QY	33	TSSYGVFISMLKALYEKKIYDIELLR-STIPES--GRVALLHNVYADETVAIDV	89
Dy	73	TKXVVAQAGDSYFLRDA-PRCAETLFTGTGDSLSLSPFGYXDLERAYGH-RDI	130
Dy	90	INWVNGHAGDSYFTEFNESNTEFAKTYFOAER-KVTLFYSNENGLDAKIREI	148
Dy	131	PIGKIOGHSYALAKXGQSTXAPASILLIIONSGAARFPIILKQKXNCSGSH	150
QY	149	PLGCPALDSATITLLEFYNNMS--ASAAFWLQISNBAARFKIIBQOGRKRDV-TIFP	204
Dy	191	DYVYMLEFSGQSGSTWQ--HSTSDVFNPNKALIXKSNFYLLKNYXK--VMSIALVL	245
QY	205	STATILENSVSNLSKDIQASINQOGEFFVYLINQKQKQVITITNVDAQVYSNALL	264

RESULT 14
 JCA840
 rRNA N-glycosidase (EC 3.2.2.22) trichoaungina - snake gourd
 C/Species: trichoaungina angulata (snake gourd)
 C/Accession: J03096 #sequence revision 24-Oct-1997 #text_change 05-Dec-1997
 R/Chow L.P., Kono M., Li J., Wang, S.H.; Teno, Y.; Tsugita, A.
 Biomed. Sci. 3:178-186 1996
 A/Titla: Amino acid of sequence of trichoaungina, a ribosomal-inactivating protein from
 A/Reference number: JCA840
 A/Accession: JCA840
 A/Molecule type: protein
 A/Residues: 1-132, 8',134-245 <CHOL>

A: Experimental source: seed
A: Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Tabl.
R: Chow, L.P.; Kamo, M.; Liu, Y.Y.; Ueno, Y.; Tagita, A.
submitted to JIPED, August 1995
A: Description: Amino acid sequence of trichogaunia, a ribosomal-inactivating protein from
A: Reference number: J06677
A: Accession: J07031
A: Molecule type: protein
A: Residues: 1-50, 1', 52-245 <CHO2>
A: Specificity: rRNA N-glycosylase; rRNA N-glycosidase homology
A: Key words: glycoprotein, glycosylase, hydrolase, phosphoprotein; seed
F: 1, 201/Binding site N-glycosylase homology <RMS>
F: 1, 201/Binding site N-glycosylase homology <RMS>
F: 10, 159, 161/Active site: Tyr, Glu, Asg Helius predicted
F: 155/Binding site: phosphate (Ser) (covalent) (y) casein kinase II Helius predicted

Query Match 23.7% Score 289.5; DB 2; Length 245;
Match Local Similarity 34.4%; Pident. No. 66-24;
Matches 83; Conservative 37; Mismatched 106; Indels 15; Gaps 7;

Query Match 23.7%; Score 289.5; DB 2; Length 245;
Best Local Similarity 34.4%; Pred. No. 6e-24;
Matches 83; Conservative 37; Mismatches 106; Indels 15; Gaps 7.

QY 13 TXKXRPFTLLADYSSGSGSPENRFLKQSTPIVPAQRCVULATNCKXSTALDY 72
Db 10 TKKSYSPFTQLKDALPTGVVYVJHLPST---ASGQRFRFPPLNNDEVTYAVDV 66
QY 73 TXKXVVAVQACDQSYFLADAPRGAEHLFTGTRDRSELPKXGXYOLERYAG-HDQIP 131
Db 67 TXVIVVAYPADAVSYFEEDTPELEFLLPAGTKYVK--LPTSGNDKDLQSGVQGDMDIE 124
QY 132 LQIHXQLQSGVAXLEKPGGSTRQARSILLIHCSTSEBAEFNPLLRKXKINSXSEFLPD 191
Db 135 LKFLPRLSSNINNVY--YDQSTGTAALLHQLSTREKAAVNTYEQQVSHIS--NFYSN 180
QY 132 XHMELESTKQSGQSYF--HSDGCHENNPKALIXGN--EYLLANVXKYZSLATL 246
Db 181 QVSIENLENNKQALSKQIQIARTGSGEPNPELYENPDGTSVYHNSAQQVKNIKLL 240
QY 247 P 247
Db 241 Y 241

247	F	247
241	Y	241

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RESULT 15
S25560
rRNA N-glycosidase (BC 3.2.2.22) monomordin II - balsam apple
C.Species: Monomorda balsamina (balsam apple)
C.Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 20-Aug-1999
C.Accession: S25560
R.Org:1990, M. Bectar, M.
Nucleic Acids Res. 20, 4662, 1992
A.Title: Monomordin II, a ribosome inactivating protein from Monomorda balsamina, is homol
A.Reference number: S25560. MUID:33027170. PMID:1408771
A.Accession: S25560
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-286 <ORT>
A.Cross-references: EMBL:Z12175; NID:G19525; PIDD:CAA78166.1; PID:G19526
A.Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
A.Keywords: glycosidase; hydrolase
A.Pathway: rRNA N-glycosidase homology <RNG>
A.Protein: rRNA N-glycosidase homology <RNG>

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Query Match	Score 281;	DB 2;	Length 286;
23.0%			

	Matches	78; Conservative	44; Mismatches	86; Indels	20; Gaps	3
Dy	13	TXEYEPFILLDYDYSSSPNN--EIEPLRQSTIPYSAQAFVLTETNOXKSDXSTRA	66			
Dy	30	IKMTITFV--EGRFALTEPHKVDYIPLLYST--ISGRFELDLDTSAVEYTSIA	89			
Dy	70	DDTNYVVAQAQAQSPFAPRACALTHFCTGTGQSTPSPYQVYQDAERAT--R	127			
Dy	87	IVTNYVVVAARQDVSIFPKSSPEAKVNIILFKGR--KTLTPGNYGNIQT--AAHRR	143			
Dy	128	DDLELQKGLDLSVAARPKGSGSTPKQAQSLILLQMSAARPPILMKRQKINSKS	187			

A:Accession: S13429
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'E',2-528 <HUN>
A:Notes-references: GB:M98344; NID:G166294; PID:AAA12624.1; EID:G166295
A:Notes: the coding region for the sequence shown is preceded by an ATG codon
A:References: 1. Kato, T., Kato, Y., Kameo, M., Yanaka, H.
Agric. Biol. Chem. 52, 1095-1097, 1988
A>Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from
A:Reference number: UT0202
A:Accession: UT0202
A:Molecule type: protein
A:Residues: 1-201,203-251 <FUN>
A:Notes: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
A:References: 1. Matsushima, A., Sugita, A.
Euk. J. Cell. Chem. 26, 6948-6952, 1991
A>Title: The complete amino acid sequence and expression of two distinct abrin A-chains.
A:Reference number: A39761; NID:J1201329; PMID:2016500
A:Accession: A39761
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 'B',2-251 <EV2>
A:Cross-references: GB:X54872
A:Notes: residues 1-8 were derived from the synthesized primer
A:References: 1. Sumitani, T., Sumitani, G.
Biochem. Biotechnol. 10, 165-169, 1993
A:Reference number: J01338; NID:J31650023; PMID:7753422
A:Accession: J01338
A:Molecule type: protein
A:Residues: 261-347,'T',349-351,'A',353-357,'L',359-528 <KIN>
A:Experimental source: seed
A:References: 1. Nielsen, A., Sundan, A.
Submitted to the EMBL Data Library, October 1990
A:Description: Direct Molecular Cloning of two distinct abrin A-chains.
A:Accession: S14471
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 'ME',2-251 <EV2>
A:Cross-references: EMBL:X54873; NID:G16090; PID:CA38655.1; PID:G16091
A:References: 1. Chow, L.P., Tsuyata, A., Lin, J.Y.
FEBS Lett. 309, 115-118, 1992
A>Title: The complete primary structure of abrin-a B chain.
A:Accession: S24133
A:Molecule type: protein
A:Residues: 265-297,'Y',299-426,'L',428-466,'P',468-482,'L',484-528 <CHE>
A:References: 1. Chow, L.P., Chen, Y.C., Lin, J.Y.
Eur. J. Biochem. 240, 564-569, 1996
A>Title: Probing the domain structure of abrin-a by tryptic digestion.
A:Reference number: S74110; NID:J9708945; PMID:8856055
A:Accession: S74110
A:Molecule type: protein
A:Residues: 1-201,203-251 <LIN>
A:Experimental source: seed
A:Accession: S74111
A:Molecule type: protein
A:Residues: 267-276,'X',278-280,329-348,369-388,399-418 <LIN>
A:Experimental source: seed
A:Comment: abrin-a is more toxic than ricin. The toxin consists of an A chain, which inhibits
A:References: 1. Kato, T., Kato, Y., Kameo, M., Yanaka, H.
Agric. Biol. Chem. 52, 1095-1097, 1988
A>Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from
A:Reference number: UT0202
A:Accession: UT0202
A:Molecule type: protein
A:Residues: 1-201,203-251 <FUN>
A:Notes: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
A:References: 1. Matsushima, A., Sugita, A.
Euk. J. Cell. Chem. 26, 6948-6952, 1991
A>Title: The complete amino acid sequence and expression of two distinct abrin A-chains.
A:Reference number: A39761; NID:J1201329; PMID:2016500
A:Accession: A39761
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 'B',2-251 <EV2>
A:Cross-references: GB:X54872
A:Notes: residues 1-8 were derived from the synthesized primer
A:References: 1. Sumitani, T., Sumitani, G.
Biochem. Biotechnol. 10, 165-169, 1993
A:Reference number: J01338; NID:J31650023; PMID:7753422
A:Accession: J01338
A:Molecule type: protein
A:Residues: 261-347,'T',349-351,'A',353-357,'L',359-528 <KIN>
A:Experimental source: seed
A:References: 1. Nielsen, A., Sundan, A.
Submitted to the EMBL Data Library, October 1990
A:Description: Direct Molecular Cloning of two distinct abrin A-chains.
A:Accession: S14471
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 'ME',2-251 <EV2>
A:Cross-references: EMBL:X54873; NID:G16090; PID:CA38655.1; PID:G16091
A:References: 1. Chow, L.P., Tsuyata, A., Lin, J.Y.
FEBS Lett. 309, 115-118, 1992
A>Title: The complete primary structure of abrin-a B chain.
A:Accession: S24133
A:Molecule type: protein
A:Residues: 265-297,'Y',299-426,'L',428-466,'P',468-482,'L',484-528 <CHE>
A:References: 1. Chow, L.P., Chen, Y.C., Lin, J.Y.
Eur. J. Biochem. 240, 564-569, 1996
A>Title: Probing the domain structure of abrin-a by tryptic digestion.
A:Reference number: S74110; NID:J9708945; PMID:8856055
A:Accession: S74110
A:Molecule type: protein
A:Residues: 1-201,203-251 <LIN>
A:Experimental source: seed
A:Accession: S74111
A:Molecule type: protein
A:Residues: 267-276,'X',278-280,329-348,369-388,399-418 <LIN>
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A:Comment: abrin-a is more toxic than ricin. The toxin consists of an A chain, which inhibits
A:References: 1. Kato, T., Kato, Y., Kameo, M., Yanaka, H.
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A>Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from
A:Reference number: UT0202
A:Accession: UT0202
A:Molecule type: protein
A:Residues: 1-201,203-251 <FUN>
A:Notes: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
A:References: 1. Matsushima, A., Sugita, A.
Euk. J. Cell. Chem. 26, 6948-6952, 1991
A>Title: The complete amino acid sequence and expression of two distinct abrin A-chains.
A:Reference number: A39761; NID:J1201329; PMID:2016500
A:Accession: A39761
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 'B',2-251 <EV2>
A:Cross-references: GB:X54872
A:Notes: residues 1-8 were derived from the synthesized primer
A:References: 1. Sumitani, T., Sumitani, G.
Biochem. Biotechnol. 10, 165-169, 1993
A:Reference number: J01338; NID:J31650023; PMID:7753422
A:Accession: J01338
A:Molecule type: protein
A:Residues: 261-347,'T',349-351,'A',353-357,'L',359-528 <KIN>
A:Experimental source: seed
A:References: 1. Nielsen, A., Sundan, A.
Submitted to the EMBL Data Library, October 1990
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A:Accession: S14471
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 'ME',2-251 <EV2>
A:Cross-references: EMBL:X54873; NID:G16090; PID:CA38655.1; PID:G16091
A:References: 1. Chow, L.P., Tsuyata, A., Lin, J.Y.
FEBS Lett. 309, 115-118, 1992
A>Title: The complete primary structure of abrin-a B chain.
A:Accession: S24133
A:Molecule type: protein
A:Residues: 265-297,'Y',299-426,'L',428-466,'P',468-482,'L',484-528 <CHE>
A:References: 1. Chow, L.P., Chen, Y.C., Lin, J.Y.
Eur. J. Biochem. 240, 564-569, 1996
A>Title: Probing the domain structure of abrin-a by tryptic digestion.
A:Reference number: S74110; NID:J9708945; PMID:8856055
A:Accession: S74110
A:Molecule type: protein
A:Residues: 1-201,203-251 <LIN>
A:Experimental source: seed
A:Accession: S74111
A:Molecule type: protein
A:Residues: 267-276,'X',278-280,329-348,369-388,399-418 <LIN>
A:Experimental source: seed
A:Comment: abrin-a is more toxic than ricin. The toxin consists of an A chain, which inhibits
A:References: 1. Kato, T., Kato, Y., Kameo, M., Yanaka, H.
Agric. Biol. Chem. 52, 1095-1097, 1988
A>Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from
A:Reference number: UT0202
A:Accession: UT0202
A:Molecule type: protein
A:Residues: 1-201,203-251 <FUN>
A:Notes: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
A:References: 1. Matsushima, A., Sugita, A.
Euk. J. Cell. Chem. 26, 6948-6952, 1991
A>Title: The complete amino acid sequence and expression of two distinct abrin A-chains.
A:Reference number: A39761; NID:J1201329; PMID:2016500
A:Accession: A39761
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 'B',2-251 <EV2>
A:Cross-references: GB:X54872
A:Notes: residues 1-8 were derived from the synthesized primer
A:References: 1. Sumitani, T., Sumitani, G.
Biochem. Biotechnol. 10, 165-169, 1993
A:Reference number: J01338; NID:J31650023; PMID:7753422
A:Accession: J01338
A:Molecule type: protein
A:Residues: 261-347,'T',349-351,'A',353-357,'L',359-528 <KIN>
A:Experimental source: seed
A:References: 1. Nielsen, A., Sundan, A.
Submitted to the EMBL Data Library, October 1990
A:Description: Direct Molecular Cloning of two distinct abrin A-chains.
A:Accession: S14471
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 'ME',2-251 <EV2>
A:Cross-references: EMBL:X54873; NID:G16090; PID:CA3

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F/247/-669,286-305,328-346,-411/-430,456-473/Disulfide bonds: #status predicted
F/288,112/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/561,401/Binding site: Carbohydrate (Asn) (covariant) #status experimental
F/500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match      18.2%   Score 467   DB 1   Length 528;
Local Similarity  42.3%   Pos Neg 5 4 43;
Matches 107; Conservative 34; Mismatches 86; Indels 26; Gaps 6;

QY 9 THQTGCKEPPFTLLRNRVYSSGSFNSLPELRLQSTIVSDAKQFVVLNQGDKSXTA 68
D 9 TEGATSGSKQFTEKLRLRL-NGGLHDIPLVDFP- TLQENNYIYVLENSDSTSEY 66
QY 69 AIDVTKYVVAQADQSYFLIDAPKQAEHLFTGTTRDSSLPPGYSXOLERYVGH- R 127
D 67 GIDVTKYVVAHQGQSYFLIDAPKQAEHLFTGTTRDSSLPPGYSXOLERSXGSK 124
QY 125 QGIPPLGKQLPHGISPFSSQGNDEKATLITVLIOGAAEAPRYSINRVSRIQTGTA 184
D 188 FEPDXYWELSTWQSGQSTGYVHSTG/FNNPRALAIKXGNFVLNVAHX----- 237
QY 185 FQPDADAIENNMWNRISGVESVQDTPFVQ-----VTLNINSEPIYDLSH 234
D 238 -VLSALIMFLVC 249
QY 235 PTVAILMFLVC 247

RESULT 3
C39761
abrin (clone 7.2) precursor - Indian licorice (fragment)
N/contains: rRNA N-glycosidase (EC 3.2.2.22)
C/species: Abrus precatorius (Indian licorice)
C/date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #extc_change 20-Aug-1999
C/position: 33481-33492, 33493-33494, 33495-33496, 33497-33498, 33499-33500, 33501-33502, 33503-33504, 33505-33506, 33507-33508, 33509-33510, 33511-33512, 33513-33514, 33515-33516, 33517-33518, 33519-33520, 33521-33522, 33523-33524, 33525-33526, 33527-33528, 33529-33530, 33531-33532, 33533-33534, 33535-33536, 33537-33538, 33539-33540, 33541-33542, 33543-33544, 33545-33546, 33547-33548, 33549-33550, 33551-33552, 33553-33554, 33555-33556, 33557-33558, 33559-33560, 33561-33562, 33563-33564, 33565-33566, 33567-33568, 33569-33570, 33571-33572, 33573-33574, 33575-33576, 33577-33578, 33579-33580, 33581-33582, 33583-33584, 33585-33586, 33587-33588, 33589-33590, 33591-33592, 33593-33594, 33595-33596, 33597-33598, 33599-33600, 33601-33602, 33603-33604, 33605-33606, 33607-33608, 33609-33610, 33611-33612, 33613-33614, 33615-33616, 33617-33618, 33619-33620, 33621-33622, 33623-33624, 33625-33626, 33627-33628, 33629-33630, 33631-33632, 33633-33634, 33635-33636, 33637-33638, 33639-33640, 33641-33642, 33643-33644, 33645-33646, 33647-33648, 33649-33650, 33651-33652, 33653-33654, 33655-33656, 33657-33658, 33659-33660, 33661-33662, 33663-33664, 33665-33666, 33667-33668, 33669-33670, 33671-33672, 33673-33674, 33675-33676, 33677-33678, 33679-33680, 33681-33682, 33683-33684, 33685-33686, 33687-33688, 33689-33690, 33691-33692, 33693-33694, 33695-33696, 33697-33698, 33699-33700, 33701-33702, 33703-33704, 33705-33706, 33707-33708, 33709-33710, 33711-33712, 33713-33714, 33715-33716, 33717-33718, 33719-33720, 33721-33722, 33723-33724, 33725-33726, 33727-33728, 33729-33730, 33731-33732, 33733-33734, 33735-33736, 33737-33738, 33739-33740, 33741-33742, 33743-33744, 33745-33746, 33747-33748, 33749-33750, 33751-33752, 33753-33754, 33755-33756, 33757-33758, 33759-33760, 33761-33762, 33763-33764, 33765-33766, 33767-33768, 33769-33770, 33771-33772, 33773-33774, 33775-33776, 33777-33778, 33779-33780, 33781-33782, 33783-33784, 33785-33786, 33787-33788, 33789-33790, 33791-33792, 33793-33794, 33795-33796, 33797-33798, 33799-33800, 33801-33802, 33803-33804, 33805-33806, 33807-33808, 33809-33810, 33811-33812, 33813-33814, 33815-33816, 33817-33818, 33819-33820, 33821-33822, 33823-33824, 33825-33826, 33827-33828, 33829-33830, 33831-33832, 33833-33834, 33835-33836, 33837-33838, 33839-33840, 33841-33842, 33843-33844, 33845-33846, 33847-33848, 33849-33850, 33851-33852, 33853-33854, 33855-33856, 33857-33858, 33859-33860, 33861-33862, 33863-33864, 33865-33866, 33867-33868, 33869-33870, 33871-33872, 33873-33874, 33875-33876, 33877-33878, 33879-33880, 33881-33882, 33883-33884, 33885-33886, 33887-33888, 33889-33890, 33891-33892, 33893-33894, 33895-33896, 33897-33898, 33899-33900, 33901-33902, 33903-33904, 33905-33906, 33907-33908, 33909-33910, 33911-33912, 33913-33914, 33915-33916, 33917-33918, 33919-33920, 33921-33922, 33923-33924, 33925-33926, 33927-33928, 33929-33930, 33931-33932, 33933-33934, 33935-33936, 33937-33938, 33939-33940, 33941-33942, 33943-33944, 33945-33946, 33947-33948, 33949-33950, 33951-33952, 33953-33954, 33955-33956, 33957-33958, 33959-33960, 33961-33962, 33963-33964, 33965-33966, 33967-33968, 33969-33970, 33971-33972, 33973-33974, 33975-33976, 33977-33978, 33979-33980, 33981-33982, 33983-33984, 33985-33986, 33987-33988, 33989-33990, 33991-33992, 33993-33994, 33995-33996, 33997-33998, 33999-34000, 34001-34002, 34003-34004, 34005-34006, 34007-34008, 34009-34010, 34011-34012, 34013-3401
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Thu Dec 11 16:09:57 2003

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Page 8

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Db 235 OVKPTALIMFVC 247

Search completed: December 11, 2003, 14:48:52
Job time : 35.4124 secs

Thu Dec 11 16:09:57 2003

us-09-601-667c-40.rapb

Page 7

STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-May-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-May-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-May-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-Dec-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-Jun-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-Nov-1991
ATTORNEY/AGENT INFORMATION:
NAME: Monicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-127-890-111
Query Match 10.8%; Score 284.5; DB 12; Length 251;
Best Local Similarity 34.0%; Pred. No. 4,6e-23;
Matches 86; Conservative 33; Mismatches 113; Indels 21; Gaps 7;
Db 8 VTHQOTXKXRPRTLLRDY--VSSGSFSENEIPILRGSTIPVSDQRFVLELNGXD 64
5 VSRSTKATYITVVFNELEARKYKKEBNSHGIFLTKRADDPKKA--FLVYALSNNGQ 62
65 SKTALIDVTXVYVAYOGAGSYAFDAAPRGAEHLFTGTRDRSLPFGSYDLEKVA 124
63 LAELIADVTSVYVGVQVRNSYFEDAPDAVEGLFQVITKTR--LHSGSYSLGEX 120
125 GHDDQIPGIXQL--IQSYALRPGSGSTXQARSILILLOWISZAAR---NPILMR 177
121 AIRETTDLGIEPLRIGIKLDENALIDNYKTEIASLVLVQVSSAARFTIENQIRNN 180
178 XKQKINSKGSFLPDXYMLELTSWQOSTVOQHS--TDGVNRPXRLAIXGNFVTLXNR 236
181 FQQRIR-----PANNITSLERKNGKLSFQIRISGANGMSSEAVLEBRANGKXYTVAVD 234
Db 237 XYTASLAINPVC 249
235 QVKKRLILKFCV 247

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Strudnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
BETTER, Marc D.,
CITY: Chicago
STREET: 500 West Madison Street, 34th floor
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-May-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-May-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-May-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-Dec-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-Jun-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-Nov-1991
ATTORNEY/AGENT INFORMATION:
NAME: Monicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-10-127-890-102
Query Match 10.7%; Score 280.5; DB 12; Length 251;
Best Local Similarity 33.6%; Pred. No. 1.3e-22;
Matches 85; Conservative 34; Mismatches 113; Indels 21; Gaps 7;
Db 8 VTHQOTXKXRPRTLLRDY--VSSGSFSENEIPILRGSTIPVSDQRFVLELNGXD 64
5 VSRSTKATYITVVFNELEARKYKKEBNSHGIFLTKRADDPKKA--DQSGCTVYALSNNGQ 62
65 SKTALIDVTXVYVAYOGAGSYAFDAAPRGAEHLFTGTRDRSLPFGSYDLEKVA 124
63 LAELIADVTSVYVGVQVRNSYFEDAPDAVEGLFQVITKTR--LHSGSYSLGEX 120
125 GHDDQIPGIXQL--IQSYALRPGSGSTXQARSILILLOWISZAAR---NPILMR 177
121 AIRETTDLGIEPLRIGIKLDENALIDNYKTEIASLVLVQVSSAARFTIENQIRNN 180
178 XKQKINSKGSFLPDXYMLELTSWQOSTVOQHS--TDGVNRPXRLAIXGNFVTLXNR 236
181 FQQRIR-----PANNITSLERKNGKLSFQIRISGANGMSSEAVLEBRANGKXYTVAVD 234
Db

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1 CURRENT FILING DATE: 2000-10-24
2 PRIOR APPLICATION NUMBER: 09/557,941
3 PRIOR FILING DATE: 2000-04-24
4 PRIOR APPLICATION NUMBER: 08/448,341
5 PRIOR FILING DATE: 1999-07-23
6 PRIOR APPLICATION NUMBER: 07/923,692
7 PRIOR FILING DATE: 1992-07-21
8 PRIOR APPLICATION NUMBER: 07/600,244
9 PRIOR FILING DATE: 1990-10-22
10 PRIOR APPLICATION NUMBER: 07/641,617
11 PRIOR FILING DATE: 1991-01-16
12 PRIOR APPLICATION NUMBER: 07/737,899
13 PRIOR FILING DATE: 1988-02-26
14 PRIOR APPLICATION NUMBER: 07/739,143
15 PRIOR FILING DATE: 1991-08-01
16 PRIOR APPLICATION NUMBER: 07/310,881
17 PRIOR FILING DATE: 1989-02-17
18 PRIOR APPLICATION NUMBER: 07/160,766
19 PRIOR FILING DATE: 1988-02-26
20 PRIOR APPLICATION NUMBER: 07/160,771
21 PRIOR FILING DATE: 1988-02-26
22 PRIOR APPLICATION DATE REMOVED - See File Wrapper or P.M.
23 NUMBER OF SEQ ID NOS: 1
24 SOFTWARE: PatentIn version 3.1
25 SEQ ID NO: 4
26 LENGTH: 289
27 TYPE: PRT
28 ORGANISM: Chinese cucumber protein alpha-trichosanthin
29 OS: 99-10-280-6798-4

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	Query Match	11.24%	Score 294	DB 12	Length 289
	Best Local Similarity	31.23%	Pred. No. 56	24	
	Matches	82	Conservative	49	Mismatches 95; Indels 14; Gaps 9
QY	13	TGXEFYPTILRDYSSGSFSNEIFPLRQSTIPVSDAGREVLVETLMQCKSKSTADIV	72		
DY	13			
DY	13	TSSSGYSFSLNRKLRKERRLDIFLR-SSGGS--GRRLALINYNMADITSLVADIV	89		
QY	73	TNNYVYVYQMGSGEYEDL-PRGEHTLPTTTRQSTIPVSGYKDLERKACH-ROD	130		
DY	73			
DY	90	TNIIMVIRAGDSTVFYFNEAALREAKYFKQAR-KTLFSGNRIETGAKKRENI	148		
QY	131	PLGIKQICGVALLKPKDGSRTQKARSLILQWISAPARENFTLWEXKQINSGSPF	190		
DY	131			
DY	149	FLDLPALDSATITFTFYNNAS--AASALMWLIGSTSEAAKFKIEQIGKREVDK--TPIP	204		
QY	151	DXTMLETSMQSGSTQV--HSTGVNNEPKALIXKNVFLKAKFX--VLSIAITEL	246		
DY	205	SLATISSEMSALSKQIDISNNKGQEPFVVLINQORWNI--NDADAVTNSILML	264		

RESULT 13
 US-10-127-890-4
 Application US/10127890
 Publication No US2003016195A1
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 Carroll, Stephen F.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

1 CORRESPONDENCE ADDRESS:
2 ADDRESS: McDonalds, Held & Mallory, Ltd.
3 Street 300 West Madison Street, 34th Floor
4 State: Illinois
5
6 COUNTRY: USA
7
8 ZIP: 60661
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS

1 SOFTWARE: PatentIn Release #1.0, Version #1.25
2
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/10/127,890
5 FILING DATE: 23-APR-2002
6
7 CLASSIFICATION: <UNKNOWN>
8
9 PRIORITY APPLICATION DATA:
10
11 APPLICATION NUMBER: US/08/646,360
12 PRIORITY DATE: 03-MAY-1997
13 PUBLICATION NUMBER: 1207/US94/05348
14 FILING DATE: 12-MAY-1994
15 APPLICATION NUMBER: US 08/064,691
16 FILING DATE: 12-MAY-1993
17 APPLICATION NUMBER: US 07/988,430
18 FILING DATE: 09-DEC-1992
19 APPLICATION NUMBER: US 07/901,707
20 FILING DATE: 19-JUN-1992
21 APPLICATION NUMBER: US 07/787,567
22 FILING DATE: 04-NOV-1991
23
24 ATTORNEY/AGENT INFORMATION:
25 NAME: McNicholas, Janet M.
26 REGISTRATION NUMBER: 32,918
27 REFERENCE/HOCKEY NUMBER: 200-70.P4
28
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 312/707-8889
31 TELEFAX: 312/707-9155
32 TELEK: 650 388-1248
33
34 INFORMATION FOR SEQ ID NO: 1:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 123 amino acids
37 TYPE: amino acid
38 TOPOLOGY: linear
39
40 MOLECULE TYPE: protein
41
42 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
43 US-10-127-890-4

Query Match	10.9%	Score 267.5	DB 12	Length 263
Best Local Similarity 33.5% <td></td> <td>Free No. 5.3e-23</td> <td></td> <td></td>		Free No. 5.3e-23		
Matches 83	Conservative 49	Mismatches 102	Indels 21	Gaps 10
Cy	13	TKGEYFPPTLIDYVSGSGSSN--EIELRGSTIPVSAQRFVLVELTQKSDSXPA 69		
Dh	10	TAKYTFE--EDFPALTLFPHSKWIDLLYST--LDSRRFTLLDTSYALETISVA 63		
Cy	70	IDVTVVVAQAQDQSYFRRAPRGAEHLFTGTNRSSLSPEFGSYADDERYACH-R 127		
Dh	63	IDVTVVVAARRDVSYFKPSKPEEVALYFKGR-KTLFPLVNGVEMNQTAARHIR 120		
Cy	128	DPIPLGKILQSLQVSLKFGSGSTRQASILLILQMSIAPARNPIMKXAKINSXS 187		
Dh	121	ENIDGSPASLSTATLLPYNNQSPH--LVLVTLIDAKARFIEHAKV--ATN 176		
Cy	188	PLPDWVLELETMSGGOSTG--QGSTDQVNNNPKLAXXGNPFLTKXVAVYASLMI 245		
Dh	177	FKFNALITLENQMSALSKQIPLANQGNKFRNPVDLIKPTGGRFOVYWDSDVVGNIK 236		
Cy	246	LPVCGSRPSSSDVAY 260		
Dh	237	LIL-NSSATLAINP 250		

RESULT 14
US-10-127-890-111
US-10-127-890-111 Application us/10127890
Publication No. US20030166196A1
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studenka, Gary M.
TITLE OF INVENTION: Immucotaxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mcandrews, Hield & Malloy, Ltd.

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QY 13 TCKEYFFFTLLRDYVSGSFSNEPIPLROSTIPVSDAORFVLELNOGXDSXTALIDV 72
DB 10 TSSSYGVFISNLRKALPBRKXLYDIPILR--SSLPGS--CRYALHILNVADEITISVALIDV 66
QY 73 TNYVAVYQAGDSGYFLDA--PRGAEFHLPFTGTRDRSSLPFGSYXDLEKRYAGH--RDQI 130
DB 67 TNYVMEYRAGDSGYFLDA--PRGAEFHLPFTGTRDRSSLPFGSYXDLEKRYAGH--RDQI 125
QY 131 PLGIXLOISYVALKXPGSTRXQNSIILIDNISAPRFLIMEXKQINSKXSLP 190
DB 126 PLGIXLOISYVALKXPGSTRXQNSIILIDNISAPRFLIMEXKQINSKXSLP 181
QY 191 DXYMLELTSNGQOSQOV--HSTGVFNPRKALIXXGNFTYLANRX--VIASIALML 246
DB 182 SLATISSENSWALSQOIASTNNGQFSFVVLINAGORVITINVDAGVYTSNIALLL 241

RESULT 10
US-10-375-209A-39
Sequence 39, Application US/10375209A
Publication No. US20030215421A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
FILE REFERENCE: 2020-601E
CURRENT FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 39
LENGTH: 247
TYPE: PRT
ORGANISM: Trichosanthens kiritlowii
US-10-375-209A-39

Query Match 11.5% Score 301; DB 12; Length 247;
Best Local Similarity 34.2%; Prid. No. 6 of 24;
Matches 83; Conservative 50; Mismatches 93; Indels 14; Gaps 9;

QY 13 TCKEYFFFTLLRDYVSGSFSNEPIPLROSTIPVSDAORFVLELNOGXDSXTALIDV 72
DB 10 TSSSYGVFISNLRKALPBRKXLYDIPILR--SSLPGS--CRYALHILNVADEITISVALIDV 66
QY 73 TNYVAVYQAGDSGYFLDA--PRGAEFHLPFTGTRDRSSLPFGSYXDLEKRYAGH--RDQI 130
DB 67 TNYVMEYRAGDSGYFLDA--PRGAEFHLPFTGTRDRSSLPFGSYXDLEKRYAGH--RDQI 125
QY 131 PLGIXLOISYVALKXPGSTRXQNSIILIDNISAPRFLIMEXKQINSKXSLP 190
DB 126 PLGIXLOISYVALKXPGSTRXQNSIILIDNISAPRFLIMEXKQINSKXSLP 181
QY 191 DXYMLELTSNGQOSQOV--HSTGVFNPRKALIXXGNFTYLANRX--VIASIALML 246
DB 182 SLATISSENSWALSQOIASTNNGQFSFVVLINAGORVITINVDAGVYTSNIALLL 241

QY 13 TCKEYFFFTLLRDYVSGSFSNEPIPLROSTIPVSDAORFVLELNOGXDSXTALIDV 72
DB 10 TSSSYGVFISNLRKALPBRKXLYDIPILR--SSLPGS--CRYALHILNVADEITISVALIDV 66
QY 73 TNYVAVYQAGDSGYFLDA--PRGAEFHLPFTGTRDRSSLPFGSYXDLEKRYAGH--RDQI 130
DB 67 TNYVMEYRAGDSGYFLDA--PRGAEFHLPFTGTRDRSSLPFGSYXDLEKRYAGH--RDQI 125
QY 131 PLGIXLOISYVALKXPGSTRXQNSIILIDNISAPRFLIMEXKQINSKXSLP 190
DB 126 PLGIXLOISYVALKXPGSTRXQNSIILIDNISAPRFLIMEXKQINSKXSLP 181
QY 191 DXYMLELTSNGQOSQOV--HSTGVFNPRKALIXXGNFTYLANRX--VIASIALML 246
DB 182 SLATISSENSWALSQOIASTNNGQFSFVVLINAGORVITINVDAGVYTSNIALLL 241

RESULT 12
US-10-280-679B-4
Sequence 4, Application US/10280679B
Publication No. US20030150019A1
GENERAL INFORMATION:
APPLICANT: Bettev, Marc D.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
US-10-280-679B-4

Query Match 11.4% Score 299; DB 12; Length 247;
Best Local Similarity 34.2%; Prid. No. 11-24;
Matches 82; Conservative 50; Mismatches 94; Indels 14; Gaps 9;

QY 13 TCKEYFFFTLLRDYVSGSFSNEPIPLROSTIPVSDAORFVLELNOGXDSXTALIDV 72
DB 10 TSSSYGVFISNLRKALPBRKXLYDIPILR--SSLPGS--CRYALHILNVADEITISVALIDV 66
QY 73 TNYVAVYQAGDSGYFLDA--PRGAEFHLPFTGTRDRSSLPFGSYXDLEKRYAGH--RDQI 130
DB 67 TNYVMEYRAGDSGYFLDA--PRGAEFHLPFTGTRDRSSLPFGSYXDLEKRYAGH--RDQI 125
QY 131 PLGIXLOISYVALKXPGSTRXQNSIILIDNISAPRFLIMEXKQINSKXSLP 190
DB 126 PLGIXLOISYVALKXPGSTRXQNSIILIDNISAPRFLIMEXKQINSKXSLP 181
QY 191 DXYMLELTSNGQOSQOV--HSTGVFNPRKALIXXGNFTYLANRX--VIASIALML 246
DB 182 SLATISSENSWALSQOIASTNNGQFSFVVLINAGORVITINVDAGVYTSNIALLL 241

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS/MS-DOS
SOFTWARE RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/27,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-May-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-May-1994
APPLICATION NUMBER: US/96/064,691
FILING DATE: 12-May-1993
APPLICATION NUMBER: US/97/888,430
FILING DATE: 09-Dec-1992
APPLICATION NUMBER: US/97/901,707
FILING DATE: 19-Jun-1992
APPLICATION NUMBER: US/97/787,567
FILING DATE: 04-Nov-1991
ATTORNEY/AGENT INFORMATION:
NAME: McAndrews, Held & Malloy, Ltd.
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-127-890-6

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Page 4

;; CURRENT FILING DATE: 2002-10-29
;; PRIOR APPLICATION NUMBER: 09/538,873
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: 60/126,826
;; PRIOR FILING DATE: 1999-03-30
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO: 1
;; LENGTH: 267
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURES:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-282-935-1

Query Match 14.3% Score 376; DB 12; Length 267;
Best Local Similarity 39.1%; Pred. No. 3.2e-33;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

QY 9 THQTGXRYPRITLADYSSGS-FSNRIPL-RSTIPVSADQFVLVETLWQSDX 66
DB 13 TGAATVOSTNIRAVRGLITQALVHEIPVLPNKGGLPN--QRFILVLSHMAELSV 70
QY 67 TLAIDVTNXYVAYQAGOSYPLR-DAPRGAE--THLFTGTRDSSLPKXSYDLERY 123
DB 71 TLALDVTNAYVYVAGNSYFPHDQDEALHTLFT-DVGNRYTFAFGYDLRBL 129
QY 124 AGH-FDQIPGLGXOLIOSYXAL--KPGGSTXQARSILLIOMISEARFPILMKRX 179
DB 130 AGNLKENIELANGPLEBIAISALYVSGTQFLTARSPFIICIMISEARFOYIEGKR 189
QY 180 QXINSKXFLPDXYMELETSWQOSTQVGHSTGVFNNPKRLAIXGNFVLNAXXYI 239
DB 190 TRIRYRSAPDPSVITLNSWGRSLTAIGSNQAFASPIQLGRNNSGFVYDVSILL 249
QY 240 ASLAIMLFCVCGRRSS 255
DB 250 PIALMYRCAPPSS 265

RESULT 8
US-10-127-890-1
;; Sequence 38, Application US/10127890
;; Publication No. US2003016136A1
;; GENERAL INFORMATION:
;; APPLICANT: Better, Marc D.
;; Studnicka, Gary M.
;; TITLE OF INVENTION: Immunopoxins Comprising Ribosome-Inactivating
;; Proteins
;; NUMBER OF SEQUENCES: 173
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/010127/890
;; FILING DATE: 13-MAY-1996
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994

;; APPLICATION NUMBER: US/08/646,360
;; FILING DATE: 13-MAY-1996
;; APPLICATION NUMBER: PCT/US94/05348
;; FILING DATE: 12-MAY-1994

;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; NAME: McAndrews, John M.
;; REGISTERED NUMBER: 32,918
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 267 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; NOTE: FILED IN: PROTEIN
US-10-127-890-1

Query Match 14.3% Score 376; DB 12; Length 267;
Best Local Similarity 39.1%; Pred. No. 3.2e-33;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

QY 9 THQTGXRYPRITLADYSSGS-FSNRIPL-RSTIPVSADQFVLVETLWQSDX 66
DB 13 TGAATVOSTNIRAVRGLITQALVHEIPVLPNKGGLPN--QRFILVLSHMAELSV 70
QY 67 TLAIDVTNXYVAYQAGOSYPLR-DAPRGAE--THLFTGTRDSSLPKXSYDLERY 123
DB 71 TLALDVTNAYVYVAGNSYFPHDQDEALHTLFT-DVGNRYTFAFGYDLRBL 129
QY 124 AGH-FDQIPGLGXOLIOSYXAL--KPGGSTXQARSILLIOMISEARFPILMKRX 179
DB 130 AGNLKENIELANGPLEBIAISALYVSGTQFLTARSPFIICIMISEARFOYIEGKR 189
QY 180 QXINSKXFLPDXYMELETSWQOSTQVGHSTGVFNNPKRLAIXGNFVLNAXXYI 239
DB 190 TRIRYRSAPDPSVITLNSWGRSLTAIGSNQAFASPIQLGRNNSGFVYDVSILL 249
QY 240 ASLAIMLFCVCGRRSS 255
DB 250 PIALMYRCAPPSS 265

RESULT 9
US-09-792-793A-39
;; Sequence 39, Application US/09792793A
;; Patent No. US20020168370A1
;; GENERAL INFORMATION:
;; APPLICANT: McAndrews, John R.
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;; FILE REFERENCE: 25020-601D
;; CURRENT APPLICATION NUMBER: US/09/792,793A
;; FILING DATE: 2001-02-22
;; NUMBER OF SEQ ID NOS: 93
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO: 39
;; LENGTH: 247
;; TYPE: PRT
;; ORGANISM: Trichostema killowii
US-09-792-793A-39

Query Match 11.5% Score 301; DB 10; Length 247;
Best Local Similarity 34.6%; Pred. No. 6.6e-25;
Matches 83; Conservative 50; Mismatches 93; Indels 14; Gaps 9;

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Page 3

SEQ ID NO 8
LENGTH: 252
TYPE: PRT
ORGANISM: viscum album
US-09-347-064-8

Query Match 44.0%; Score 1155; DB 9; Length 252;
Best Local Similarity 91.3%; Pred. No. 4 4e-120;
Matches 232; Conservative 1; Mismatches 19; Indels 2; Gaps 1;

QY 1 YERLRVTHQTCXEFRIITLADYSSGSFSEIPLRQSTIPVSDAQREVLVELTN 60
DB 1 YERLRVTHQTCXEFRIITLADYSSGSFSEIPLRQSTIPVSDAQREVLVELTN 60
QY 61 QGDSITAIADVTNNXYVAAYOGQSYFLRDPARGAETHLFTGTTDRSSLPKXSYXOL 120
DB 61 QGDSITAIADVTNNXYVAAYOGQSYFLRDPARGAETHLFTGTTDRSSLPKXSYXOL 118
QY 121 ERYAGRDQIPDIGIXOLIGSVALLKPGGSTRXKRSIILQWISSEARPNILMXKQ 180
DB 119 ERYAGRDQIPDIGIXOLIGSVALLKPGGSTRXKRSIILQWISSEARPNILMXKQ 178
QY 181 XINSGXSLPDXYMLEETSMQGSTOVGHSTGVNNPRLAIXGNPVTILANRYVIA 240
DB 179 YINSGXSLPDXYMLEETSMQGSTOVGHSTGVNNPRLAIPGNVTLNVRDVI 238
QY 241 SLATMLFVCGERP 254
DB 239 SLATMLFVCGERP 252

RESULT 5
US-09-347-064-2
Sequence 2, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: ECK, Jürgen
INVENTOR: ECK, Jürgen
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe viscum
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 252
TYPE: PRT
ORGANISM: viscum album
US-09-347-064-2

Query Match 43.8%; Score 1151; DB 9; Length 252;
Best Local Similarity 91.3%; Pred. No. 1,2e-119;
Matches 231; Conservative 1; Mismatches 19; Indels 2; Gaps 1;

QY 1 YERLRVTHQTCXEFRIITLADYSSGSFSEIPLRQSTIPVSDAQREVLVELTN 60
DB 2 YERLRVTHQTCXEFRIITLADYSSGSFSEIPLRQSTIPVSDAQREVLVELTN 61
QY 61 QGDSITAIADVTNNXYVAAYOGQSYFLRDPARGAETHLFTGTTDRSSLPKXSYXOL 120
DB 62 QGDSITAIADVTNNXYVAAYOGQSYFLRDPARGAETHLFTGTTDRSSLPKXSYXOL 119
QY 121 ERYAGRDQIPDIGIXOLIGSVALLKPGGSTRXKRSIILQWISSEARPNILMXKQ 180
DB 120 ERYAGRDQIPDIGIXOLIGSVALLKPGGSTRXKRSIILQWISSEARPNILMXKQ 179

QY 181 XINSGXSLPDXYMLEETSMQGSTOVGHSTGVNNPRLAIXGNPVTILANRYVIA 240
DB 180 YINSGXSLPDXYMLEETSMQGSTOVGHSTGVNNPRLAIPGNVTLNVRDVI 239
QY 241 SLATMLFVCGERP 253
DB 240 SLATMLFVCGERP 252

RESULT 6
US-10-282-935-3
Sequence 3, Application US/10282935
Publication No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GREITE, VICTOR F.
APPLICANT: SHALISHA, JOAN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: TOXIC COMPOUNDS
FILE REFERENCE: US20030143193A1
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 251
LENGTH: 251
TYPE: PRT
ORGANISM: Abrus precatorius
US-10-282-935-3

Query Match 17.6%; Score 461; DB 12; Length 251;
Best Local Similarity 41.9%; Pred. No. 9.9e-43;
Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;

QY 9 TQHTGKXFRITLADYSSGSFSEIPLRQSTIPVSDAQREVLVELTNQKXKXTRA 68
DB 9 TQHTGKXFRITLADYSSGSFSEIPLRQSTIPVSDAQREVLVELTNQKXKXTRA 66
QY 69 AIDVTNNXYVAAYOGQSYFLRDPARGAETHLFTGTTDRSSLPKXSYXOL 127
DB 67 AIDVTNNXYVAAYOGQSYFLRDPARGAETHLFTGTTDRSSLPKXSYXOL 124
QY 128 DQEPDIGIXOLIGSVALLKPGGSTRXKRSIILQWISSEARPNILMXKXKX 187
DB 125 DQEPDIGIXOLIGSVALLKPGGSTRXKRSIILQWISSEARPNILMXKXKX 184
QY 188 PDPXYMLEETSMQGSTOVGHSTGVNNPRLAIXGNPVTILANRYVIA 240
DB 186 PDPXYMLEETSMQGSTOVGHSTGVNNPRLAIXGNPVTILANRYVIA 234
QY 238 PTVATMLMFC 249
DB 235 PTVATMLMFC 247

RESULT 7
US-10-282-935-1
Sequence 1, Application US/10282935
Publication No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GREITE, VICTOR F.
APPLICANT: SHALISHA, JOAN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: TOXIC COMPOUNDS
FILE REFERENCE: US20030143193A1
CURRENT APPLICATION NUMBER: US/10/282,935

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Page 2

QY 391 VQTLDTYTLGGWMLAGNDTAPREVTITGPRDLCESSNGSXSWTEWCSSQXNOXWALYD 450
DB 121 VQTLDTYTLGGWMLAGNDTAPREVTITGPRDLCESSNGSXSWTEWCSSQXNOXWALYD 179
QY 451 GSIRPKXNDQCLTGRDVSIVTINIVSCSXSSXXQKWFTEKXALINLKKXXXXVYQAQ 510
DB 180 GSIRPKXNDQCLTGRDVSIVTINIVSCSXSSQKWFTEKXALINLKKGLAMVYQAQ 239
QY 511 NPKLRITITYPATGKFNQWMLPV 533
DB 240 NPKLRITITYPATGKFNQWMLPV 262

RESULT 2
US-09-347-064-4
Sequence 4, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Beck, Jürgen
APPLICANT: Schmidt, Arno
APPLICANT: Wenzel, Holger
TITLE OF INVENTION: Ribosome-Inactivating Proteins Based on
TITLE OF INVENTION: Album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
EARLIER FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 4
LENGTH: 267
ORGANISM: Vascum album
US-09-347-064-4

Query Match 48.3%; Score 1267.5; DB 9; Length 267;
Best Local Similarity 91.6%; Pred. No. 1,46-132;
Matches 241; Conservative 1; Mismatches 20; Indels 1; Gaps 1;
QY 271 DDTGCSASEPTNRIKRGKXKUVVDDPHGQNTQIMRSKNDPQVLTREDYTR 330
DB 1 DDTGCSASEPTNRIKRGKXKUVVDDPHGQNTQIMRSKNDPQVLTREDYTR 60
QY 331 NSGCLTYGTAGYVYMIPEQNTAVREAITQIKXGIIINPSNVLAASSGIKETTL 390
DB 61 NSGCLTYGTAGYVYMIPEQNTAVREAITQIKXGIIINPSNVLAASSGIKETTL 120
QY 391 VQTLDTYTLGGWMLAGNDTAPREVTITGPRDLCESSNGSXSWTEWCSSQXNOXWALYD 450
DB 121 VQTLDTYTLGGWMLAGNDTAPREVTITGPRDLCESSNGSXSWTEWCSSQXNOXWALYD 179
QY 451 GSIRPKXNDQCLTGRDVSIVTINIVSCSXSSXXQKWFTEKXALINLKKXXXXVYQAQ 510
DB 180 GSIRPKXNDQCLTGRDVSIVTINIVSCSXSSQKWFTEKXALINLKKGLAMVYQAQ 239
QY 511 NPKLRITITYPATGKFNQWMLPV 533
DB 240 NPKLRITITYPATGKFNQWMLPV 262

RESULT 3
US-10-083-336A-1
Sequence 3, Application US/10083336A
Patent No. US20030181655A1
GENERAL INFORMATION:
APPLICANT: Olsson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wememacher, Robert W

TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (R10-01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 576
ORGANISM: Ricinus communis
US-10-083-336A-1

Query Match 46.8%; Score 1229.5; DB 12; Length 576;
Best Local Similarity 49.2%; Pred. No. 7,2e-128;
Matches 264; Conservative 76; Mismatches 176; Indels 21; Gaps 12;
QY 9 TQDTGKXEFRETILRDYVSSGS-FSNEIFEL-RQSTIPVSDAQRFVLTETKQKDX 66
DB 48 TQDTGKXEFRETILRDYVSSGS-FSNEIFEL-RQSTIPVSDAQRFVLTETKQKDX 105
QY 67 TLAIDTYVYVAYQAGDQSFYR-DAPRGE--THTFTGTRDRESLPXSYXDERY 123
DB 106 TLAIDTYVYVAYQAGDQSFYR-DAPRGE--THTFTGTRDRESLPXSYXDERY 164
QY 124 AGH-RDQIPGIXDLSYVLA--RXDGSSTRKQARSLLTQWISAPRPILMRX 179
DB 165 AGH-RDQIPGIXDLSYVLA--RXDGSSTRKQARSLLTQWISAPRPILMRX 224
QY 180 QXINSXSELPDXIMLETFKQSGTOVQHTQVNNPKXALIXGNTVILXNXYI 239
DB 225 TRIMRKSAPDSVITLKNRSLTILQENQAPASPQQRNQSAPSVYDIL 284
QY 240 ASLAIWLVGCRSSDVRWVYRFLAD--DYTCASSEPTNRIKRGKXKUVVDD 296
DB 285 TRIMRKSAPDSVITLKNRSLTILQENQAPASPQQRNQSAPSVYDIL 339
QY 297 DDTGCSASEPTNRIKRGKXKUVVDDPHGQNTQIMRSKNDPQVLTREDYTR 356
DB 340 DDTGCSASEPTNRIKRGKXKUVVDDPHGQNTQIMRSKNDPQVLTREDYTR 399
QY 357 ENATQIKXGIIINPSNVLAASSGIKETTLVQTLDTYTLGGWMLAGNDTAPREVTI 416
DB 400 ENATQIKXGIIINPSNVLAASSGIKETTLVQTLDTYTLGGWMLAGNDTAPREVTI 459
QY 417 GPRDLCESSNGSXSWTEWCSSQXNOXWALYDQSIIRPKXNDQCLTGRDVSIVTINI 476
DB 460 GPRDLCESSNGSXSWTEWCSSQXNOXWALYDQSIIRPKXNDQCLTGRDVSIVTINI 518
QY 477 VSCSXSSXXQKWFTEKXALINLKKXXXXVYQAQNPFLRRITITYPATGKFNQWMLPV 533
DB 519 VSCSXSSXXQKWFTEKXALINLKKXXXXVYQAQNPFLRRITITYPATGKFNQWMLPV 575

RESULT 4
US-09-347-064-8
Sequence 8, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Beck, Jürgen
APPLICANT: Schmidt, Arno
APPLICANT: Wenzel, Holger
TITLE OF INVENTION: Ribosome-Inactivating Proteins Based on
TITLE OF INVENTION: Album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
EARLIER FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1

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Page 1

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Run on: December 11, 2003, 14:01:14 / Search time 34.4124 Seconds
(without alignments)

2865.029 Million cell updates/sec

Title: US-09-601-667C-40
Accession: 2628
Sequence: 1 FENLRALVHTQITCKEYTRF.....RRIITPTATKXNOMLPIVX 534

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Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*
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18: /cgn2_6/prodata/1/pubpa/US10_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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3	1229.5	46.3	252	9	US-09-347-064-10
4	1155	44.0	252	9	US-09-347-064-10
5	1151	43.8	252	9	US-09-347-064-10
6	461	17.6	251	12	US-10-287-933-3
7	376	14.3	267	12	US-10-287-933-1
8	301	11.5	247	10	US-09-792-793A-39
9	301	11.5	247	10	US-09-792-793A-39
10	299	11.4	247	12	US-10-127-890-6
11	299	11.4	247	12	US-10-127-890-6
12	287.5	10.9	263	12	US-10-127-890-4
13	287.5	10.9	263	12	US-10-127-890-4
14	286.5	10.7	261	12	US-10-127-890-11
15	286.5	10.7	261	12	US-10-127-890-102

16	278.5	10.6	247	10	US-09-792-793A-34	Sequence 34, App1
17	278.5	10.6	247	12	US-10-375-209A-34	Sequence 34, App1
18	275.5	10.5	251	12	US-10-127-890-101	Sequence 101, App
19	275.5	10.5	251	12	US-10-127-890-101	Sequence 101, App
20	272.5	10.5	331	9	US-09-765-527-253	Sequence 253, App
21	274.5	10.5	251	12	US-10-127-890-99	Sequence 99, App1
22	273.5	10.4	316	12	US-10-074-596-1	Sequence 1, App1
23	272.5	10.4	251	12	US-10-127-890-109	Sequence 109, App
24	272.5	10.4	251	12	US-10-127-890-109	Sequence 109, App
25	271.5	10.3	251	9	US-09-765-527-247	Sequence 247, App
26	271.5	10.3	251	12	US-10-127-890-2	Sequence 2, App1
27	271.5	10.3	251	12	US-10-127-890-103	Sequence 103, App
28	271.5	10.3	251	12	US-10-127-890-108	Sequence 108, App
29	271.5	10.3	251	12	US-10-074-596-11	Sequence 11, App1
30	271.5	10.3	507	12	US-10-074-596-11	Sequence 11, App1
31	270.5	10.3	251	12	US-10-127-890-106	Sequence 106, App
32	268.5	10.2	293	12	US-10-127-890-107	Sequence 107, App
33	268.5	10.2	293	9	US-09-765-527-253	Sequence 253, App
34	268.5	10.2	309	9	US-09-765-527-253	Sequence 253, App
35	268.5	10.2	309	9	US-09-765-527-253	Sequence 253, App
36	263	10.0	198	12	US-10-083-336A-3	Sequence 3, App1
37	263	10.0	198	12	US-10-083-336A-7	Sequence 7, App1
38	263	10.0	199	12	US-10-083-336A-5	Sequence 5, App1
39	263	10.0	200	12	US-10-083-336A-10	Sequence 10, App1
40	263.5	9.7	263	12	US-10-127-890-7	Sequence 7, App1
41	249.5	9.5	185	12	US-10-083-336A-9	Sequence 9, App1
42	241	9.2	188	12	US-10-083-336A-8	Sequence 8, App1
43	241	9.2	188	12	US-10-083-336A-8	Sequence 8, App1
44	241	9.2	188	12	US-10-083-336A-8	Sequence 8, App1
45	241	9.2	190	12	US-10-083-336A-11	Sequence 11, App1

ALIGNMENTS

RESULT 1
US-09-347-064-10
Sequence 10, Application US/09347064A
Residue No.: 2620045208A1
APPLICANT: Eck, Jorgen
APPLICANT: Schmidt, Arno
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347 064A
EARLIER FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/E998/00009
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 10
LENGTH: 263
ORGANISM: Viscum album
US-09-347-064-10
Query Match: 48.3%, Score 1267.5, DB 9, Length 263,
Best local similarity 93.6%, PID 4, Indels 1,
Matches 241, Conservative 1, Mismatches 20,
QY 271 DVTCSAEPYTRIVGKKVQVYDDPDNDGQIQWPSKNNDDPDLTKTKRXTYS 330
DB 1 DVTCSAEPYTRIVGKKVQVYDDPDNDGQIQWPSKNNDDPDLTKTKRXTYS 60
QY 331 NGSCITTYGTAGVYVWIFDGNVARENTIOWIXNGTINPRSNVYLAASGIGCTTT 390
DB 61 NGSCITTYGTAGVYVWIFDGNVARENTIOWIXNGTINPRSNVYLAASGIGCTTT 120

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Qy 240 ASLAIMLVCGGERPS 255
Db 250 PIALMYRCAPPSS 265

RESULT 15

US-08-425-336-1
Sequence 1: 581083
Sequence 2: 581083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: D30
PRIORITY NUMBER: 123
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: 36,989
PRACTICE NUMBER: 31354
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-1

Query Match 14.3%; Score 376; DB 1; Length 267;
Best Local Similarity 39.1%; Pred. No. 8, 2e-34;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

Qy 9 THGTTQKYEYFETLLIDYVSSG-FSNEIPL-ROSTIPVSDQRFVLYELVWGXDSX 66
Db 13 TGAATVOSYTNFIRAVRRLTADVRHEIPLNVEGLPLN-CRFLIVSHRAELSV 70
Qy 67 TAAIDVNNKTYRQAGOSYR-DAPRGA-THLFTGTRDSSLPFGXSYDIERY 123
Db 71 TLADVNNAYVGRANNAIFHPDQEDAAITLFT-DYGRYTFAGGVDRIDQL 129
Qy 124 AGH-RDQIPAGIXOLIQSYAL---KFGSGSTRQASITLILQISEARFPIIMRXR 179
Db 130 AGHRENIENGPLEAISALYYISGTQLPTLARSPICIQIISDARFOYIEGMR 189

Qy 180 QXINSGSELPDXMYMLETSWGQSGTQVGHSTGVFNNPRLAIXGFEVLNVRXYI 239
Db 190 TRIRYRNSAPDPVITLENMGRISTAIQSNQAFASFTQLGRMNSKFSYDVSTILI 249
Qy 240 ASLAIMLVCGGERPS 255
Db 250 PIALMYRCAPPSS 265

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Job time: 19.4882 secs

Thu Dec 11 16:09:56 2003

us-09-601-667c-40.rai

Page 7

Db 250 P11AMVYRCAPPSS 265

RESULT 13

/ Sequence 1, Application US/07988430

/ Patent No. 5416202

/ GENERAL INFORMATION:

/ APPLICANT: Bernhardt, Susan L.

/ APPLICANT: Better, Marc D.

/ APPLICANT: Carroll, Stephen P.

/ APPLICANT: Lane, Julie A.

/ APPLICANT: Lee, Chuan-Ping

/ TITLE OF INVENTION: Methods and Means for the Preparation and Use of Ribosome-Inactivating Proteins

/ NUMBER OF SEQUENCES: 101

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Marshall, O'Toole, Garstein, Murray &

/ STREET: Two First National Plaza, 20 South Clark

/ CITY: Chicago

/ STATE: Illinois

/ COUNTRY: USA

/ ZIP: 60603

/ COMPUTER: IBM PC COMPATIBLE

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/07988430

/ FILING DATE: 19921209

/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 07/901,707

/ FILING DATE: 1992-01-19

/ PRIORITY INFORMATION:

/ APPLICATION NUMBER: US 07/787,567

/ FILING DATE: 04-NOV-1991

/ ATTORNEY/AGENT INFORMATION:

/ NAME: No. 5416202 and, Greer B.

/ REGISTRATION NUMBER: 35302

/ REFERENCE/DOCKET NUMBER: 31133

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (312) 346-5750

/ FAX: (312) 984-9740

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 267 amino acids

/ TYPE: AMINO ACID

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

/ US-07-988-430-1

/ Query Match 14.3%; Score 376; DB 1; Length 267;

/ Best Local Similarity 39.1%; Pred. No. 8.2e-34;

/ Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

/ Db 250 P11AMVYRCAPPSS 265

/ Qy 9 THQTKGKHYRFTITLADYSSGS-FSNEIPL-RQSTIPVSDAQRFLVLTNQGDXK 66

/ Db 13 TQATVQSYTNFIAVAGRLTGADVRHILVLPKRVGLPIN-QRFLVLSNARSLAV 70

/ Qy 67 TLAIDVYKVVAVYQAGQSYLR-DAPRQAE--THLFTGTTRPSGLPFGSYXDIEY 123

/ Db 71 TLADVYKVVAVYQAGQSYLR-DAPRQAE--THLFTGTTRPSGLPFGSYXDIEY 129

/ Qy 124 AGH-RQIPIGIXQILQSYVAL--RXPQGSTXQASRILILQMSARFNPILWPKR 179

/ Db 130 AGNUNREILGNCPLEHLSALVYISTGTGTOPLTARSPICQIMSEALRFOYIEBMR 199

Db 250 P11AMVYRCAPPSS 265

RESULT 14

/ Sequence 16, Application US/08218303

/ Patent No. 5547867

/ GENERAL INFORMATION:

/ APPLICANT: Kato, Shunpandra V.

/ APPLICANT: Hockney, Robert C.

/ APPLICANT: Hockney, Robert C.

/ TITLE OF INVENTION: FERMENTATION PROCESS

/ NUMBER OF SEQUENCES: 23

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Cushman, Darby & Cushman

/ STREET: 1615 L Street, N.W.

/ CITY: Washington

/ STATE: D.C.

/ COUNTRY: U.S.A.

/ ZIP: 20036-5601

/ COMPUTER: REMARKABLE FORM:

/ OPERATING SYSTEM: IBM PC COMPATIBLE

/ SOFTWARE: Patent Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08218303

/ FILING DATE: 19921209

/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 07/841,533

/ FILING DATE: 26-FEB-1992

/ PRIORITY INFORMATION:

/ APPLICATION NUMBER: US 07/773,773

/ FILING DATE: 04-NOV-1991

/ ATTORNEY/AGENT INFORMATION:

/ NAME: No. 5547867 and, Greer B.

/ REGISTRATION NUMBER: 35302

/ REFERENCE/DOCKET NUMBER: 31133

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 202-861-3000

/ FAX: 202-861-3000

/ INFORMATION FOR SEQ ID NO: 16:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 267 amino acids

/ TYPE: amino acid

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

/ US-08-218-303-16

/ Query Match 14.3%; Score 376; DB 1; Length 267;

/ Best Local Similarity 39.1%; Pred. No. 8.2e-34;

/ Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

/ Db 250 P11AMVYRCAPPSS 265

/ Qy 9 THQTKGKHYRFTITLADYSSGS-FSNEIPL-RQSTIPVSDAQRFLVLTNQGDXK 66

/ Db 13 TQATVQSYTNFIAVAGRLTGADVRHILVLPKRVGLPIN-QRFLVLSNARSLAV 70

/ Qy 67 TLAIDVYKVVAVYQAGQSYLR-DAPRQAE--THLFTGTTRPSGLPFGSYXDIEY 123

/ Db 71 TLADVYKVVAVYQAGQSYLR-DAPRQAE--THLFTGTTRPSGLPFGSYXDIEY 129

/ Qy 124 AGH-RQIPIGIXQILQSYVAL--RXPQGSTXQASRILILQMSARFNPILWPKR 179

/ Db 130 AGNUNREILGNCPLEHLSALVYISTGTGTOPLTARSPICQIMSEALRFOYIEBMR 199

/ Qy 190 QXINSKSFIPDXVMELETSNQGQSTOVGHSTGVNPNPKRLATIXGNFVTLKXNVXYI 239

/ Db 190 TRIRNRSSADPFSVITLNSMWRSLTAIGSNQCAFSPFQLORRNSKFSVYDVSIIL 249

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us-09-601-667c-40.1rat

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 17,829
ADDRESS/DOCKET NUMBER: CRP-053
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-356-786-10

Query Match 15.3%; Score 403; DB 2; Length 534;
Best Local Similarity 27.9%; Pred. No. 2,2e-36;
Matches 143; Conservative 78; Mismatches 167; Indels 124; Gaps 23;

QY 9 THQTGKXKRPFTLLRDYVSSGS-FSNEIPL-ROSTIPVSDARFVIVETLVNQKXGX 66
DB 16 TAGATVOSTYNTFRAVGRRLTTGADVHEIPVLRVGLPTN--GRFLVLSNHAELSV 73
QY 67 TAAIDVTKXVAVAGQGYPLR-DAPGAE--THLTGTTRDSSLFPKSGIXYLER 123
DB 74 TLADVTNAVVGIRGNSALFHFHPDQDMSALHILF-DYGNVTFRFGNDLDEL 132
QY 124 AGH-RPOIPLGIXLOSYAL--RXPQSGTRXQASLILLOMISEARFNYLWXR 179
DB 133 AGNLRENIELGNGPLREISALVYVSGTQPLARSPFICIQMISEARFOYIGER 192
QY 180 QXINSGKSPLEPXWLELFTSMQOSTGVGHTGVNNEPKALIXGNFTLVNPKXYI 239
DB 193 TRIRNRBSADPPSVITLNSMGRSLTAIOENQGFASPTOLQRNGKFSYVDVSI 252
QY 240 ASLAIMFVCGRRSSDVRWPLVTRVADDTGCASEPTFRIYQKXMYVDHDDF 259
DB 253 FIKNAVYRQAPRSG--FSLIRVYPRNNDVQWDEIGLV----- 264
QY 300 HDNGOILMPSKSNNDPQLTIRKXITIRKSGCLTYG----- 339
DB 295 QSGPELK-----KFGK--TVK--ISCAAGTYFANQMMWKOAGKGLWGWINT 342
QY 340 YTA-GVYV-----MIFDGNVREXTI-----WQIKXNTINE 372
DB 343 YTGSTVADDFKRRFASLETSATTAHQINLRNEDSATFCARFPAWQGLIVSY 402
QY 373 KSNVLAASGICITLTITVQILDVTLQGMHNDTPRZYITIGRDLQMSNGSIW 432
DB 403 SASI--SSSGGGS-----GGSGSG-----GDSIDMNGSPSLA 437
QY 433 E-----TKSSQ--XNCKM-ALYGDGSR 454

DB 438 SICRVSITCRASODIGNSLTMISSCPDGTIK 469
RESULT 12
US-07-901-707-1
Sequence 1, Application US/07901707
Patent No. 5376546
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greca E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 57129/30910
TELEPHONE: (312) 346-5780
TELEFAX: (312) 984-5750
TIREX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-901-707-1

Query Match 14.3%; Score 376; DB 1; Length 267;
Best Local Similarity 39.1%; Pred. No. 8,2e-34;
Matches 100; Conservative 43; Mismatches 101; Indels 12; Gaps 8;

QY 9 THQTGKXKRPFTLLRDYVSSGS-FSNEIPL-ROSTIPVSDARFVIVETLVNQKXGX 66
DB 13 TAGATVOSTYNTFRAVGRRLTTGADVHEIPVLRVGLPTN--GRFLVLSNHAELSV 70
QY 67 TAAIDVTKXVAVAGQGYPLR-DAPGAE--THLTGTTRDSSLFPKSGIXYLER 123
DB 71 TLADVTNAVVGIRGNSALFHFHPDQDMSALHILF-DYGNVTFRFGNDLDEL 129
QY 124 AGH-RPOIPLGIXLOSYAL--RXPQSGTRXQASLILLOMISEARFNYLWXR 179
DB 130 AGNLRENIELGNGPLREISALVYVSGTQPLARSPFICIQMISEARFOYIGER 189
QY 180 QXINSGKSPLEPXWLELFTSMQOSTGVGHTGVNNEPKALIXGNFTLVNPKXYI 239
DB 190 TRIRNRBSADPPSVITLNSMGRSLTAIOENQGFASPTOLQRNGKFSYVDVSI 249

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Page 5

APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESS: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION/DOCKET NUMBER: 33651
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ. ID NO. 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-761a-71

Query Match 17.3%, Score 453.5, DB 1, Length 250;
Best Local Similarity 41.9%, Freq. No. 1,56-42;
Matches 106, Conservative 34, Mismatches 86, Indels 27, Gaps 7;
DB 9 THQTTKXEFREFTLLRDVSSGGSFSENPILRGSTIPVSDAQRVAVELTNGQXDSXTA 68
69 AIDVTNXYVAYQADQSYFLRDAPRGAETHLFTGTRDSLSLFFXGSYXDLERYAGH-R 127
DB 9 TEGATSGYKQFTEALRERL-RGLLHDIPLVDPPT-TLQERNRYITVELNSDTSIEV 66
QY 69 AIDVTNXYVAYQADQSYFLRDAPRGAETHLFTGTRDSLSLFFXGSYXDLERYAGH-R 127
DB 67 GIDVTNAYVAYRAGTQSYFLRDAPSSADYLFYGT-DQHSLEFYGVGLERMAHQSR 124
QY 128 DQPLGLXQGLQSYVYALRXGGSSTKQASILLIQLNISEAARENPILMEXQXINSXS 187
DB 125 QQLHDLQALHNGISFRBSGDNDEKATLVIYIOWAELARRYISNRVFSIQGTGA 184
QY 188 FLDPDXMLETSMGQSTQVQSTQVGNPNPRLAIXGNFVTLXVWX----- 237
DB 185 FQPDAMTISLENNW-DNLRGVQSSVQDTPNQ-----VLTNINRNPVYDLSH 233
QY 238 -VIASLAIMLFC 249
DB 234 PTVAVIALMLFC 246

RESULT 10
US-08-485-286-71
Sequence 71, Application US/09485286
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESS: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION/DOCKET NUMBER: 33651
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ. ID NO. 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-71

Query Match 17.3%, Score 453.5, DB 1, Length 250;
Best Local Similarity 41.9%, Freq. No. 1,56-42;
Matches 106, Conservative 34, Mismatches 86, Indels 27, Gaps 7;
DB 9 THQTTKXEFREFTLLRDVSSGGSFSENPILRGSTIPVSDAQRVAVELTNGQXDSXTA 68
69 AIDVTNXYVAYQADQSYFLRDAPRGAETHLFTGTRDSLSLFFXGSYXDLERYAGH-R 127
DB 9 TEGATSGYKQFTEALRERL-RGLLHDIPLVDPPT-TLQERNRYITVELNSDTSIEV 66
QY 69 AIDVTNXYVAYQADQSYFLRDAPRGAETHLFTGTRDSLSLFFXGSYXDLERYAGH-R 127
DB 67 GIDVTNAYVAYRAGTQSYFLRDAPSSADYLFYGT-DQHSLEFYGVGLERMAHQSR 124
QY 128 DQPLGLXQGLQSYVYALRXGGSSTKQASILLIQLNISEAARENPILMEXQXINSXS 187
DB 125 QQLHDLQALHNGISFRBSGDNDEKATLVIYIOWAELARRYISNRVFSIQGTGA 184
QY 188 FLDPDXMLETSMGQSTQVQSTQVGNPNPRLAIXGNFVTLXVWX----- 237
DB 185 FQPDAMTISLENNW-DNLRGVQSSVQDTPNQ-----VLTNINRNPVYDLSH 233
QY 238 -VIASLAIMLFC 249
DB 234 PTVAVIALMLFC 246

RESULT 11
US-08-356-786-10
Sequence 10, Application US/08356786
Patent No. 587305
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Herman
APPLICANT: Houston, L. L.
APPLICANT: King, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer

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STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-77

Query Match
41.9%; Score 1101; DB 1; Length 540;
Matches 242; Conservative 81; Mismatches 193; Indels 20; Gaps 11;

9 THOTTGKYEYREITLADVSSGS-FSNEIPL-RSTIFVSDAQRFVLEINQGXDSX 66
13 TADATVSYNPIAVRSHITTDADVHEIPVLENEVGLDIS--QRFIVLEINSHASLV 70
67 TADITNXYVAVQAGQSYPLR-DAPGAE--TETFTTRDSSLPFYKSYKOLEY 123
71 TADITNXYVAVQAGQSYPLR-DAPGAE--TETFTTRDSSLPFYKSYKOLEY 123
124 AGHROCPGLXOLIOSYKX--RPGSTKXQASILLIOMISAPAFNELIMEXRQ 180
130 GGFREIEIGTGPLLEDAISALTYSTGTQCFPLASFWICQWISAPAFVIEZEWAT 189
181 XINSQXSLPDXMLELTSWQOSTVGHSTGVFNNKRLAIXGNFVILANVAVYA 240
190 RIXYKRSAPDSVITLNSKNSLTAIGSQGASAPFQIQRRNSFENVYDVSILIP 249
241 STALPVCSEPPSSQVWYHYRPHAD--DTTCSASEPTTATYKXKQVTRD 297
250 IIALVYKCAPPSQ---PSLIRVYVNNADV-CQPEHIVRIYVBNGLCDVTVGS 304
298 DFHGNQIOLWPSKNNPDLTKIKDYIISNGSCITTYGVYGVYVMEPCNFAVR 357
305 RFPDNPQLWPCSKNDPMDLTKIKDYIISNGSCITTYGVYGVYVMEPCNFAVR 357
358 ATTQWQKNGTITNRSNVLAASSGKIGTLYVQTLDTLQYGLAAGDTAPREYVIT 417
365 NIKQWQKNGTITNRSNVLAASSGKIGTLYVQTLDTLQYGLAAGDTAPREYVIT 417
418 FRLCMEKXGKSVYVTCSSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 477
425 LYMCLOANSGKWLBPCTSEKAO-QMALYADBSIRPQQRNCLITPANIKGIVYKIL 483
478 SCSSXSSXQXQVFTNEKALIMLXXXXXXDVAQAFGRIRIIIPATKXNQMPLV 533
484 SCQPASSSQRMWPKNDGTLINLVNGLVDRSPSLKQIIVHPFHQNMQIMLP 539

RESULT 7
US-08-776-059-39
Sequence 39, Application US/08776059B
Patent No. 6271368

GENERAL INFORMATION:
APPLICANT: LEWISZSN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: ECK, Jürgen
APPLICANT: ECK, Jürgen
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 059B
EARLIER FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
NUMBER OF SEQ ID NOS: 36
SEQUENCE: Patent Ver. 2.0
LENGTH: 235
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-39

Query Match
40.9%; Score 1073; DB 3; Length 235;
Best Local Similarity 91.6%; Pred. No. 3, 6e-112;

Matches 217; Conservative 0; Mismatches 18; Indels 2; Gaps 1;

18 FRIITLADVSSGSFSENEIPLARQSTIFVSDAQRFVLEINQGXSTADITNXY 77
1 FRIITLADVSSGSFSENEIPLARQSTIFVSDAQRFVLEINQGXSTADITNXY 60
78 VAYQAGQSYPLRPAQAEHLFTGTTRDSSLPFXGXYDEYAGRQIPLGIXOL 137
61 VAYQAGQSYPLRPAQAEHLFTGTTRDSSLPFXGXYDEYAGRQIPLGIXOL 118
138 IGSVLAERPGSTKXQASILLIOMISAPAFNELIMEXRQXINSKXSLPDXMLEL 197
119 IGSVLAERPGSTKXQASILLIOMISAPAFNELIMEXRQXINSKXSLPDXMLEL 178
198 FTSWQOSTVGHSTGVFNNKRLAIXGNFVILANVAVYA 254
179 FTSWQOSTVGHSTGVFNNKRLAIXGNFVILANVAVYA 235

RESULT 8
US-09-538-873-3
Sequence 3, Application US/09538873
Patent No. 6565500

GENERAL INFORMATION:
APPLICANT: ELLIN S
APPLICANT: ELLIN S
APPLICANT: ELLIN S
APPLICANT: ELLIN S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
FILE REFERENCE: US/09/538, 873
CURRENT APPLICATION NUMBER: US/09/538, 873
EARLIER FILING DATE: 2000-03-30
EARLIER APPLICATION NUMBER: 98/067426, 826
NUMBER OF SEQ ID NOS: 19
SEQUENCE: Patent Ver. 2.1
SEQ ID NO 3
LENGTH: 251
TYPE: PRT
ORGANISM: Abtus precatorius
US-09-538-873-3

Query Match
17.6%; Score 461; DB 4; Length 251;
Matches 106; Conservative 34; Mismatches 87; Indels 26; Gaps 6;

9 THOTTGKYEYREITLADVSSGSFSENEIPLARQSTIFVSDAQRFVLEINQGXSTA 68
9 TEGATSGYKQFIRALRELU-RGCHIDIPVDPF-TLQERRKRTIVELSSSTISLV 66
63 AIDTNNXYVAVQAGQSYPLRPAQAEHLFTGTTRDSSLPFXGXYDEYAGRQIPLGIXOL 127
67 GIDTNNXYVAVQAGQSYPLRPAQAEHLFTGTTRDSSLPFXGXYDEYAGRQIPLGIXOL 124
128 DCPPLGIXOLIOSYKX--RPGSTKXQASILLIOMISAPAFNELIMEXRQXINSKXSLPDXMLEL 187
125 QOILDLQALHTGISFPFGSGDNNEKARLLVLIQVAAAFYVSNRVSIGTGA 184
188 FLPDXMLELTSWQOSTVGHSTGVFNNKRLAIXGNFVILANVAVYA 251
185 FLPDXMLELTSWQOSTVGHSTGVFNNKRLAIXGNFVILANVAVYA 234
238 -VISLALNPLVC 249
235 FVAVLALNPLVC 247

RESULT 9
US-08-378-761A-71
Sequence 71, Application US/08378761A
Patent No. 5635984
GENERAL INFORMATION:

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Page 3

Db 2 YERIKLVHTQTESEYFRFTLLADYVSSSPSENEILRQSTIPVSDARPLVETLN 61
Qy 61 QGKQSTNAIDYNNXYVVAQAGDSYFLRDAFPGATLHFTGTRDSGLPFGSYXDL 120
Db 62 QGDSIRNADYNNXYVVAQAGDSYFLRDAFPGATLHFTGTRDSGLPFGSYXDL 119
Qy 121 ERYAGHRDOIPLGIXOLIOGVYAL--EXPAGSTRXQASSTILLIOMISEARFELMXEQ 180
Db 120 ERYAGHRDOIPLGIXOLIOGVYAL--EXPAGSTRXQASSTILLIOMISEARFELMXEQ 179
Qy 181 XINSKSGFLPDYVMELESTMGQOSTVQVSHDGVNNPKRLAIXKGNPVLNAXRVYA 240
Db 180 YINSKSGFLPDYVMELESTMGQOSTVQVSHDGVNNPKRLAIXKGNPVLNAXRVYA 239
Qy 241 SLATMEFVCGERS 254
Db 240 SLATMEFVCGERS 253

RESULT 5

US-08-378-761A-77
Sequence 77, Application US/08378761A
Patent No. 5635384

GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D

APPLICANT: KOSMAN, ALICE ER
TITLE OF INVENTION: INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN

COUNTRY: US
ZIP: 46268

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-378-761A-77

Query Match 41.9%, Score 1101, DB 1, Length 540;
Best Local Similarity 45.1%, Pred No 9, Seq-115

Matches 242; Conservative 81, Mismatches 193, Indels 20, Gaps 11;

Qy 9 THDTGKEYFRITLADYVSSG--FNEIPL--RSTIPVSDARPLVETLNQKXSK 66
Db 13 TADATVSTNPLAVRSHLTADYVHEPLVLRVNGPLPS--GRFLVSHSLHSLSV 70
Qy 67 TLAIDVNNXYVVAQAGDSYFLR--DAPRGA--TLHFTGTRDSGLPFGSYXDLERY 123

Db 71 TLAIDVNNXYVVAQAGDSYFLR--DAPRGA--TLHFTGTRDSGLPFGSYXDLERY 129
Qy 124 AGHRDOIPLGIXOLIOGVYAL--EXPAGSTRXQASSTILLIOMISEARFELMXEQ 180
Db 130 GGLNENIELGHRDLMSLITVSTQGIPTLAKSPVYCLOMISEARFELMXEQ 189
Qy 181 XINSKSGFLPDYVMELESTMGQOSTVQVSHDGVNNPKRLAIXKGNPVLNAXRVYA 240
Db 180 RRYNERSADPSEVITLNSWGLSLTAIOBNQAFAPFLOQRNRSKENVYDVSLILP 249
Qy 241 SLATMEFVCGERSSDRYMPLVIRPVAD--DYCSASEPVRIVGKXKXDVYAD 297
Db 250 ILALMYRCAAPSSQ---FSLIRPVVFNPAVY--CNDEPVLIVRNGLCVDVYGE 304
Qy 298 DPHNQIQLMPSKNNDPNQTITRQXNINRSGCLTITGTAGVYMTPOCTANFE 357
Db 305 EPPQNFQLMPSKNNDPNQTITRQXNINRSGCLTITGTAGVYMTPOCTANFE 364
Qy 358 ATIMQIKNKGITLINPRNMLYLAASGIGKTTLVQTLDTLGGQMLAGNDAPREYTVG 417
Db 365 ATRMQIMNRTIINPRSGVLAATSNGSGTLVQTLNIVYSGQMLPTNNTOPFTTVG 424
Qy 418 FPDLCNESKSGYVETCKSSQXQXNALYGDGSIIPKQNDQCTKGRDSYVINYI 477
Db 425 IYMGCLNNSGKVMLEDCSTERAQ--QNALYAGSIRPQNDQCTKGRDSYVINYI 483
Qy 478 SCSSKXKQRMVETEXALINIKKXKXNDVQAQAPRLRIIYVANGKQMWLV 533
Db 484 SCGRASSGQRMVETEXALINIKKXKXNDVQAQAPRLRIIYVANGKQMWLV 539

RESULT 6

US-08-485-286-77
Sequence 77, Application US/08485286
Patent No. 5645026

GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D

APPLICANT: KOSMAN, ALICE ER
TITLE OF INVENTION: INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN

COUNTRY: US
ZIP: 46268

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid

Thu Dec 11 16:09:56 2003

us-09-601-667c-40.rat

Page 2

Db 332 DNMOTLMSKSNNDPMOATWIKRGTSSNSCLTGTGAGVYWMIPDCTVREATL 391
QY 361 MOIWNGTIIINFRSNIVLAASGIGTTLTVOGLDYLTCGSMAGNDTAPREVTIGFRD 420
Db 392 MOIWNGTIIINFRSNIVLAASGIGTTLTVOGLDYLTCGSMAGNDTAPREVTIGFRD 451
QY 421 LCMESNGSVWETFCSSXONXWALVYDGFREFKQMOGCTKGRDSYFTVNTVSCS 480
Db 452 LCMESNGSVWETFCSSXONXWALVYDGFREFKQMOGCTKGRDSYFTVNTVSCS 510
QY 481 XXSXQWVFTNEXATILNXXXXXDDVAONPKLRITIIYPATGKPNQWMLPV 533
Db 511 AGSSQWVFTNEXATILNXXXXXDDVAONPKLRITIIYPATGKPNQWMLPV 563

RESULT 2
US-08-776-059-43
Sequence 43, Application US/0876059B
Best Local Similarity 91.6%; Pred. No. 6,3e-134;
Matches 241; Conservative 1; Mismatches 20; Indels 1; Gaps 1;
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: BAKR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER PUBLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 43
LENGTH: 263
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-43

Query Match 48.3%; Score 1267.5; DB 3; Length 263;
Best Local Similarity 91.6%; Pred. No. 6,3e-134;
Matches 241; Conservative 1; Mismatches 20; Indels 1; Gaps 1;
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QY 1 DDTCSASEPTVRIYGRXGKXWVYDDDPHNOGLOLPSKSNNDPMOATWIKRGTSS 60
Db 331 NSGCLTGTGAGVYWMIPDCTVREATILWQIXNGTIIINFRSNIVLAASGIGTTLT 390
QY 61 NSGCLTGTGAGVYWMIPDCTVREATILWQIXNGTIIINFRSNIVLAASGIGTTLT 120
Db 391 VOTLDYTLGQSMAGNDTAPREVTIGFRDLCMESNGSVWETFCSSXONXWALVYD 450
QY 121 VOTLDYTLGQSMAGNDTAPREVTIGFRDLCMESNGSVWETFCSSXONXWALVYD 179
Db 451 GSIRPKONODCTKGRDSYFTVNTVSCSXQWVFTNEXATILNXXXXXDDVAON 510
QY 180 GSIRPKONODCTKGRDSYFTVNTVSCSXQWVFTNEXATILNXXXXXDDVAON 239
Db 511 NPKLRITIIYPATGKPNQWMLPV 533
QY 240 NPKLRITIIYPATGKPNQWMLPV 262

RESULT 3
US-08-776-059-33
Sequence 33, Application US/0876059B
Best Local Similarity 91.6%; Pred. No. 6,271368
Matches 232; Conservative 1; Mismatches 19; Indels 2; Gaps 1;
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: BAKR, Jurgen

APPLICANT: BAKR, Axel
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER PUBLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 33
LENGTH: 264
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-33

Query Match 48.3%; Score 1267.5; DB 3; Length 264;
Best Local Similarity 91.6%; Pred. No. 6,3e-134;
Matches 241; Conservative 1; Mismatches 20; Indels 1; Gaps 1;
Db 271 DDTCSASEPTVRIYGRXGKXWVYDDDPHNOGLOLPSKSNNDPMOATWIKRGTSS 61
QY 2 DDTCSASEPTVRIYGRXGKXWVYDDDPHNOGLOLPSKSNNDPMOATWIKRGTSS 121
Db 331 NSGCLTGTGAGVYWMIPDCTVREATILWQIXNGTIIINFRSNIVLAASGIGTTLT 390
QY 62 NSGCLTGTGAGVYWMIPDCTVREATILWQIXNGTIIINFRSNIVLAASGIGTTLT 121
Db 391 VOTLDYTLGQSMAGNDTAPREVTIGFRDLCMESNGSVWETFCSSXONXWALVYD 450
QY 122 VOTLDYTLGQSMAGNDTAPREVTIGFRDLCMESNGSVWETFCSSXONXWALVYD 180
Db 451 GSIRPKONODCTKGRDSYFTVNTVSCSXQWVFTNEXATILNXXXXXDDVAON 510
QY 181 GSIRPKONODCTKGRDSYFTVNTVSCSXQWVFTNEXATILNXXXXXDDVAON 240
Db 511 NPKLRITIIYPATGKPNQWMLPV 533
QY 241 NPKLRITIIYPATGKPNQWMLPV 263

RESULT 4
US-08-776-059-31
Sequence 31, Application US/0876059B
Best Local Similarity 91.6%; Pred. No. 6,271368
Matches 232; Conservative 1; Mismatches 19; Indels 2; Gaps 1;
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: BAKR, Jurgen
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003 US/08/776, 059B
CURRENT APPLICATION NUMBER: US/08/776, 059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER PUBLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 31
LENGTH: 253
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-31

Query Match 44.0%; Score 1155; DB 3; Length 253;
Best Local Similarity 91.3%; Pred. No. 2,5e-121;
Matches 232; Conservative 1; Mismatches 19; Indels 2; Gaps 1;
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: BAKR, Jurgen
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003 US/08/776, 059B
CURRENT APPLICATION NUMBER: US/08/776, 059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER PUBLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 31
LENGTH: 253
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-31

Thu Dec 11 16:09:56 2003

US-09-601-667C-40.rai

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 11, 2003, 13:53:18 ; Search time 18.4882 Seconds
(without alignments) 1222.073 Million cell updates/sec

Title: US-09-601-667C-40
Perfect score: 2626
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310859 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgm2_5/prodate/1/aa/backfield.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2504.5	95.4	564	3	US-08-776-059-35 Sequence 35, Appl
2	1267.5	48.3	263	3	US-08-776-059-43 Sequence 43, Appl
3	1267.5	48.3	264	3	US-08-776-059-33 Sequence 33, Appl
4	1155	44.0	253	3	US-08-776-059-31 Sequence 31, Appl
5	1101	41.9	540	1	US-08-378-761A-77 Sequence 77, Appl
6	1101	41.9	540	1	US-08-488-286-77 Sequence 77, Appl
7	1073	40.2	235	3	US-08-776-059-39 Sequence 39, Appl
8	1073	40.2	235	3	US-08-776-059-39 Sequence 39, Appl
9	453.5	17.3	250	1	US-08-378-761A-71 Sequence 71, Appl
10	453.5	17.3	250	1	US-08-378-761A-71 Sequence 71, Appl
11	403	15.3	534	2	US-08-488-286-71 Sequence 71, Appl
12	376	14.3	267	1	US-07-901-707-1 Sequence 1, Appl
13	376	14.3	267	1	US-07-988-430-1 Sequence 1, Appl
14	376	14.3	267	1	US-08-218-303-16 Sequence 16, Appl
15	376	14.3	267	1	US-08-425-336-1 Sequence 1, Appl
16	376	14.3	267	1	US-08-488-113B-1 Sequence 1, Appl
17	376	14.3	267	1	US-08-477-488B-1 Sequence 1, Appl
18	376	14.3	267	2	US-08-546-360-1 Sequence 21, Appl
19	376	14.3	267	2	US-08-546-360-1 Sequence 21, Appl
20	376	14.3	267	3	US-08-838-782-61 Sequence 1, Appl
21	376	14.3	267	3	US-08-838-782-61 Sequence 1, Appl
22	376	14.3	267	4	US-09-610-838-1 Sequence 1, Appl
23	376	14.3	267	4	US-09-610-838-1 Sequence 1, Appl
24	376	14.3	267	5	PCT-US92-09487-1 Sequence 1, Appl
25	376	14.3	268	5	US-08-356-786-8 Sequence 8, Appl
26	372	14.2	290	1	US-08-378-761A-27 Sequence 27, Appl
27	372	14.2	290	1	US-08-488-286-27 Sequence 27, Appl

28	372	14.2	290	6	US-08-324-301-15 Sequence 15, Appl
29	326	12.4	282	1	US-08-778-761A-74 Sequence 74, Appl
30	301	11.5	267	1	US-08-488-286-74 Sequence 74, Appl
31	301	11.5	267	1	US-08-488-286-74 Sequence 74, Appl
32	299	11.4	247	1	US-08-477-488B-6 Sequence 6, Appl
33	299	11.4	247	1	US-08-477-488B-6 Sequence 6, Appl
34	299	11.4	247	2	US-08-483-502-4 Sequence 4, Appl
35	299	11.4	247	3	US-08-483-502-4 Sequence 4, Appl
36	299	11.4	247	3	US-08-483-502-4 Sequence 4, Appl
37	299	11.4	247	3	US-08-483-502-4 Sequence 4, Appl
38	294	11.2	289	1	US-08-184-237-4 Sequence 4, Appl
39	294	11.2	289	2	US-08-482-920-4 Sequence 4, Appl
40	294	11.2	289	3	US-08-484-341-4 Sequence 4, Appl
41	294	11.2	289	3	US-08-484-341-4 Sequence 4, Appl
42	294	11.2	289	3	US-08-483-502-4 Sequence 4, Appl
43	294	11.2	289	3	US-08-483-502-4 Sequence 4, Appl
44	287.5	10.9	263	1	US-07-501-707-4 Sequence 4, Appl
45	287.5	10.9	263	1	US-07-501-707-4 Sequence 4, Appl

ALIGNMENTS

```
RESULT 1
US-08-776-059-35
Sequence 35, Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: EXX, Orlgen
APPLICANT: BUNN, Axel
APPLICANT: BUNN, Axel
TITLE OF INVENTION: MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776,059B
CURRENT FILING DATE: 1999-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
US-08-776-059-35
ORGANISM: Viscum album
Query Match 95.4%, Score 2504.5, DB 3, Length 564;
Best Local Similarity 91.7%, Pred. No. 2.5e-272;
Matches 489; Conservative 2; Mismatches 39; Indels 3; Gaps 2.
QY 1 YERLARVHTQTKEXYFRITLARDVSSGSSSNIFLRQSTIPYSQARFLVETRN 60
61 QGXSTAIIDVNNXYVAVAGQSGVFLAPRGAEHLFTGTRDRSLPXSXYND 120
34 YERLARVHTQTKEXYFRITLARDVSSGSSSNIFLRQSTIPYSQARFLVETRN 93
QY 1 YERLARVHTQTKEXYFRITLARDVSSGSSSNIFLRQSTIPYSQARFLVETRN 60
121 EVYGRHDDIPLDIOLOSVAFKPGKSTROKRSITLILQWISPAARFETLRRKQ 180
152 EVYGRHDDIPLDIOLOSVAFKPGKSTROKRSITLILQWISPAARFETLRRKQ 211
181 XNKGASRTPDYMTAELEFISVQSGTVOGSDTCFNNPKYLLXKNTLXNRYXIA 240
212 YNKGASRTPDYMTAELEFISVQSGTVOGSDTCFNNPKYLLXKNTLXNRYXIA 271
241 SLATMFVCGRRSSGVRKMLVTPYADDTGASAEPTVRAIVGKXVVRDDPDP 300
272 SLATMFVCGRRSSGVRKMLVTPYADDTGASAEPTVRAIVGKXVVRDDPDP 331
QY 301 DNDQIDLPKSKSNDDPMQMTIKEDXTIRSNKSCLTGYAGYVWIPDNTAIREATI 360
```

DR N-PSDB; AA029120.
XX Preparation of mistletoe lectins in heterologous systems,
PY particularly for use as anticancer agents and immunostimulants
XX
XX Disclosure; Fig 18B; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The 286 amino acid
CC ribosome. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B5 protein.
SQ Sequence 265 AA:

Query Match 49.1%; Score 1290; DB 20; Length 265;
Best Local Similarity 32.4%; Pred. No. 3,6e-134;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 271 DDTGSASEPTVAVKXKXVVDVDDPHDQNLQIWPFSKSNDDPQMLWTIKEDXTIRS 330
DB 1 DDTGSASEPTVAVKXKXVVDVDDPHDQNLQIWPFSKSNDDPQMLWTIKEDXTIRS 60
QY 331 NSGCLTGYGTAQVYMTFDCNTVREACTIQIMKXGTTINRSGNITLAASGIGKTTTF 390
DB 61 NSGCLTGYGTAQVYMTFDCNTVREACTIQIMKXGTTINRSGNITLAASGIGKTTTF 120
QY 391 VQTLDTYTLGGWLAGNDPAPEVITYGFEDLCMSKXGSYWEFCXSOXQXWALYED 450
DB 121 VQTLDTYTLGGWLAGNDPAPEVITYGFEDLCMSKXGSYWEFCXSOXQXWALYED 180
QY 451 GSIRKXNODQCLTXGRDSYVTVINIVSCXKXKXQWFTNEXAIIINIKXXXXVYAK 510
DB 181 GSIRKXNODQCLTXGRDSYVTVINIVSCXKXKXQWFTNEXAIIINIKXXXXVYAK 240
QY 511 NPKLRRIIYPATGKXNQMLFV 533
DB 241 NPKLRRIIYPATGKXNQMLFV 263

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Accession	Sequence	Score	DB	Length
XX	Claim 9; Fig 12b; 79pp; German.			
CC	This invention describes a novel mistletoe lectin (I) and its fragments			
CC	CC which have antitumour and immunostimulatory activity. The A-chain (MA)			
CC	of the mistletoe lectin binds to, and inactivates, the 28S subunit of			
CC	ribosomes. Non-cytotoxic forms of (I) activate T-cell and			
CC	lymphokine-producing macrophages, so stimulate immunity. (I) and its			
CC	fragments are used to treat uncontrolled cell growth, particularly			
CC	immune response, bacterial infection, or a cytotoxic disease. Strength of the			
CC	(tumour-associated, bacterial or viral). The method allows production of			
CC	mistletoe lectin, and its individual chains, in many different isoforms			
CC	and on a large scale, at any time of the year. Recombinant products are			
CC	free from toxins present in natural mistletoe extracts. This sequence			
CC	represents a fragment of a mistletoe lectin B5 protein.			
XX	Sequence 264 AA;			
XX				
Query Match:	49.1%;	Score 1260;	DB 20;	Length 264;
Best Local Similarity	97.4%;	Pred 130;	Seq 130;	
Matches 243;	Conservative 0;	Mismatches 20;	Indels 0;	Gaps 0;
QY	271 DVTGSSASPEPTVIRYVKRCKXQYVADDDPFHGNQIQLPWSEKSNNDPQQLMTIRKEDYTRIS 330			
Db	1 DVTGSSASPEPTVIRYVGRKSRVDVADDDPFHGNQIQLPWSEKSNNDPQQLMTIRKEDYTRIS 60			
QY	31 NSGCLITFTGNGAYVIMFPCQTAIVREATTQIMXNGTIIINRSNLYLASSGIGKDTLT 390			
Db	61 NSGCLITFTGNGAYVIMFPCQTAIVREATTQIMXNGTIIINRSNLYLASSGIGKDTLT 120			
QY	391 VQDLYLYLQGLNLGNDAIPREVIYGFDPDCWESKXSGYVWEFCXSSQXQXVALYGP 450			
Db	121 VQDLYLYLQGLNLGNDAIPREVIYGFDPDCWESKXSGYVWEFCXSSQXQXVALYGP 180			
QY	451 GSIRPNQNDQCLIXGRGSVSTVNIYVCSXXSXQRWVETWEAIIINLKXXXDXVAAQ 510			
Db	181 GSIRPNQNDQCLIXGRGSVSTVNIYVCSGXSGRWVETWEAIIINLKSSLDVDAQA 240			
QY	511 NPTLRRIITTYPAKCKNQNMQLP 533			
Db	241 NPTLRRIITTYPAKCKNQNMQLP 263			
XX	RESULT 15			
XX	AAVZ5996			
XX	AAVZ5996 standard; Protein; 265 AA.			
XX	AAVZ5996;			
XX	18-OCT-1999 (first entry)			
XX	Mistletoe lectin B5 variant protein fragment.			
XX	Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;			
XX	lymphocyte 28S subunit; non-cytotoxic; T-cell activation; immune response;			
XX	lymphokine-producing macrophage; uncontrolled cell growth; treatment;			
XX	cancer; cytotoxicity; antigen; isoform; lectin B5.			
XX	Vicium album.			
XX	DEJ9804210-AL.			
XX	12-AUG-1999.			
XX	03-FEB-1998; 98DE-1004210.			
XX	03-FEB-1998; 98DS-1004210.			
XX	(BIOS)-BIOSYN ARANIMITTEL CMH.			
XX	Morris P, Stiefel T, Woelfel W, Woelfel P,			
XX	WPI; 1999-445335/38.			

XX Sequence 265 AA;
 SQ Query Match 49.2%; Score 1291; DB 20; Length 265;
 Best Local Similarity 92.4%; Pred. No. 2.8e-134;
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 271 DDTCSASEPTVRIVSGKXGVVDVDDDFHDNSQIQLPKSNNDPQWLTIKXITRS 330
 DB 1 DDTCSASEPTVRIVSGKXGVVDVDDDFHDNSQIQLPKSNNDPQWLTIKXITRS 60
 QY 331 NSGCLTGYTAGVYVMEFDQNTAVREATIQIKXNGIIMPESNVLAAASGIKGTLT 390
 DB 61 NSGCLTGYTAGVYVMEFDQNTAVREATIQIKXNGIIMPESNVLAAASGIKGTLT 120
 QY 391 VOTLDYTLGGWLAGNDTAPREVTIYGFRLDCKESNGSVWETCSQXQXWALYGD 450
 DB 121 VOTLDYTLGGWLAGNDTAPREVTIYGFRLDCKESNGSVWETCSQXQXWALYGD 180
 QY 451 GSIRPKQNOQCLTXGRDSVSTVINIVSGSXSKXQRMVFTNEZAIINLKXXXXXVDAQA 510
 DB 181 GSIRPKQNOQCLTXGRDSVSTVINIVSGSXSKXQRMVFTNEZAIINLKXXXXXVDAQA 240
 QY 511 NPKLRRIITYPATGKPNQWMLPV 533
 DB 241 NPKLRRIITYPATGKPNQWMLPV 263

RESULT 12
 AAY25993
 ID AAY25993 standard; Protein; 265 AA.
 XX AAY25993;
 DT 18-OCT-1999 (first entry)
 DB Mistletoe lectin B2 variant protein fragment.
 XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B2.
 XX Viscum album.
 XX DB19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelker W, Welters P;
 DR WPI; 1999-44535/38.
 DR N-PEDS; AA209117.
 PT Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants
 PS Disclosure; Fig 15B; 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC of the mistletoe lectin and its ribozyme activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to and inactivates the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B2 protein.
 XX Sequence 265 AA;
 SQ Query Match 49.2%; Score 1291; DB 20; Length 265;
 Best Local Similarity 92.4%; Pred. No. 2.8e-134;
 Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 271 DDTCSASEPTVRIVSGKXGVVDVDDDFHDNSQIQLPKSNNDPQWLTIKXITRS 330
 DB 1 DDTCSASEPTVRIVSGKXGVVDVDDDFHDNSQIQLPKSNNDPQWLTIKXITRS 60
 QY 331 NSGCLTGYTAGVYVMEFDQNTAVREATIQIKXNGIIMPESNVLAAASGIKGTLT 390
 DB 61 NSGCLTGYTAGVYVMEFDQNTAVREATIQIKXNGIIMPESNVLAAASGIKGTLT 120
 QY 391 VOTLDYTLGGWLAGNDTAPREVTIYGFRLDCKESNGSVWETCSQXQXWALYGD 450
 DB 121 VOTLDYTLGGWLAGNDTAPREVTIYGFRLDCKESNGSVWETCSQXQXWALYGD 180
 QY 451 GSIRPKQNOQCLTXGRDSVSTVINIVSGSXSKXQRMVFTNEZAIINLKXXXXXVDAQA 510
 DB 181 GSIRPKQNOQCLTXGRDSVSTVINIVSGSXSKXQRMVFTNEZAIINLKXXXXXVDAQA 240
 QY 511 NPKLRRIITYPATGKPNQWMLPV 533
 DB 241 NPKLRRIITYPATGKPNQWMLPV 263

RESULT 13
 AAY25986
 ID AAY25986 standard; Protein; 264 AA.
 XX AAY25986;
 DT 18-OCT-1999 (first entry)
 DB Mistletoe lectin B1 protein fragment.
 XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B1.
 XX Viscum album.
 XX DB19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelker W, Welters P;
 DR WPI; 1999-44535/38.
 DR N-PEDS; AA209110.
 PT Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants
 PS Claim 9; Fig 8B; 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of

QY 331 NGSCLTITVGTAGTWTWIEHCNTAVREALTWQWKNGTIINFSNITVLAASGIGTITLT 390
 DB 61 NGSCLTITVGTAGTWTWIEHCNTAVREALTWQWKNGTIINFSNITVLAASGIGTITLT 120
 QY 391 VQTLIDYTLTGQGMWLAGNDTAPREAVTITGFRDLQMESNKGSVWVECTCSQXNKGKALYGD 450
 DB 121 VQTLIDYTLTGQGMWLAGNDTAPREAVTITGFRDLQMESNKGSVWVECTCSQXNKGKALYGD 180
 QY 451 GSIRPKQNDQCLTYGRDVSSTVNTIVSGSXSSXKQWVFTEKXALIMLXXXXXDVPAQA 510
 DB 181 GSIRPKQNDQCLTYGRDVSSTVNTIVSGSXSSXKQWVFTEKXALIMLXXXXXDVPAQA 240
 QY 511 NPKLRRIITTPATKRNQWMLPV 533
 DB 241 NPKLRRIITTPATKRNQWMLPV 263

RESULT 10

AAV25988
 ID AAV25988 standard; Protein; 264 AA.

AAV25988;
 AC

XX 18-OCT-1999 (first entry)
 XX

XX Mistletoe lectin B3 protein fragment.
 XX

XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin B3.

XX Viscum album.
 OS

XX DE1904210-A1.
 KM

XX 12-AUG-1999.
 KM

XX 03-FEB-1998; 98DE-1004210.
 PF

XX 03-FEB-1998; 98DE-1004210.
 PR

XX 03-FEB-1998; 98DE-1004210.
 PA

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 PA

XX Morris P, Stiefel T, Voelter W, Welters P;
 PI

XX WPI: 1999-445335/38.
 DR

XX N-PSDB; AA009112.
 DX

XX Preparation of mistletoe lectins in heterologous systems.
 PT

XX Particularly for use as anticancer agents and immunostimulants
 PT

XX Claim 9; Fig 10B; 78pp; German.
 PS

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC of tumour-associated, bacterial or viral). The method allows production of the
 CC (tumour-associated, bacterial or viral). The method allows production of the
 CC immune response, particularly to a co-administered antigen
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B3 protein.

XX Sequence 264 AA;
 SQ

Query March 49 28; Score 1291; DB 20; Length 264;
 Best Local Similarity 92.48; Field No. 2.7e-14;

Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 271 DVVTSASBPYRIVRKQKQVYVDDPFNDQNOIQLPSSKSNPNQWLTKIDXTIRS 330
 DB 1 DVVTSASBPYRIVRKQKQVYVDDPFNDQNOIQLPSSKSNPNQWLTKIDXTIRS 60
 QY 331 NGSCLTITVGTAGTWTWIEHCNTAVREALTWQWKNGTIINFSNITVLAASGIGTITLT 390
 DB 61 NGSCLTITVGTAGTWTWIEHCNTAVREALTWQWKNGTIINFSNITVLAASGIGTITLT 120
 QY 391 VQTLIDYTLTGQGMWLAGNDTAPREAVTITGFRDLQMESNKGSVWVECTCSQXNKGKALYGD 450
 DB 121 VQTLIDYTLTGQGMWLAGNDTAPREAVTITGFRDLQMESNKGSVWVECTCSQXNKGKALYGD 180
 QY 451 GSIRPKQNDQCLTYGRDVSSTVNTIVSGSXSSXKQWVFTEKXALIMLXXXXXDVPAQA 510
 DB 181 GSIRPKQNDQCLTYGRDVSSTVNTIVSGSXSSXKQWVFTEKXALIMLXXXXXDVPAQA 240
 QY 511 NPKLRRIITTPATKRNQWMLPV 533
 DB 241 NPKLRRIITTPATKRNQWMLPV 263

RESULT 11

AAV25994
 ID AAV25994 standard; Protein; 265 AA.

AAV25994;
 AC

XX 18-OCT-1999 (first entry)
 XX

XX Mistletoe lectin B3 variant protein fragment.
 XX

XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin B3.

XX Viscum album.
 OS

XX DE1904210-A1.
 KM

XX 12-AUG-1999.
 KM

XX 03-FEB-1998; 98DE-1004210.
 PF

XX 03-FEB-1998; 98DE-1004210.
 PR

XX 03-FEB-1998; 98DE-1004210.
 PA

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 PA

XX Morris P, Stiefel T, Voelter W, Welters P;
 PI

XX WPI: 1999-445335/38.
 DR

XX N-PSDB; AA009118.
 DX

XX Preparation of mistletoe lectins in heterologous systems.
 PT

XX Particularly for use as anticancer agents and immunostimulants
 PT

XX Disclosure; Fig 16B; 78pp; German.
 PS

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MLA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC of tumour-associated, bacterial or viral). The method allows production of the
 CC (tumour-associated, bacterial or viral). The method allows production of the
 CC immune response, particularly to a co-administered antigen
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B3 protein.

KW Mistletoe; galactose-recognising mistletoe lectin; MLI1.
XX Viscum album.
XX Key location/Qualifiers
XX Misc-difference 223 /note= "Encoded by ATG"
FT Misc-difference 251 /note= "Encoded by TTT"
FT Misc-difference 344 /note= "Encoded by TCG"
FT Misc-difference 380 /note= "Encoded by GCC"
FT Misc-difference 488 /note= "Encoded by GTG"
XX DE10044027-A1.
XX 14-MAR-2002.
XX 06-SEP-2000; 2000DE-1044027.
XX 06-SEP-2000; 2000DB-1044027.
XX (VISC-) VISCUM AG.
XX Kieff S;
XX MPI; 2002-316737/36.
XX N-PSDB; AB156947.
XX New nucleic acid encoding preprotein of mistletoe lectin, useful as
XX diagnostic and therapeutic agents, also encodes polypeptide -
XX Claim 1; Fig 1; 6pp; German.
XX The invention relates to a nucleic acid molecule (AB156947) that encodes
XX a preprotein (AB156948) which, after processing, has the biological
XX activity of the galactose-recognising mistletoe lectin (MLI1) the MLI1
XX encoding nucleic acid molecule, primers specific to it or complements of
XX it, and encoded (oligomeric) polypeptides are useful as diagnostic and
XX therapeutic agents.
SQ Sequence 551 AA;
Query Match 83.3%; Score 2187; DB 23; Length 551;
Best Local Similarity 83.6%; Pred. No. 3,46-233;
Matches 429; Conservative 14; Mismatches 62; Indels 8; Gaps 3;
1 YERLALVTHQTTGDEYFRITLADYVSSGSPNFIILROSTIPYSRQRFVLELTM 60
34 YERLALVTHQTTGDEYFRITLADYVSSGSPNFIILROSTIPYSRQRFVLELTM 93
61 QGDEXTPAIDVNMVVAOAGDSYFLRDPAGLTHFTVTTRDRSSLPFGSYNDI 120
94 QGDSITPAIDVNMVVAOAGDSYFLRDPAGLTHFTVTTRDRSSLPFGSYNDI 151
121 ERYAGHRDQPIGLXGLTQSVALKKXGSTRXQANSLILQMTSMAARNPILMRKQ 180
152 ERYAGHRDQPIGLXGLTQSVALKKXGSTRXQANSLILQMTSMAARNPILMRKQ 211
181 XINSGKSLPDYWMLELTSWGQSTOVOSTDGVNPRIRALISTGNVTLISWADYIA 240
212 DINGSEFLPDYWMLELTSWGQSTOVOSTDGVNPRIRALISTGNVTLISWADYIA 271
241 SLALMLFVCGEPSSSDVYKVPVYIRPVI-----ADVTCSABEPTVRYGKXVAVVR 295
272 SLALMLFVCGEPSSSDVYKVPVYIRPVI-----ADVTCSABEPTVRYGKXVAVVR 331
296 DDDPFDENQIQMSKSNNDNQMTTKRQXTINSGLCTTGTGATGYVAFIDCNRAV 355
332 DGFTHNRPIDQMCRTKPTDNPWTINRGDILSNRNCLETTATGATVWALDCAVAV 391

QY 356 RENTMOTIXKNTIIPRNSLTLAASGKIGTTLTWGLDYTLGGCHANDTAPREVTI 415
DB 392 RENTMOTIXKNTIIPRNSLTLAASGKIGTTLTWGLDYTLGGCHANDTAPREVTI 451
QY 416 YGRDLCEBNKXSVWERTCSQXQXKXWALYQDSIRPKNOQCITXGSDSVTVN 475
DB 452 YGRDLCEBNKXSVWERTCSQXQXKXWALYQDSIRPKNOQCITXGSDSVTVN 510
QY 476 IVSCSXKX 508
DB 511 IVSCSXKX 543
RESULT 9
AAV25987
ID AAV25987 standard; Protein; 264 AA.
XX AAV25987;
XX 18-OCT-1999 (first entry)
XX DE
XX Mistletoe lectin B2 protein fragment.
XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX ribosome 268 subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B2.
XX Viscum album.
XX DE19804210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris F, Stiefel T, Voelter W, Welters P;
XX MPI; 1999-445335/38.
XX N-PSDB; AA209111.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 9; Fig 9B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (WLA)
XX of the mistletoe lectin binds to, and inactivates, the 26S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of
XX cancers) and if they lack cytotoxicity, to increase antigen
XX immune response, particularly to viral antigens.
XX Mistletoe lectin (I) is a glycoprotein. The method allows production of
XX recombinant mistletoe lectin and its individual chains. In many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B2 protein.
SQ Sequence 264 AA;
Query Match 49.2%; Score 1291; DB 20; Length 264;
Best Local Similarity 92.4%; Pred. No. 2,76-134;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 271 DNTVCSABEPTVRYGKXVAVVR-----ADVTCSABEPTVRYGKXVAVVR 330
DB 1 DNTVCSABEPTVRYGKXVAVVR-----ADVTCSABEPTVRYGKXVAVVR 391

Query Match 95.4%; Score 2504.5; DB 18; Length 564;
 Best Local Similarity 91.7%; Pred. No. 2.2e-268;
 Matches 489; Conservative 2; Mismatches 39; Indels 3; Gaps 2;

1 YERLALHTVOTTKKXFRRTTLTLDYSSSSSSNFIPLRSGSTIPYDAQRVLYELTN 60
 34 YERLALHTVOTTKKXFRRTTLTLDYSSSSSSNFIPLRSGSTIPYDAQRVLYELTN 93
 61 QGDSXTPAIDVTNYYVAVQAGDSYFLRPAFGAETHLFTGTRDRSSLPFGSYXDL 120
 94 QGDSITPAIDVTNYYVAVQAGDSYFLRPAFGAETHLFTGTT--SSLPFGSYXDL 151
 121 ERYAGHDQIPGIXQLTQSVYALRXPQGSTKQARSLTLTQMTSARPNELIMEXQ 180
 152 ERYAGHDQIPGIXQLTQSVYALRXPQGSTKQARSLTLTQMTSARPNELIMEXQ 211
 181 XINSKSLPDXVMELETSWQSGTQVHSTQVFNPRFALPQGVTLNVEVIA 240
 212 YINSKSLPDXVMELETSWQSGTQVHSTQVFNPRFALPQGVTLNVEVIA 271
 241 SLALMFLVCGERPSSESVRYWPIVRPVIADVTCSASEPTVIRVGNKXCVDRDDFH 300
 272 SLALMFLVCGERPSSESVRYWPIVRPVIADVTCSASEPTVIRVGNKXCVDRDDFH 331
 301 DNGOQLMPSKSNNDPQNLTKREDXTISNSGCLTGYGTAGVYVLPDCTNVRPNT 360
 332 DNGOQLMPSKSNNDPQNLTKREDXTISNSGCLTGYGTAGVYVLPDCTNVRPNT 391
 361 MOIYKNGTINPRSNVLAASGIGKTLTYQTLDTYLGQGMALNDPAPREVTIYGRD 420
 392 MOIYKNGTINPRSNVLAASGIGKTLTYQTLDTYLGQGMALNDPAPREVTIYGRD 451
 421 LCHESNGSVWETCSQXKXKXALYDGSIRPKNODCLTKGRDSVTVINVSQS 480
 452 LCHESNGSVWETCSQXKXKXALYDGSIRPKNODCLTKGRDSVTVINVSQS 510
 481 XKSXKXKXWETNEKATILNKKKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 533
 511 AGSGQRWVFTNEGALILNKKKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 563

RESULT 7
 AAV90127
 ID AAV90127 standard; Protein; 564 AA.

AAV90127;
 DT 20-MAR-2003 (updated)
 DT 30-APR-1999 (first entry)
 XX Mistletoe lectin prepro-protein.
 XX Mu, mistletoe; lectin; Mu; transgenic plant; glycosylation;
 XX dimer; immunotoxin; large-scale production; diagnostic; therapeutic;
 XX cancer.
 XX Viscum album.
 XX EP84388-AL.
 XX 16-DEC-1998.
 XX 26-JUN-1995; 98EP-0105660.
 XX 26-JUN-1995; 95EP-0109949.
 XX 26-JUN-1995; 98EP-0105660.
 XX (MADU) MADUS KOEHL AG.
 XX Baur A, Eck J, Lentzen H, Zinke H;
 XX WFI; 1999-026582/03.

DR N-PSDB; AAV74182.

XX New transgenic plant expressing mistletoe lectin - useful for
 FT producing recombinant lectin in e.g. cancer diagnosis and therapy

XX Claim 1a; Fig 4c; 30pp; German.

XX This invention describes a novel transgenic plant transformed with a
 CC vector capable of encoding a mistletoe (Viscum album) lectin
 CC preproprotein or a biologically active fragment. The specific
 CC also describes a polypeptide produced by a plant where the polypeptide
 CC exhibits at least one enzymatic modification other than the glycosylation
 CC that occurs in Viscum album or the polypeptide is a fusion protein, a
 CC mistletoe lectin polypeptide dimer and an immunotoxin comprising the
 CC polypeptide or the polypeptide dimer. The plants are used for large-scale
 CC production of mistletoe lectin for diagnostic or therapeutic purposes
 CC e.g. in cancer therapy.
 CC The method of the invention represents the mistletoe lectin
 CC (Updated on 20-MAR-2003 to correct PF field.)

XX Sequence 564 AA;

Query Match 95.4%; Score 2504.5; DB 20; Length 564;
 Best Local Similarity 91.7%; Pred. No. 2.2e-268;
 Matches 489; Conservative 2; Mismatches 39; Indels 3; Gaps 2;

1 YERLALHTVOTTKKXFRRTTLTLDYSSSSSSNFIPLRSGSTIPYDAQRVLYELTN 60
 34 YERLALHTVOTTKKXFRRTTLTLDYSSSSSSNFIPLRSGSTIPYDAQRVLYELTN 93
 61 QGDSXTPAIDVTNYYVAVQAGDSYFLRPAFGAETHLFTGTRDRSSLPFGSYXDL 120
 94 QGDSITPAIDVTNYYVAVQAGDSYFLRPAFGAETHLFTGTT--SSLPFGSYXDL 151
 121 ERYAGHDQIPGIXQLTQSVYALRXPQGSTKQARSLTLTQMTSARPNELIMEXQ 180
 152 ERYAGHDQIPGIXQLTQSVYALRXPQGSTKQARSLTLTQMTSARPNELIMEXQ 211
 181 XINSKSLPDXVMELETSWQSGTQVHSTQVFNPRFALPQGVTLNVEVIA 240
 212 YINSKSLPDXVMELETSWQSGTQVHSTQVFNPRFALPQGVTLNVEVIA 271
 241 SLALMFLVCGERPSSESVRYWPIVRPVIADVTCSASEPTVIRVGNKXCVDRDDFH 300
 272 SLALMFLVCGERPSSESVRYWPIVRPVIADVTCSASEPTVIRVGNKXCVDRDDFH 331
 301 DNGOQLMPSKSNNDPQNLTKREDXTISNSGCLTGYGTAGVYVLPDCTNVRPNT 360
 332 DNGOQLMPSKSNNDPQNLTKREDXTISNSGCLTGYGTAGVYVLPDCTNVRPNT 391
 361 MOIYKNGTINPRSNVLAASGIGKTLTYQTLDTYLGQGMALNDPAPREVTIYGRD 420
 392 MOIYKNGTINPRSNVLAASGIGKTLTYQTLDTYLGQGMALNDPAPREVTIYGRD 451
 421 LCHESNGSVWETCSQXKXKXALYDGSIRPKNODCLTKGRDSVTVINVSQS 480
 452 LCHESNGSVWETCSQXKXKXALYDGSIRPKNODCLTKGRDSVTVINVSQS 510
 481 XKSXKXKXWETNEKATILNKKKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 533
 511 AGSGQRWVFTNEGALILNKKKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 563

RESULT 8

AB79450
 ID AB79450 standard; Protein; 551 AA.

AB79450;
 DT 08-JUL-2002 (first entry)
 XX Galactose-recognition mistletoe lectin.

Db 61 GQXKXKALDVTNXXVYVAKQGGQSVFLFQAPRASTHLFGVTR-XESLFFKSGSYDL 119
Qy 131 ERYAGHPDIPFGIXOLIOSVAKAPFGSGTRKQASILLIOMISEAPAPFIMEXQ 180
Db 130 ERYAGHPDIPFGIXOLIOSVAKAPFGSGTRKQASILLIOMISEAPAPFIMEXQ 179
Qy 181 XINSKXFLPXWLELETSNQSGTQVQSHSTGVPNPRALIXKNTVTLANVXIA 240
Db 180 XINSKXFLPXWLELETSNQSGTQVQSHSTGVPNPRALIXKNTVTLANVXIA 239
Qy 241 SLATMLFQCGRPSSSDVRWPLVRPIADDTVCASSEPTVRIYVGRXCMQVDRDDPF 300
Db 240 SLATMLFQCGRPSSSDVRWPLVRPIADDTVCASSEPTVRIYVGRXCMQVDRDDPF 299
Qy 301 DGNQIOLMPSKSNNDPQLTIRKXITIRKNSGLTGYTGAGVYVAFEDCNVREXAT 360
Db 300 DGNQIOLMPSKSNNDPQLTIRKXITIRKNSGLTGYTGAGVYVAFEDCNVREXAT 359
Qy 361 WQIWKNGTINRSNLVLAASGKGTLYVQGLDITTCQGMAGNDVAPREPTIKGRD 420
Db 360 WQIWKNGTINRSNLVLAASGKGTLYVQGLDITTCQGMAGNDVAPREPTIKGRD 419
Qy 421 LCMENSGSWTCSSQONKQWALYQPSIPRONQOCITKGRDVSFTINIVCS 480
Db 420 LCMENSGSWTCSSQONKQWALYQPSIPRONQOCITKGRDVSFTINIVCS 479
Qy 481 XSEXKQWVFTKXALIMKKXXXDVQANFKLR111YPATKPKQWMLPV 533
Db 480 XSEXKQWVFTKXALIMKKXXXDVQANFKLR111YPATKPKQWMLPV 532

RESULT 2

NA125976
NA125976 standard; protein; 533 AA.AA125976;
AA125976;

18-OCT-1999 (first entry)

Mistletoe lectin protein consensus sequence 3.

XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MAb; immunity;
XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform.
XX
OS Viscum album.

Viscum album.

Key Location/Qualifiers
FT Misc-difference 15 /label= Asp, Gln
FT Misc-difference 63 /label= Gly, Gln
FT Misc-difference 66 /label= Ile, Val
FT Misc-difference 7 /label= Leu, Ala
FT Misc-difference 107 /label= Asp, none
FT Misc-difference 113 /label= Aen, Thr
FT Misc-difference 117 /label= Pro, Thr
FT Misc-difference 134 /label= Asp, Gln
FT Misc-difference 141 /label= Ser, Tyr
FT Misc-difference 145 /label= Phe, Tyr
FT Misc-difference 152 /label= Thr, Ala
FT Misc-difference 177

FT /label= Ala, Tyr
FT Misc-difference 180 /label= Tyr, Asp
FT Misc-difference 185 /label= Ala, Gln
FT Misc-difference 191 /label= Val, Met
FT Misc-difference 218 /label= Ile, Phe
FT Misc-difference 224 /label= Pro, Ser
FT Misc-difference 225 /label= Thr, Ser
FT Misc-difference 232 /label= Asp, Ser
FT Misc-difference 236 /label= Aen, Ser
FT Misc-difference 287 /label= Cys, Arg
FT Misc-difference 290 /label= Gly, Asn
FT Misc-difference 325 /label= Gly, Asn
FT Misc-difference 364 /label= Gly, Asp
FT Misc-difference 426 /label= Gly, Gln
FT Misc-difference 435 /label= Val, Asp
FT Misc-difference 439 /label= Gln, Lys
FT Misc-difference 442 /label= Gly, none
FT Misc-difference 443 /label= Arg, Lys
FT Misc-difference 464 /label= Cys, Ser, Val
FT Misc-difference 480 /label= Ala, Gly
FT Misc-difference 481 /label= Gly, Ala
FT Misc-difference 483 /label= Ser, Gly
FT Misc-difference 484 /label= Gly, Ser
FT Misc-difference 493 /label= Gly, Tyr
FT Misc-difference 500 /label= Asn, Ser, Thr, Lys
FT Misc-difference 501 /label= Ser, Gly
FT Misc-difference 502 /label= Leu, Pro
FT Misc-difference 504 /label= Ala, Met
FT Misc-difference 504 /label= Met, Val
FT Misc-difference 533 /label= Pro, Phe
XX DB19904210-A1.
XX 12-AUG-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BROS-) BIOSYN ARZENEMITTEL GmbH.
XX Morris P, Stiefel T, Voelter W, Welters P,
XX MPI; 1999-44535/38.
XX DR

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RESULT 2
AA125973 standard; protein; 533 AA.
AA125973;
AA125973;
18-OCT-1999 (first entry)
DE Mistletoe lectin protein consensus sequence 2.
XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform.
XX
OS Viscum album.
XX
XX Key Location/Qualifiers
FH MISC-difference 15 /label= Asp, Glu
FT MISC-difference 63 /label= Gly, Glu
FT MISC-difference 66 /label= Ile, Val
FT MISC-difference 75 /label= Leu, Ala
FT MISC-difference 107 /label= Asp, Arg, none
FT MISC-difference 113 /label= Asn, Thr
FT MISC-difference 117 /label= Pro, Thr
FT MISC-difference 134 /label= Asp, Glu
FT MISC-difference 141 /label= Ser, Thr
FT MISC-difference 145 /label= Phe, Tyr
FT MISC-difference 152 /label= Thr, Ala
FT MISC-difference 177 /label= Ala, Tyr
FT MISC-difference 180 /label= Tyr, Asp
FT MISC-difference 185 /label= Ala, Glu
FT MISC-difference 191 /label= Val, Met
FT MISC-difference 219 /label= Ile, Phe
FT MISC-difference 220 /label= Phe, Ser
FT MISC-difference 225 /label= Pro, Thr
FT MISC-difference 232 /label= Thr, Ser
FT MISC-difference 236 /label= Asp, Ser
FT MISC-difference 289 /label= Asn, Ser
FT MISC-difference 320 /label= Cys, Arg
FT MISC-difference 325 /label= Gly, Asn
FT MISC-difference 364 /label= Gly, Asp
FT MISC-difference 427 /label= Gly, Glu
FT MISC-difference 435 /label= Val, Asp
FT MISC-difference 439 /label= Glu, Lys
FT MISC-difference 442
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FT MISC-difference 443 /label= Gly, none
FT MISC-difference 443 /label= Arg, Lys
FT MISC-difference 464 /label= Cys, Ser, Val
FT MISC-difference 480 /label= Ala, Gly
FT MISC-difference 481 /label= Gly, Ala
FT MISC-difference 483 /label= Ser, Gly
FT MISC-difference 484 /label= Ser, Gly
FT MISC-difference 493 /label= Gly, Tyr
FT MISC-difference 500 /label= Asn, Ser, Thr, Lys
FT MISC-difference 502 /label= Ser, Gly
FT MISC-difference 502 /label= Ser, Gly
FT MISC-difference 503 /label= Leu, Pro
FT MISC-difference 503 /label= Leu, Pro
FT MISC-difference 504 /label= Ala, Met
FT MISC-difference 504 /label= Met, Val
FT MISC-difference 533 /label= Pro, Phe
FT MISC-difference 533 /label= Pro, Phe
XX DB19804210-AL.
XX 12-NOV-1999.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welteers P;
XX WPI, 1999-44535/38.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 4; Page 28-29; 78bp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX of which have antitumour and immunostimulatory activity. The A-chain (MA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a consensus sequence of the mistletoe lectin described in the
XX specification.
XX
XX Sequence 533 AA;
XX
XX Query Match 96.1%; Score 2524.5; DB 20; Length 533;
XX Best Local Similarity 99.6%; Pred. No. 132-270;
XX Matches 533; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX
XX QY 1 YERLRARFQQTGKGEFFFTLLRDYVSSGSPNRPILRQSTIVSPADRFVVELTN 60
XX 1 YERLRARFQQTGKGEFFFTLLRDYVSSGSPNRPILRQSTIVSPADRFVVELTN 60
XX DB 61 GQDXYTAIDVNNYVAVQAGDSYFLDAPRQAGTHLFGTTRDSLPFXSGSYXD 120
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Thu Dec 11 16:09:55 2003

PT	Misc-difference	134	/label= Asp, Glu
PT	Misc-difference	141	/label= Ser, Thr
PT	Misc-difference	145	/label= Phe, Tyr
PT	Misc-difference	152	/label= Thr, Ala
PT	Misc-difference	172	/label= Ala, Tyr
PT	Misc-difference	180	/label= Tyr, Asp
PT	Misc-difference	185	/label= Val, Glu
PT	Misc-difference	191	/label= Val, Met
PT	Misc-difference	213	/label= Ile, Phe
PT	Misc-difference	224	/label= Pro, Ser
PT	Misc-difference	225	/label= Pro, Thr
PT	Misc-difference	232	/label= Thr, Ser
PT	Misc-difference	236	/label= Asp, Ser
PT	Misc-difference	257	/label= Asn, Ser
PT	Misc-difference	280	/label= Cys, Arg
PT	Misc-difference	325	/label= Gly, Asn
PT	Misc-difference	364	/label= Gly, Asp
PT	Misc-difference	426	/label= Gly, Gln
PT	Misc-difference	435	/label= Val, Asp
PT	Misc-difference	440	/label= Gln, Lys
PT	Misc-difference	442	/label= Gly or none
PT	Misc-difference	443	/label= Arg, Lys
PT	Misc-difference	464	/label= Cys, Ser, Val
PT	Misc-difference	490	/label= Ala, Gly
PT	Misc-difference	483	/label= Gly, Ala
PT	Misc-difference	483	/label= Ser, Gly
PT	Misc-difference	484	/label= Gly, Ser
PT	Misc-difference	493	/label= Gly, Tyr
PT	Misc-difference	500	/label= Asn, Ser, Thr, Lys
PT	Misc-difference	501	/label= Ser, Gly
PT	Misc-difference	502	/label= Leu, Pro
PT	Misc-difference	503	/label= Ala, Met
PT	Misc-difference	504	/label= Met, Val
PT	Misc-difference	533	/label= Pro, Phe
XX	DE3.9804210-AL1.		
XX	12-AUG-1999.		
XX			

GenCore version 5.1.6
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OM protein - protein search, using fw model

Run on: December 11, 2003, 13:53:18 : Search time 52.7657 Seconds

[without alignments]
1606.345 Million cell updates/sec

Title: US-09-601-667c-40

Sequence: 1 YERLRNRYHTQTXEYFRF.....RRILYPAKPKRQMLPVX 534

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107663 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107663

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: A: Geneseq, 19Jun03:*

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24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best hit being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2524.5	96.1	533	20	AA125970
2	2524.5	96.1	533	20	AA125970
3	2524.5	96.1	533	20	AA125970
4	2518.5	95.9	531	20	AA125970
5	2518.5	95.9	531	20	AA125970
6	2504.5	95.4	564	18	AA10021
7	2504.5	95.4	564	18	AA10021
8	2187	83.3	551	23	AA10021
9	1291	49.2	264	20	AA125970

10	1291	49.2	264	20	AA125988	Mistletoe lectin B
11	1291	49.2	265	20	AA125994	Mistletoe lectin B
12	1291	49.2	265	20	AA125993	Mistletoe lectin B
13	1290	49.1	264	20	AA125986	Mistletoe lectin B
14	1290	49.1	264	20	AA125990	Mistletoe lectin B
15	1290	49.1	265	20	AA125996	Mistletoe lectin B
16	1290	49.1	265	20	AA125992	Mistletoe lectin B
17	1290	49.1	265	20	AA125992	Mistletoe lectin B
18	1286	48.0	264	20	AA125978	Mistletoe lectin B
19	1286	48.0	264	20	AA125978	Mistletoe lectin B
20	1286	48.0	264	20	AA125978	Mistletoe lectin B
21	1286	48.0	264	20	AA125978	Mistletoe lectin B
22	1277.5	48.6	264	20	AA125985	Mistletoe lectin B
23	1277.5	48.6	264	20	AA125991	Mistletoe lectin B
24	1267.5	48.3	263	19	AA10023	Mistletoe lectin B
25	1267.5	48.3	264	18	AA10023	Mistletoe lectin B
26	1267.5	48.3	264	18	AA10023	Mistletoe lectin B
27	1267.5	48.3	267	19	AA10023	Mistletoe lectin B
28	1267.5	48.3	267	19	AA10023	Mistletoe lectin B
29	1229.5	46.8	576	18	AA125987	Mistletoe lectin B
30	1229.5	46.8	576	21	AA125982	Mistletoe lectin B
31	1229.5	46.8	576	21	AA125982	Mistletoe lectin B
32	1229.5	46.8	576	22	AA125930	Mistletoe lectin B
33	1229.5	46.8	576	22	AA125930	Mistletoe lectin B
34	1228.5	46.8	565	6	AA10016	Mistletoe lectin B
35	1228.5	46.8	565	22	AA10016	Mistletoe lectin B
36	1228.5	46.8	574	9	AA10016	Mistletoe lectin B
37	1228.5	46.8	574	9	AA10016	Mistletoe lectin B
38	1213.5	46.2	576	22	AA10016	Mistletoe lectin B
39	1213.5	46.2	576	22	AA10016	Mistletoe lectin B
40	1194	45.5	256	20	AA125981	Mistletoe lectin A
41	1194	45.5	256	20	AA125984	Mistletoe lectin A
42	1193.5	45.0	267	19	AA125984	Mistletoe lectin A
43	1180.5	44.4	562	10	AA10019	Mistletoe lectin A
44	1180.5	44.4	562	10	AA10019	Mistletoe lectin A
45	1165	44.4	254	20	AA125983	Mistletoe lectin A

ALIGNMENTS

RESULT 1
ID: AA125970 standard; protein; 533 AA.

AA125970; (first entry)

19-OCT-1999 (first entry)

Mistletoe lectin protein consensus sequence 1.

Mistletoe lectin; antitumor; immunostimulant; A-chain; MAb; immunity;

ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

lymphokine-producing macrophage; uncontrolled cell growth; treatment;

cytotoxicity; antigen; isoform.

Viscum album.

Viscum album.

Viscum album.

Viscum album.

Viscum album.

Viscum album.

Viscum album.

Viscum album.

Viscum album.

Viscum album.

Query Match 37.2%; Score 977; DB 10; Length 251;
Best Local Similarity 80.6%; Pred. No. 1, 28-31;
Matches 203; Conservative 7; Mismatches 36; Indels 6; Gaps 3;
QY 1 YERLRLVYHTGTGXEYFRFPITLLADYVSSGSPFENEIPLROSTIPYSDAORFYLVELTN 60
DB 1 YERLRLVYHTGTGDEYFRFPKILRDSVSSGSPFENDIDILPPE-IPVSAORFYLVELTN 59
QY 61 Q---GDVXKALIDVTNKYVAYOXGDQYFPLDAPRGALTEHLFTGTRDSSSLPFXSY 117
DB 60 QGKRWEDSTLKNIDVINDYVAYOXGDQYFPLDAPRGALTEHLFTGTRDSSSLPFXSY 117
QY 118 XDLERYAGHRQIPFLIGLXQLTQSVKALXPGSTRXQARSLILITOMISEAARNPILAR 177
DB 118 ADLERYAGHRQIRPLREPLIRSVADYFGSTRPAQSSILIVLQWISEAARNPILAR 177
QY 178 XROXINGXSEFLPDXYMLELETSWGQOSTQVGHSTQGVFNNPYRLATYXGNFTLLANRX 237
DB 178 ARQYINGVSYLPDYVMLELETSWGQOSTQVGHSTQGVFNNPYRLGISTGNFWLSNTRD 237
QY 238 VIASLAIIMLFVC 249
DB 238 VINSIGIMVFC 249

Search completed: December 11, 2003, 14:01:06
Job time : 42.16 secs

RX MEDLINE-2156752; PubMed-11710524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
 mistletoe (Viscum album coloratum).";
 RL Mol. Cells 13:215-220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RX MEDLINE-2156752; PubMed-11710524;
 RA Do M.-S., Song S.K.; to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AF508915; AA046933.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 KW Hydrolase; Toxin.
 FT NON_TER 1
 FT NON_TER 249
 SQ SEQUENCE 249 AA; 27821 MW; 3C6870F839BDAB5 CRC64;
 Query Match 40.1%; Score 1054; DB 10; Length 249;
 Best Local Similarity 83.9%; Pred No. 1.7e-99;
 Matches 209; Conservative 13; Mismatches 25; Indels 2; Gaps 1;

QY 1 YERLRATVHTQCKEYFRITLLRDYVSASGSEHEFELRGSTIPVSDAQRPVLYELRN 60
 DB 1 YERLRATVHTQCKEYFRITLLRDYVSASGSEHEFELRGSTIPVSDAQRPVLYELRN 60
 QY 61 QGDSXTAIDVNTKYYAVAKGDSYFLRDAPRGAETHLFTGTDRSSLPFGSYXDL 120
 DB 61 QGDSXTAIDVNTKYYAVAKGDSYFLRDAPRGAETHLFTGTDRSSLPFGSYXDL 120
 QY 121 ERYAGROIFGICXKIOSVAPRPGSTYKASRIILICWIGEAAPPTIMRXXO 180
 DB 121 ERYAGROIFGICXKIOSVAPRPGSTYKASRIILICWIGEAAPPTIMRXXO 180
 QY 181 XINGSGSPDPXYMLETSMGQSGTQVSHSTGTVFNNPRLATXXGNFTLLKNRVYA 240
 DB 179 YISSGSPDPXYMLETSMGQSGTQVSHSTGTVFNNPRLATXXGNFTLLKNRVYA 238
 QY 241 STATMLFVC 249
 DB 239 STATMLFVC 247

RESULT 14
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 AC OBLKO1
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Lectin chain B isoform 3 (Fragment).
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotys;
 OC NCBI_TaxID=159976; Viscum.
 RX MEDLINE-2156752; PubMed-11710524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
 mistletoe (Viscum album coloratum).";
 RL Mol. Cells 13:215-220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RX MEDLINE-2156752; PubMed-11710524;
 RA Do M.-S., Song S.K.; to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AF508915; AA046933.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 KW Hydrolase; Toxin.
 FT NON_TER 1
 FT NON_TER 251
 SQ SEQUENCE 251 AA; 28090 MW; A11777489012E989 CRC64;

RX Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RA EMBL; AF508915; AA046933.1; -.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 FT NON_TER 1
 FT NON_TER 263
 SQ SEQUENCE 263 AA; 29071 MW; 3F9C4AD86CF061D CRC64;
 Query Match 39.2%; Score 1029.5; DB 10; Length 263;
 Best Local Similarity 71.5%; Pred No. 5.3e-97;
 Matches 196; Conservative 19; Mismatches 47; Indels 1; Gaps 1;

QY 271 DVTGSASEPTVRIYGRKXKGVYDDPHDQIQCLPSSKNNDPQLMTIKEDXTIRS 330
 DB 1 DDTCTSEPTVRIYVAGLCLVDVHAKPHDGNPQLPCKSTDRNQLMTIRADGTIRS 60
 QY 331 NSGCLTYGTATGVYVIMFDQNAVREANTIQWKNGTIIPRSMVLAAASGIGKSTLT 390
 DB 61 NSGCLTYGTATGVYVIMFDQNAVREANTIQWKNGTIIPRSMVLAAASGIGKSTLT 120
 QY 391 VQTLDTYLQGMLAGNDTPRERTTYGFRDLCHNSKXSWTETCKSSQXNXXALYED 450
 DB 121 VQGMKXQGMKLSHDIRRETIYGFNDJHMGSSVYVLCVHQND-KMLYED 179
 QY 451 GSIRKRNQDQCLXGRDSVTVIYVSCSXKXQRPWFTEKXALINLKXXXXXVQA 510
 DB 180 GSIRKRNQDQCLXGRDSVTVIYVSCSXKXQRPWFTEKXALINLKXXXXXVQA 239
 QY 511 NPLRLRIIYPAATGKFNQMLLPV 533
 DB 240 NPLRLRIIYPAATGKFNQMLLPV 262

RESULT 15
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 AC OBLKO1
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Lectin chain A isoform 3 (EC 3.2.2.22) (RNA N-glycosidase)
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotys;
 OC NCBI_TaxID=159976; Viscum.
 RX MEDLINE-2156752; PubMed-11710524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
 mistletoe (Viscum album coloratum).";
 RL Mol. Cells 13:215-220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RX MEDLINE-2156752; PubMed-11710524;
 RA Do M.-S., Song S.K.; to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AF508915; AA046933.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 KW Hydrolase; Toxin.
 FT NON_TER 1
 FT NON_TER 251
 SQ SEQUENCE 251 AA; 28090 MW; A11777489012E989 CRC64;

OC Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophytes;
OC Spermatophytes; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC Eusidia; I. Fabales; Fabaceae; Papilionoideae; Aretaceae; Aduzeae.
OC [1] _taxidb:3310;
RP SEQUENCE FROM N. A.
RX MEDLINE=20102702; PubMed=10616890;
RX Lin C.L., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Hwang M.J.,
RA Lin J.Y., Structure and Function Analysis of the Abnase Precolector
RT alpha-Helix H1 Imprints Protein Synthesis Inhibitory Activity." *Antibiotics*
CC 2019; 8(12):1937-1947. doi:10.3390/ant8121937.
CC J.- CATALYTIC ACTIVITY: ENDOPOLYSACCHARIDASE OF THE N-D-GLUCOSIDIC BOND AT ONE
CC SPECIFIC AMBOSIONS ON THE 2BS RNA.
CC 1. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR PDB: 1L14QJ; IASB.
DR Interpro: IPR000772; Rctin B_lectin.
DR Interpro: IPR001574; RLP.
DR Pfam: PF00652; Rctin B_lectin; 6.
DR Pfam: PF00161; xfp1.
DR SMART: SM00389; SUGARACTN.
DR SMART: SM00389; SUGARACTN.
DR PROSITE: PS00231; Rctin B_lectin; 2.
DR PROSITE: PS00275; SHCA_Rctin; 1.
KW Hydrolase; Toxin.
KW SEQUENCE 547 AA, 61248 MW, 3554325C35A1AD CRC64;

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Best Local Similarity	43.7%	Pred. No. 1.4e-101;		
Matches 234;	Conservative 79;	Mismatches 190;	Indels 32;	Gaps 10;

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Dh	28	TQSTNPRASQPIIDAKRRLRTELIG-IVYDPS-7YENQWYTELSTQVSTQL	95
Qy	69	AIDVXXVYVAQADQSYFELDEPDAFETHEFTTTRRPSISLPEVGSYDLENYGHR	123
Dh	96	GIDIDVAYVAYVAAQSSFEFFNAPASVAFYFVL-QQVSLPEQNYDDELEMAOR	143
Qy	123	DQIPGIXHOLDSVZALKRSGSTRQAKRSILTIQISBEAENETPLMKRQXINSGAS	160
Dh	144	QOISPELEAKQOIGETLRSQASDDEIRLITLITVQVAFVLEINQKQSTKXA	200
Qy	188	FLPFXVHEBETNMOQOSTVOYGHSTGVFNNPELXVQVAFVLEINQKQSTKXA	223
Dh	204	POPPPSLSLNTWMEPLSRVGHVQDTE--PQN-----TLINRQOEYVSSLSH	226
Qy	238	-VLSGIAINLPEVCGERSSDRQWPLVTRPVADVTCNS-EPYAVIQRKXWAVYR	253
Dh	254	PSVSLALDVLQCNPLRATS---PILASIVSQAQSCSHREPVALQSGDLQVDS	300
Qy	326	DQDHEGQIDLPKSKNDNPPQCLITIRKXIBNSQCTITGTAQVYVMEIDQVYR	353
Dh	310	DVANNNGNPIILKQCQLEVNQVLTLSQDPIRKQCTILITGVAPRNVWIDYDSNV	360
Qy	356	REAVIYQIXXNGIILNPSNVLAAASGIKGTLITVQTLDTAGQVLAQNTLPEEYTI	411
Dh	370	AARVYQWIDMDGIIINPISGLVLSAESSWQGLITVQKDVYRQVQKNTNIPRVLIS	420
Qy	416	YQDRLQMSKXQSVWETVCSAQXQKMAIYQDSIRPKQXQDQCIKXGDSVSYV	477
Dh	430	APBPKLOKBERGKQWLVQDITHEBO-QNVPYVSLNPEQNTLQENKSGATV	484
Qy	476	IYSCSXKXQXWVETREKALINLKXXXXQVQAKXKRLIITRYRQKXQW	530
Dh	489	NMGCSNNAASQKRVYTESGIVYINLMDVWYVDSQDSLSKLIILMPTVGNQDM	543

RESULT 12
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AC Q8JAK2; 2002 (TrEMBLref). 22, (Created)
DT 01-OCT-2002 (TrEMBLref). 22, Last update
DI 01-OCT-2002 (TrEMBLref). 22, Last annotation update)
DR 01-MAR-2003 (TrEMBLref). 27, Last annotation update)
OS Mus musculus (Mus musculus)
PE Viscum album subsp. *V. album*
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliopsida; eudicotyledons, core eudicots;
OC Santalales; Viscaceae; Viscum.
NCBI_TextID=159976; OX
[1]
RN SEQUENCE FROM N.A.
RP EX MERRILL=1167552; PubMed=1170524;
RP DA M.-S. Kang S.-H., Kang T.-B., Lee K.-H., Yoon T.-U., Kim J.-B.,
RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
LT mistleee (*Viscum album coloratum*).";
ET Mol. Cells 12:215-220(2001) .

RN [2]
SEQUENCE FROM N.A.
RA PAX C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RD M.-S., Song S.K.
RE Submitted May 11, 2002, to the EMBL/GenBank/DBJ databases.
RF EMBL: AF098678; Genbank: AF098678; F011 lectin.
RG Pfam: PF00653; Rctln_B lectin_5.
RH SMART: SMO0458; RCTIN_7.
RI PROSITE: PSS0231; RCTIN_B_LECTIN_2.
RJ
RK NON_TER 1
RL FT_NON_TER 263 263
RM NO SEQUENCE 263 AA; 26150 MW; B685BCFC7C9CBDF CRC64;

Query Match	Similarity	% ID*	Score	DB ID*	Length
Matches	2001	Conservative	191	Mismatches	493
				Indels	1
				Gaps	1
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DY	1	DDDTCTATSTVETVYVVRKXKXVVDDEDDFHGNGIDLPVSKSNPNPQMLTKKDTYTS	330		
QY	321	NSGCTATSTVETVYVVRKXKXVVDDEDDFHGNGIDLPVSKSNPNPQMLTKKDTYTS	330		
DY	61	NSGCTATSTVETVYVVRKXKXVVDDEDDFHGNGIDLPVSKSNPNPQMLTKKDTYTS	330		
QY	391	VQDLDYTLGKGLAAGMTAPREVTYVDFPLCHESKXSVVETFKSSQNNQXVALLSD	450		
DY	121	VQDLDYTLGKGLAAGMTAPREVTYVDFPLCHESKXSVVETFKSSQNNQXVALLSD	450		
QY	451	GSIRPKNDQGLTQKRPQSVSTVYIVSCSXKXSVVETFKSSQNNQXVALLSD	450		
DY	180	GSIRPKNDQGLTQKRPQSVSTVYIVSCSXKXSVVETFKSSQNNQXVALLSD	450		
QY	511	NPELRITITVPTKQNMMLTV	533		
DY	240	NPELRITITVPTKQNMMLTV	262		

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REQUEST 13
1 BBLN03
2 AC
3 Q8RKH5. PRELIMINARY. PRT. 249 AA.
4
5 DT 01-OCT-2002 (TRMBL021_22, Created)
6 DT 01-OCT-2002 (TRMBL021_22, Last sequence update)
7 DT 01-MAR-2003 (TRMBL021_23, Last annotation update)
8 DT 1-ECT chain A isocform 2 (BC 3.2.2.22) (tRNA N-glycosylase)
9 DE (Fragment)
10
11 DE Viscum album subsp. coloratum.
12 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
13 OC Streptales; Viciales; Viciales; Viciales; Viciales; Viciales; Viciales;
14 OC NCBI_TaxID=159976;
15 RX [1]_TextID=159976;
16
17 SEQUENCE FROM N.A.

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Db 301 IAWKCKRLEENQWLTAKSDLTFRNSKCLITTBGVAAPNVMYVCCSNVNAETVMEID 360
QY NGTIINPRSNVLAASSGKIKGTTLVCTDVTYLGQGMLAGNDAPREVTIGPFDLQES 425
Db 361 NGTIINPRSNVLAASSGKIKGTTLVCTDVTYLGQGMLAGNDAPREVTIGPFDLQES 420
QY 426 NKGWVETKSSQKQXKXALYGGGIRKQNDQCTKGRDVSFTVNIWCSXSSX 485
Db 421 QGSMVWALDQWNRKQD QKALYDSSISVGNVNCCLTSKQKQSPVYKRCSSGMS 479
QY 486 QKVVPTNEXALINLXXXXXDVAKNPKLRRIIYFANGKPNQML 531
Db 480 QKVLFPNDGSIYSYDQWVQVMSDPSLKQIILWPTGRNQITVL 525

RESULT 9

ID Q8KXK7 PRELIMINARY; PRT: 249 AA.
AC Q8KXK7, 2002 (T-EMBLrel. 21, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Lectin chain A isoform 2 (EC 3.2.2.22) (RNA N-glycosidase)
DS (Fragment).
OS Viscum album (European mistletoe).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=3972;
RN 11 SOURCE FROM N.A.
RC Tissue=leaf;
RA Paramesitium M., Srinivasan A., Singh T.P.;
RT "Viscum Album (Indian) mRNA for Mistletoe Lectin Chain A, isoform 2,"
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOGLYCOSYLASE OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S rRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AY081148; AML87005.1; -.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
KW Hydroxylase; Toxin.
FT NON-TER 1
FT 249
SQ SEQUENCE 249 AA; 27944 MW; 89FABP7309A633 CRC64;

Query Match

Best Local Similarity 42.4%; Score 1113; DB 10; Length 249;
Matches 223; Conservative 3; Mismatches 23; Indels 2; Gaps 1;

QY 1 YERLRVHTQTKGKXFFRFTLLRDVSSGSSFSNEIPLRQSTIFVSDAQRPVLYELTN 60
Db 1 YERLRVHTQTKGKXFFRFTLLRDVSSGSSFSNEIPLRQSTIFVSDAQRPVLYELTN 60
QY 61 GCMXSTALIDVNNYNNYVNAQAGDSTFLRDPAGATLFTCTTRQSSSPFXGSIYDL 120
Db 61 GCMXSTALIDVNNYNNYVNAQAGDSTFLRDPAGATLFTCTTRQSSSPFXGSIYDL 118
QY 121 ERYAGHRDQIPGIXOLIGVVALKPGSGTRKQASITLILQWISGAARFNPIIMKRO 180
Db 119 ERYAGHRDQIPGIXOLIGVVALKPGSGTRKQASITLILQWISGAARFNPIIMKRO 178
QY 181 XINSKXSFDPXVMELETSMQOSTOVQSHSTGVFNNPRLAIXGNPVLXNVAYIA 240
Db 179 DINSKXSFDPXVMELETSMQOSTOVQSHSTGVFNNPRLAIXGNPVLXNVAYIA 238
QY 241 SLAINLFCGRR 251
Db 239 SLAINLFCGRR 249

RESULT 10

Q81K06 PRELIMINARY; PRT: 254 AA.
AC Q81K06;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Lectin chain A isoform 1 (EC 3.2.2.22) (RNA N-glycosidase)
DS (Fragment).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
OX NCBI_TaxID=159976;
RN 11 SOURCE FROM N.A.
RC Tissue=leaf;
RA MEDLINE=2156752; PubMed=11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
RT mistletoe (Viscum album coloratum).";
RT Mol. Cells 12:215-220(2001).
RN 121
RS SOURCE FROM N.A.
RC Tissue=leaf;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
RA Do M.-S., Song S.K.;
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOGLYCOSYLASE OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S rRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF508914; AAM46932.1; -.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00196; SHIGARICIN.
KW Hydroxylase; Toxin.
FT NON-TER 1
FT 254
SQ SEQUENCE 254 AA; 28446 MW; 6DBECB18FAFE80 CRC64;

Query Match

Best Local Similarity 41.7%; Score 1094; DB 10; Length 254;
Matches 219; Conservative 8; Mismatches 27; Indels 2; Gaps 1;

QY 1 YERLRVHTQTKGKXFFRFTLLRDVSSGSSFSNEIPLRQSTIFVSDAQRPVLYELTN 60
Db 1 YERLRVHTQTKGKXFFRFTLLRDVSSGSSFSNEIPLRQSTIFVSDAQRPVLYELTN 60
QY 61 GCMXSTALIDVNNYNNYVNAQAGDSTFLRDPAGATLFTCTTRQSSSPFXGSIYDL 120
Db 61 GCMXSTALIDVNNYNNYVNAQAGDSTFLRDPAGATLFTCTTRQSSSPFXGSIYDL 118
QY 121 ERYAGHRDQIPGIXOLIGVVALKPGSGTRKQASITLILQWISGAARFNPIIMKRO 180
Db 119 ERYAGHRDQIPGIXOLIGVVALKPGSGTRKQASITLILQWISGAARFNPIIMKRO 178
QY 181 XINSKXSFDPXVMELETSMQOSTOVQSHSTGVFNNPRLAIXGNPVLXNVAYIA 240
Db 179 YISGSGSFDPVTLILQETSMQOSTOVQSHSTGVFNNPRLAIXGNPVLXNVAYIA 238
QY 241 SLAINLFCGRR 256
Db 239 SLAINLFCGRR 254

RESULT 11

ID Q9W659 PRELIMINARY; PRT: 547 AA.
AC Q9W659;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-DEC-2000 (T-EMBLrel. 23, Last annotation update)
DE Preproagglutinin (EC 3.2.2.22) (RNA N-glycosidase).
GN AAG.
OS Abrus precatorius (Indian licorice) (Crab's eye).

RESULT 7
 Q94BMS PRELIMINARY; PRT; 581 AA.
 ID Q94BMS, 2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinnamomin I precursor
 DE (EC 3.2.2.22) (RNA N-glycosidase).
 OS Cinnamomum camphora (Camphor tree).
 OC Burkariaceae; Viciales; Fabaceae; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 NCBI_TaxID=13429;
 RX SOURCE FROM N.A.
 RA Yang O, Geop Z Z, Liu W Y;
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinnamomin proteins and study of their expression
 RT patterns".
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC EMBL; AF039801; AA042458.1; .
 DR InterPro: IPR000772; Ricin_B_lectin.
 DR Pfam: PF00652; Ricin_B_lectin; 5.
 DR PRINTS: PRO0161; RIP_1; RLP_1; SHIGARICIN.
 DR SMART: SM00458; RICIN; 2.
 DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
 KW Hydrolyase; Signal; Toxin.
 FT SIGNAL 1 32
 FT CHAIN 33 581
 FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CINNAMOMIN I
 SEQUENCE 581 AA; 64215 MW; 68375876236 CRC64;
 Query Match 45.5%; Score 1195; DB 10; Length 581;
 Best Local Similarity 48.7%; Pred. No. 1.9e-113;
 Matches 266; Conservative 70; Mismatches 184; Indels 26; Gaps 13;
 QY 9 THQTKKYEPRITLADVSSGSSSEKPELQSTIVSDAQRVAVLTLNQKXS-X 66
 DB 40 TKAKTKSYQTELEAGLQSGSEPRGLIVERRESTRV--DKRFELVELSNMAHSEV 97
 QY 67 TLAIDWYVYVAVQAGDQSYVPR-DAPKATRLPTGTTPSSGSPKXGYDERRAG 125
 DB 98 TLAVDTNAVVAVYKSGSFFRNDPDALEMLDPT--KYPFFSGSYDLDEGAVG 155
 QY 126 -HDDQPLGKXOLGOSVYALXRG-GSTRQKRSILILQWISSEARFNPILMXKQKXIN 183
 DB 156 ERREETILGMDPLEKMLISALWISNNOGRALSLIVYQWAEVAFEFIEKRVAGSIS 215
 QY 184 SGKSLPDKVYLETSWQGSQVQVSTG-DVNNPKKLAIXKQVTLKAVV-YVLA 241
 DB 216 PAKRFPPDPNLSLEKMSALSNVQSGGVSSEVLELSIKKPVSGSDENYISG 275
 QY 242 LAIMLFVC--GSPSSDQVYVLPVPLVAD-----DYCCASAPPTVAVGXG 289
 DB 276 LAIMEFLCRSTRASSDQFIPLMLNFRILVIVAEVATDANDNDQDDEPTVVISGNG 335
 QY 290 KAVIVRDPDHPGNOIQIWPESKNDPQOLMTRKEDTRISNGSLTYGTAGVYVIF 349
 DB 336 LCVDAVDKQNNNGPQLMPCQNSDQVQWTLNRGALHSEKELTYNGVADADVWY 395
 QY 350 DQCTARATQIQWAGTINPRSNVYLAASGQKTLTYGTDTLCOGQTAQNTA 409
 DB 396 DCFPTVASIQFMANGTILINQSAVLASGSRPTLLQNAVITASQKMLANITE 455
 QY 410 PRVITVGRDLQESNKGSTWECSSQXKQXVALYKSGSIFPKQND--CCTIGR 467
 DB 456 PVTYSIVGFNDLCQANEDAMWVECESSKAO--KVALPQSGIRHPQDEGRACELLDN 514

RESULT 8
 Q06076 PRELIMINARY; PRT; 528 AA.
 ID Q06076, 1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Abtin-d (EC 3.2.2.22) (RNA N-glycosidase) (Fragment).
 OS Abrus precatorius (Indian licorice) (Crab's eye).
 OC Burkariaceae; Viciales; Fabaceae; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucoside II; Fabales; Fabaceae; Papilionoideae; Abrus.
 NCBI_TaxID=3816;
 RX SOURCE FROM N.A.
 RA MEDLINE=9112759; PubMed=642112; LBN J-Y;
 RT "Primary structure of three distinct isoforms determined by cDNA
 RT sequencing: conservation and significance".
 RL J. Mol. Biol. 229:263-267(1993).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC EMBL; M83446; AA03626.1; .
 DR HSP; P11140; IABR; Ricin_B_lectin.
 DR InterPro: IPR001574; RLP_1; SHIGARICIN.
 DR Pfam: PF00652; Ricin_B_lectin; 6.
 DR PRINTS: PRO0396; SHIGARICIN.
 DR SMART: SM00458; RICIN; 2.
 DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolyase; Toxin.
 FT NON-TER 1 528
 FT SIGNAL 529 528
 SEQUENCE 528 AA; 58870 MW; 628242F8F60F8 CRC64;
 Query Match 43.3%; Score 1137; DB 10; Length 528;
 Best Local Similarity 46.0%; Pred. No. 1.5e-107;
 Matches 242; Conservative 83; Mismatches 189; Indels 12; Gaps 9;
 QY 9 THQTKKYEPRITLADVSSGSSSEKPELQSTIVSDAQRVAVLTLNQKXS-X 68
 DB 9 TEGATSGYQTELEAGLQSGSEPRGLIVERRESTRV--DKRFELVELSNMAHSEV 97
 QY 69 TLAIDWYVYVAVQAGDQSYVPR-DAPKATRLPTGTTPSSGSPKXGYDERRAG 127
 DB 67 TLAVDTNAVVAVYKSGSFFRNDPDALEMLDPT--KYPFFSGSYDLDEGAVG 154
 QY 126 DDQPLGKXOLGOSVYALXRG-GSTRQKRSILILQWISSEARFNPILMXKQKXIN 184
 DB 126 EELSLQALTRVAFSGSNDKARFLVLIQWAEARIRISNVGVSIRGTA 184
 QY 188 PLDPVXVLETSWQGSQVQVSTGQVPRERKLAIXKQVTLKAVV-RVYLAIAV 246
 DB 185 TQPPKPSGSDQVYVLPVPLVAD-----DYCCASAPPTVAVGXG 289
 QY 242 PTCGPPSSDQVYVLPVPLVADVQASL-PTVYVQKQWCVDDPDDPQNDI 305
 DB 245 PVND--PRANQ--PLIRISVIESKICSSAYEPTVIRIGRGQWCVDDYDGHNNRI 300
 QY 306 QUNBSKNDPQNLTKEDTRISNGSLTYGTAGVYVIFDQNTAVRATVQW 365

NCBI_TaxID=3988;
[1]
SEQUENCE FROM N.A.
MEDLINE=9238377; PubMed=163311;
RA ROBERTS L.M., Tregear J.W., Lord J.N.,
RT Molecular cloning of Ricin B.
R Ricin B subunit cDNA (GenBank accession
CC C001471) Activity: Endo-1,4-beta-D-glucosylase; EC=3.2.2.22 (1992)
CC -1- SIMILARITY: BELONGS TO THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: S40366; AA02282.1; -
DR HSP: P02879; IPR6.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIF.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00181; RIF; 1.
DR SMART: SM00456; RIBGALICIN.
DR SMART: SM00459; RIBGALICIN.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
KW Hydroxylase; Toxin.
FT NON_TER 1
SQ SEQUENCE 541 AA; 60281 MW; 28782CDEPF2E9D3 CRC64;
Query Match 46.8%; Score 1228.5; DB 10; Length 541;
Best Local Similarity 45.0%; Pred. No. 6,56-117; Matches 263; Conservative 78; Mismatches 175; Indels 21; Gaps 12;
9 THQTTQKYEFRITLADYVSSGSENEIFLRQ-STIPSDQRFVLEINQKDSX 66
13 TAGATVQSTNFIARQGLITGADVDHDIYLPKRYGLIN-QNIIYVLSMAHLSY 70
67 TLAIDVYKXVYVAYOAGDSYFEL-DAPRGAE--THLPTGRSSLPFGSYDLEHY 123
71 TLADVYKXVYVAYOAGDSYFEL-DAPRGAE--THLPTGRSSLPFGSYDLEHY 129
124 AGR-RDQIFPGIXOLIGVYAL--KXFGSTKXQANSLILQWISPAARFPIIMKX 179
130 AGRKENTELANGHELEISALYVSTGDTPLARSPFICICWISPAARFPIIMKX 189
180 QKINSQKSEFLPKYMLSEFNSGQOSTVQNSTDGVFNKXKLAIXKFFLTXKXVI 239
190 TRIRYKRSAPDPSVITLNSKASSTALQSNQKSTPISQKQKRSKSTISL 249
240 ASIALMLFVCGERSSDVPYVPIVPIAD--DYTCASSEPTFRVYKXAVYDRO 296
250 PIIALVYKCAPPSQ---PSLIRFPVFNRAVD-CMDEPVIYIGANGICVDRO 304
257 DDFDQNGQIQLPKSKNSDNQVLMITIKDITRSNGSCITTYGTAGYVWIMDKTVR 356
305 GRTNKGNAIQLPKSKNSDNQVLMITIKDITRSNGSCITTYGTAGYVWIMDKTVR 364
357 EATIMQKNGITINRSNNTYLAASGICGTLTQVTLDTYTGQNTLADYAPREVIT 416
365 DATIMQKNGITINRSNNTYLAASGICGTLTQVTLDTYTGQNTLADYAPREVIT 424
417 GFRDLCMBNSGVSWEYTCSSQKXKXWALYGGSGIFPQXQDQCLTGKSDYVYNI 476
425 GLVGLCLQNSGQVWIECCSKRBAQ-QWALYDGSIFPQXQDQCLTGKSDYVYNI 483
477 VSCXKXKXQVWFTNEXALINLKKXKXVDAQANPKLEIITTPATGKPNQWMLPV 533
484 LSCGPKSGCQKXKXQVWFTNEXALINLKKXKXVDAQANPKLEIITTPATGKPNQWMLPV 540

RESULT 6
ID Q9FV22 PRELIMINARY; FRT; 549 AA.
AC Q9FV22;
DT 01-MAR-2001 (TRENBERG, 16, Created)
DT 01-MAR-2001 (TRENBERG, 16, Last sequence update)

01-OCT-2002 (TRENBERG, 22, Last annotation update)
DE Type II ribosome-inactivating protein cinnamomun (BC 3.2.2.22) (ENM
DE N-glycosylase) (Fragment)
OS Cinnamomum camphora (Camphor tree)
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI_TaxID=13429;
[1]
SEQUENCE FROM N.A.
RA ROBERTS L.M., Tregear J.W., Lord J.N.,
RT Molecular cloning of cinnamomun A., B-chain and the expression,
R Ricin B subunit cDNA (GenBank accession
CC C001471) Activity: Endo-1,4-beta-D-glucosylase; EC=3.2.2.22 (1992)
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AF259548; AA68978.2; -
DR HSP: P02879; 2A01.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIF.
DR Pfam: PF00652; Ricin_B_lectin; 5.
DR Pfam: PF00181; RIF; 1.
DR SMART: SM00456; RIBGALICIN.
DR SMART: SM00459; RIBGALICIN.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
KW Hydroxylase; Toxin.
FT NON_TER 1
SQ SEQUENCE 549 AA; 60648 MW; 02607F607CA4B0 CRC64;
Query Match 45.5%; Score 1196; DB 10; Length 549;
Best Local Similarity 48.7%; Pred. No. 1,48-113; Matches 266; Conservative 71; Mismatches 183; Indels 26; Gaps 13;
9 THQTTQKYEFRITLADYVSSGSENEIFLRQ-STIPSDQRFVLEINQKDSX 66
8 TKGITSTYQIFELALQAGSGEHOITVKNESIVV--DSKRIYVLSMAHLSY 65
67 TLAIDVYKXVYVAYOAGDSYFEL-DAPRGAE--THLPTGRSSLPFGSYDLEHY 125
66 TLADVYKXVYVAYOAGDSYFEL-DAPRGAE--THLPTGRSSLPFGSYDLEHY 123
126 -HRDQIFPGIXOLIGVYAL--KXFGSTKXQANSLILQWISPAARFPIIMKX 183
184 SGRSEFLPKYMLSEFNSGQOSTVQNSTDGVFNKXKLAIXKFFLTXKXVI 239
194 TRIRYKRSAPDPSVITLNSKASSTALQSNQKSTPISQKQKRSKSTISL 249
184 SGRSEFLPKYMLSEFNSGQOSTVQNSTDGVFNKXKLAIXKFFLTXKXVI 239
184 SGRSEFLPKYMLSEFNSGQOSTVQNSTDGVFNKXKLAIXKFFLTXKXVI 239
242 LAIHLVPC--GSPSSDVPYVPIVPIAD--DYTCASSEPTFRVYKXAVYDRO 296
244 LAIHLVPC--GSPSSDVPYVPIVPIAD--DYTCASSEPTFRVYKXAVYDRO 296
244 LAIHLVPC--GSPSSDVPYVPIVPIAD--DYTCASSEPTFRVYKXAVYDRO 296
290 KXVYVADDFHQNQIQLPKSKNSDNQVLMITIKDITRSNGSCITTYGTAGYVWIMDKTVR 356
304 LCVADVADDFHQNQIQLPKSKNSDNQVLMITIKDITRSNGSCITTYGTAGYVWIMDKTVR 364
350 KXVYVADDFHQNQIQLPKSKNSDNQVLMITIKDITRSNGSCITTYGTAGYVWIMDKTVR 364
364 DCRPTVLAIVQPRANGITINRSNNTYLAASGICGTLTQVTLDTYTGQNTLADYAPREVIT 416
410 PREVTIYGFRLCMBNSGVSWEYTCSSQKXKXWALYGGSGIFPQXQDQCLTGKSDYVYNI 476
424 PREVTIYGFRLCMBNSGVSWEYTCSSQKXKXWALYGGSGIFPQXQDQCLTGKSDYVYNI 483
468 DSVYVADDFHQNQIQLPKSKNSDNQVLMITIKDITRSNGSCITTYGTAGYVWIMDKTVR 356
483 HPGSTIILISSCSRSSGRRVAVNDGVLINLNGALVMDVGSNPLQIILWPTAKEN 542
528 QMFLPV 533
543 HEMFLP 546

KM Hydroxylase; Signal; Toxin.
 FT SIGNAL 1 32
 FT CHAIN 33 580
 SEQUENCE 580 AA; 64265 MW; 3764289CCEGAPF CRC64;
 Query Match 47.4%; Score 1244.5; DB 10; Length 580;
 Best Local Similarity 50.3%; Pred. No. 1.6e-118;
 Matches 274; Conservative 69; Mismatches 177; Indels 25; Gaps 13;

QY 9 THQTGKEFRFTLLADYVSSGSFSNEIPLRQ-STIPVSDAQRFVYVELTNGQXDSX 67
 DB 40 TKNATKISTYQFLEALRQALSGEPRGHEIVKEDGSTVE--DSKRFILVLSNMAADSPV 97
 QY 68 A-AIDVTNKKYVVAQAGDSYR-DAPRGAETHLFGTTDRSSLPFGSKYDLERYAG 125
 DB 98 ALAVDTNAYVVAFRGSGSFLEADNPDALENLPDT--KRTFFSGSYTDLERYAG 155
 QY 126 H-RDQIFGIXQILOSVALKXPG-GSTRXQASILLIQMISEAARPNILFXRXQYN 183
 DB 156 ELKEEILLGMDPLENLSALMTSNLNOORALNSLIVYQVAVARFRFEYVRESIT 215
 QY 184 SGXSFDPDXMLELSTWQOQTOYQSTD-GVFNNEPKRLAIKXGNVTLNVR-XVLA 241
 DB 216 RAEFRPDPALSLKMKASLNVQSNQGVSSPVELKSIKMKYVVSVDVLSG 275
 QY 242 LAIMEFVC--GEPSSSDVRYVYRPIVAD-----DVTGASEPTVAVGXG 289
 DB 276 LAIMEFICSSDRTSSDQFIDMLKRIIVYADVADADNDQCADPEPTVAVISGN 335
 QY 290 KAYVDADDPDHGNQIQLPKSKNNDNOLMTIKEDXITIRNSGCLTYGTAGYVWIP 349
 DB 336 LCVDYDQKYNKGNPQLMPCKNSDYNQWLRLRGGITIRNSCKLTITNGSAGDYV 395
 QY 350 DONTAVREATINQWKGITINRSNIVLAASGIGKITLTGYOTLQGLMAQNDTA 409
 DB 396 DCRPTVTAISIVQFANGLINOSALVLSASSENRTITLVANATYASRQMLANNTE 455
 QY 410 PREVTIYGRDLCMSNGSWTWCSSGXQXKXALVGDSSIFPQMOQCLT-XGRD 468
 DB 456 PFTSIVGMNDCQANDDMWVVCSSKSAQ-KMAYTPDSIRPHQDRKCLISTDNH 514
 QY 469 SVSTVITNVCSSXSKXQKRWFTNEXALINLKKXXXKXVQANPKRLRIIYPATGR 528
 DB 515 SGGIILLISCSFGSGQRMVPMNDGITLNLKNGLVWVKSNPFLHQLIIMPATCKN 574
 QY 529 MWLPV 533
 DB 575 QWLEL 579

RESULT 4
 ID Q94BW3 PRELIMINARY; PRT: 580 AA.
 AC Q94BW3;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Type 2, Ribosome-inactivating protein cinnamomol III precursor
 DE 183 (3.2.2) (rRNA N-glycosidase).
 OS Cinnamomum (Cannaceae) (Streptococci).
 OC Eukaryota; Viridiplantae; Streptococci.
 OC Spermatophyta; Magnoliophyta; Laurales; Euphorbia; Tracheophyta;
 OC NCBI_TaxID=13429;

RP SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating proteins) genes encoding cinnamomol proteins and study of their expression patterns";
 RI Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ENDOHYDROLYSTS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 26S RRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL: AY039803; AK02460.1; -;
 DR Interpro: IPR00772; RICH_B_lectin.
 DR Interpro: IPR001574; RIP__B_lectin.
 DR Pfam: PF00652; RICH_B_lectin; 6.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00453; RICHIN_2; LECTIN; 2.
 DR PROSITE: PS00453; RICHIN_2; LECTIN; 2.
 DR SIGNAL 1 32
 FT SIGNAL 32
 FT CHAIN 33 580
 SEQUENCE 580 AA; 64421 MW; 940D10F0LEFB58 CRC64;
 Query Match 47.3%; Score 1241.5; DB 10; Length 580;
 Best Local Similarity 50.3%; Pred. No. 3.3e-118;
 Matches 274; Conservative 71; Mismatches 175; Indels 25; Gaps 13;

QY 9 THQTGKEFRFTLLADYVSSGSFSNEIPLRQ-STIPVSDAQRFVYVELTNGQXDSX 66
 DB 40 TKNATKISTYQFLEALRQALSGEPRGHEIVKEDGSTVE--DSKRFILVLSNMAADSPV 97
 QY 67 TAAIDVTNKKYVVAQAGDSYR-DAPRGAETHLFGTTDRSSLPFGSKYDLERYAG 125
 DB 98 ALAVDTNAYVVAFRGSGSFLEADNPDALENLPDT--KRTFFSGSYTDLERYAG 155
 QY 126 -HRDQIFGIXQILOSVALKXPG-GSTRXQASILLIQMISEAARPNILFXRXQYN 183
 DB 156 ERREELILLGMDPLENLSALMTSNLNOORALNSLIVYQVAVARFRFEYVRESIT 215
 QY 184 SGXSFDPDXMLELSTWQOQTOYQSTD-GVFNNEPKRLAIKXGNVTLNVR-XVLA 241
 DB 216 RAEFRPDPALSLKMKASLNVQSNQGVSSPVELKSIKMKYVVSVDVLSG 275
 QY 242 LAIMEFVC--GEPSSSDVRYVYRPIVAD-----DVTGASEPTVAVGXG 289
 DB 276 LAIMEFICSSDRTSSDQFIDMLKRIIVYADVADADNDQCADPEPTVAVISGN 335
 QY 290 KAYVDADDPDHGNQIQLPKSKNNDNOLMTIKEDXITIRNSGCLTYGTAGYVWIP 349
 DB 336 LCVDYDQKYNKGNPQLMPCKNSDYNQWLRLRGGITIRNSCKLTITNGSAGDYV 395
 QY 350 DONTAVREATINQWKGITINRSNIVLAASGIGKITLTGYOTLQGLMAQNDTA 409
 DB 396 DCRPTVTAISIVQFANGLINOSALVLSASSENRTITLVANATYASRQMLANNTE 455
 QY 410 PREVTIYGRDLCMSNGSWTWCSSGXQXKXALVGDSSIFPQMOQCLT-XGRD 468
 DB 456 PFTSIVGMNDCQANDDMWVVCSSKSAQ-KMAYTPDSIRPHQDRKCLISTDNH 514
 QY 469 SVSTVITNVCSSXSKXQKRWFTNEXALINLKKXXXKXVQANPKRLRIIYPATGR 528
 DB 515 SGGIILLISCSFGSGQRMVPMNDGITLNLKNGLVWVKSNPFLHQLIIMPATCKN 574
 QY 529 MWLPV 533
 DB 575 QWLEL 579

RESULT 5
 ID Q41174 PRELIMINARY; PRT: 541 AA.
 AC Q41174;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Proctid A chain (EC 3.2.2.2) (rRNA N-glycosidase)
 DE (Fragment).
 OS Ricinus communis (Castor bean).
 CC Eukaryota; Viridiplantae; Streptophyta; Euphorbia; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.

Matches 483; Conservative 5; Mismatches 42; Indels 3; Gaps 2;

QY 1 YERLRLVHTQTKXEVFRFTLLRLDYSSGSPSNEILRLRSTIIPVSDAQRFVLELTN 60
 DB 1 YERLRLVHTQTKXEVFRFTLLRLDYSSGSPSNEILRLRSTIIPVSDAQRFVLELTN 60

QY 61 CGDSTALADVTNLYVAVQAGDQSTFLADPRGATFLPCTTRDSSGSPKSYDYL 120
 DB 61 CGDSTALADVTNLYVAVQAGDQSTFLADPRGATFLPCTTRDSSGSPKSYDYL 118

QY 121 ERYAGHRDQIPGIGXOLIGVYALXPGSGTRKQASLILILQWISBARFPIILRXQ 180
 DB 119 ERYAGHRDQIPGIGDOLIGVYALXPGSGTRKQASLILILQWISBARFPIILRXQ 178

QY 181 XINSKSEFLPDXYMLELTSWGQSTOVQSHTDGVNPNPKALIXXGNFVLAVRYVIA 240
 DB 179 YINSKSEFLPDXYMLELTSWGQSTOVQSHTDGVNPNPKALIXXGNFVLAVRYVIA 238

QY 241 SLALMFCGSPSSDVRVWPLVIRPVADVTCSASEPTVIRVGRKXQVREDDEH 300
 DB 239 SLALMFCGSPSSDVRVWPLVIRPVADVTCSASEPTVIRVGRKXQVREDDEH 298

QY 301 DGNQIOLMPKSNNDPNOQLTIKXDTIRNSGCLITGYTAGVYVWIPDNTAVBATI 360
 DB 299 DGNQIOLMPKSNNDPNOQLTIKXDTIRNSGCLITGYTAGVYVWIPDNTAVBATI 358

QY 361 WQIWKGTINRSNLVLAASSGIGKTLTVQTLDTYLLQSGMLAGNDTAPREVTIYGRD 420
 DB 359 WQIWKGTINRSNLVLAASSGIGKTLTVQTLDTYLLQSGMLAGNDTAPREVTIYGRD 418

QY 421 LCMENKSGVWETCKSSQXKXKXALXGDSIPRQNOQCLTGKDSVSTVYNVSCS 480
 DB 419 LCMENKSGVWETCKSSQXKXKXALXGDSIPRQNOQCLTGKDSVSTVYNVSCS 477

QY 481 XKSXKXQWVFTENXALINLKKXKXKXDVQANFKRLRIIYATGKPNQMLPV 533
 DB 478 AGSSQQRWFTENXALINLKKXKXKXDVQANFKRLRIIYATGKPNQMLPV 530

RESULT 2

ID Q8W243 PRELIMINARY; PRT; 565 AA.

AC Q8W243; 01-MAR-2002 (Tremblrel. 20, Created)

DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)

DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)

DB VCA precursor (BC 3.2.2.22) (rRNA N-glycosidase).

OS Viscum album subsp. coloratum.

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.

OC [1]_taxid=15976;

EN [1]_taxid=15976;

RP SEQUENCE FROM N.A.
 RA Park W.-B., Liu S.;
 RT "Cloning of Viscum album subsp. coloratum (Korean mistletoe).",
 RL Biochem. Biophys. Res. Commun. 0:0-0(2002).

CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC EMBL: AF369961; AL040417.1; -
 DB EMBL: AF369961; AL040417.1; -
 DB Interpro: IPRO01574; Ricin_B_lectin.6.
 DB Pfam: PF00652; Ricin_B_lectin.6.
 DB PRINTS: PR00396; SHIGARICIN.
 DB SMART: SM00458; RICIN_2.
 DB PROSITE: PS50231; RICIN_B_LECTIN; 2.
 KW Hydrolase; Signal; Toxin.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 273 VCA ALPHA CHAIN.
 FT CHAIN 309 565 VCA BETA CHAIN.
 SQ SEQUENCE 565 AA; 62401 MW; 991E394D005511 CRC64;

Query Match 84.7%; Score 2224; DB 10; Length 565;
 Best Local Similarity 81.6%; Pred. No. 6.2e-219;
 Matches 439; Conservative 18; Mismatches 69; Indels 12; Gaps 4;

QY 1 YERLRLVHTQTKXEVFRFTLLRLDYSSGSPSNEILRLRSTIIPVSDAQRFVLELTN 60
 DB 34 YERLRLVHTQTKXEVFRFTLLRLDYSSGSPSNEILRLRSTIIPVSDAQRFVLELTN 93

QY 61 CGDSTALADVTNLYVAVQAGDQSTFLADPRGATFLPCTTRDSSGSPKSYDYL 120
 DB 94 CGDSTALADVTNLYVAVQAGDQSTFLADPRGATFLPCTTRDSSGSPKSYDYL 151

QY 121 ERYAGHRDQIPGIGXOLIGVYALXPGSGTRKQASLILILQWISBARFPIILRXQ 180
 DB 152 ERYAGHRDQIPGIGIEIGVYALXPGSGTRKQASLILILQWISBARFPIILRXQ 211

QY 181 XINSKSEFLPDXYMLELTSWGQSTOVQSHTDGVNPNPKALIXXGNFVLAVRYVIA 240
 DB 212 YINSKSEFLPDXYMLELTSWGQSTOVQSHTDGVNPNPKALIXXGNFVLAVRYVIA 271

QY 241 SLALMFCGSPSSDVRVWPLVIRPVADVTCSASEPTVIRVGRKXQVREDDEH 300
 DB 272 SLALMFCGSPSSDVRVWPLVIRPVADVTCSASEPTVIRVGRKXQVREDDEH 331

QY 299 DGNQIOLMPKSNNDPNOQLTIKXDTIRNSGCLITGYTAGVYVWIPDNTAVBATI 360
 DB 332 DGNQIOLMPKSNNDPNOQLTIKXDTIRNSGCLITGYTAGVYVWIPDNTAVBATI 387

QY 361 WQIWKGTINRSNLVLAASSGIGKTLTVQTLDTYLLQSGMLAGNDTAPREVTIYGRD 420
 DB 356 WQIWKGTINRSNLVLAASSGIGKTLTVQTLDTYLLQSGMLAGNDTAPREVTIYGRD 415

QY 421 LCMENKSGVWETCKSSQXKXKXALXGDSIPRQNOQCLTGKDSVSTVYNVSCS 480
 DB 388 LCMENKSGVWETCKSSQXKXKXALXGDSIPRQNOQCLTGKDSVSTVYNVSCS 447

QY 481 XKSXKXQWVFTENXALINLKKXKXKXDVQANFKRLRIIYATGKPNQMLPV 533
 DB 448 YKQCNLCWENAGASVETCKSSQXKXKXALXGDSIPRQNOQCLTGKDSVSTVYNVSCS 506

DB 507 IVSCSSGQQRWFTENXALINLKKXKXKXDVQANFKRLRIIYATGKPNQMLPV 564

RESULT 3

ID Q94BW4 PRELIMINARY; PRT; 580 AA.

AC Q94BW4; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

DB Type 2 ribosome-inactivating protein cinnamon II precursor
 (BC 3.2.2.22) (rRNA N-glycosidase).

CC Cinnamomum camphora (Camphor tree).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.

OC [1]_taxid=11429;

EN [1]_taxid=11429;

RP SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinnamon proteins and study of their expression
 RT patterns."

CC Submitted (JUN-2001) to the EMBL/Genbank/DDBJ databases.

CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.

CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC EMBL: AY039802; AA029459; -
 DB EMBL: AY039802; AA029459; -
 DB Interpro: IPRO01574; Ricin_B_lectin.6.
 DB Pfam: PF00652; Ricin_B_lectin.6.
 DB PRINTS: PR00396; SHIGARICIN.
 DB SMART: SM00458; RICIN_2.
 DB PROSITE: PS50231; RICIN_B_LECTIN; 2.

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Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 : Search time 41.16 Seconds

3347.915 Million cell updates/sec

Title: US-09-601-667c-40

Perfect score: 2626

Sequence: 1 YERLRVTHQTCXEPFP.....RRIIVPATKRNQMLPYX 534

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mus:*
- 8: sp_rabbit:*
- 9: sp_rhesus:*
- 10: sp_rhesus:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeo:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Match length	DB	ID	Description
1	2477.5	94.3	531	10	Q8W2E8	Q8W2E8 vitiscum albu
2	2224	84.7	565	10	Q8W2E8	Q8W2E8 vitiscum albu
3	1244.5	47.4	580	10	Q8W2E8	Q8W2E8 vitiscum albu
4	1244.5	47.3	580	10	Q8W2E8	Q8W2E8 vitiscum albu
5	1228.5	46.8	541	10	Q8W2E8	Q8W2E8 vitiscum albu
6	1195	45.5	549	10	Q8W2E8	Q8W2E8 vitiscum albu
7	1195	45.5	581	10	Q8W2E8	Q8W2E8 vitiscum albu
8	1137	43.3	528	10	Q8W2E8	Q8W2E8 vitiscum albu
9	1137	43.3	528	10	Q8W2E8	Q8W2E8 vitiscum albu
10	1074	41.7	524	10	Q8W2E8	Q8W2E8 vitiscum albu
11	1074	41.7	524	10	Q8W2E8	Q8W2E8 vitiscum albu
12	1060.5	40.1	263	10	Q8W2E8	Q8W2E8 vitiscum albu
13	1029.5	39.2	263	10	Q8W2E8	Q8W2E8 vitiscum albu
14	977	37.2	251	10	Q8W2E8	Q8W2E8 vitiscum albu
15	969	36.9	592	10	Q8W2E8	Q8W2E8 vitiscum albu

ALIGNMENTS

17	964	36.7	573	10	Q8W2E8	Q8W2E8 vitiscum albu
18	949	36.1	266	10	Q8W2E8	Q8W2E8 vitiscum albu
19	879	33.5	570	10	Q8W2E8	Q8W2E8 vitiscum albu
20	876.5	33.4	382	10	Q8W2E8	Q8W2E8 vitiscum albu
21	873.5	33.3	564	10	Q8W2E8	Q8W2E8 vitiscum albu
22	851	32.3	570	10	Q8W2E8	Q8W2E8 vitiscum albu
23	848	32.3	567	10	Q8W2E8	Q8W2E8 vitiscum albu
24	829	31.6	565	10	Q8W2E8	Q8W2E8 vitiscum albu
25	829	31.6	565	10	Q8W2E8	Q8W2E8 vitiscum albu
26	821	31.3	563	10	Q8W2E8	Q8W2E8 vitiscum albu
27	819	31.2	563	10	Q8W2E8	Q8W2E8 vitiscum albu
28	815	31.0	564	10	Q8W2E8	Q8W2E8 vitiscum albu
29	814.5	31.0	566	10	Q8W2E8	Q8W2E8 vitiscum albu
30	766	29.2	603	10	Q8W2E8	Q8W2E8 vitiscum albu
31	726.5	27.7	569	10	Q8W2E8	Q8W2E8 vitiscum albu
32	526.5	20.0	316	10	Q8W2E8	Q8W2E8 vitiscum albu
33	523.5	19.9	316	10	Q8W2E8	Q8W2E8 vitiscum albu
34	503.2	19.0	320	10	Q8W2E8	Q8W2E8 vitiscum albu
35	494.5	18.6	320	10	Q8W2E8	Q8W2E8 vitiscum albu
36	494.5	18.6	320	10	Q8W2E8	Q8W2E8 vitiscum albu
37	493	18.2	307	10	Q8W2E8	Q8W2E8 vitiscum albu
38	467	17.6	252	10	Q8W2E8	Q8W2E8 vitiscum albu
39	461	17.6	251	10	Q8W2E8	Q8W2E8 vitiscum albu
40	460	17.5	251	10	Q8W2E8	Q8W2E8 vitiscum albu
41	454	17.3	251	10	Q8W2E8	Q8W2E8 vitiscum albu
42	443	16.9	252	10	Q8W2E8	Q8W2E8 vitiscum albu
43	302	11.5	289	10	Q8W2E8	Q8W2E8 vitiscum albu
44	301	11.5	289	10	Q8W2E8	Q8W2E8 vitiscum albu
45	297.5	11.3	299	10	Q8W2E8	Q8W2E8 vitiscum albu

RESULT 1

10	Q8W2E8	PRELIMINARY:	PF1: 531 AA.
20	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Created)	
30	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
40	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
50	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
60	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
70	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
80	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
90	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
100	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
110	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
120	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
130	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
140	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
150	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
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190	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
200	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
210	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
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270	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
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290	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
300	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
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320	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
330	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
340	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
350	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
360	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
370	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
380	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
390	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
400	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
410	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
420	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
430	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
440	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	
450	Q8W2E8	Q8W2E8_2002 (TREMUR_21, Last annotation update)	

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Page 15

Db 218 FIENOINNNPOQRIR-----PANNTISLHKKWGLSFOIRTSANGWFSSEAVELEBANG 271
QY 228 NPTLXNVEXVIALMIFV 248
Db 272 KRIYVYANDOVREHILKFEV 292

Search completed: December 11, 2003, 14:09:09
Job time : 10.26 secs

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CC or send an email to license@sib.ch).
CC
DR EMBL; AF055086; AAD02686.1; -.
DR HSSP; P33185; 1BRX.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; FALSE NEG.
KW Ribosome; protein synthesis inhibitor; Hydrolase; Toxin;
KW Glycoprotein; signal.
FT SIGNAL 1 19
FT CHAIN 20 264
FT TYPE 1 RIBOSOME-INACTIVATING PROTEIN
FT TRICHONANTHA.
FT PROPEP 265 294
FT ACT SITE 177 177 BY SIMILARITY.
FT ACT SITE 180 180 BY SIMILARITY.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (PROBALE).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. .) (PROBALE).
FT CONFLICT 51 51 C->Y (IN REF. 2).
FT CONFLICT 65 65 W->R (IN REF. 2).
FT CONFLICT 85 85 N->D (IN REF. 2).
FT CONFLICT 154 154 A->S (IN REF. 2).
FT CONFLICT 174 174 A->S (IN REF. 2).
FT CONFLICT 245 245 N->H (IN REF. 2).
SQ SEQUENCE 294 AA; 32234 MW; DA4FB7C33290994 CRC64;
Query Match 10.6%; Score 278.5; DB 1; Length 294;
Best Local Similarity 32.5%; Pred. No. 1e-19;
Matches 82; Conservative 40; Mismatches 115; Indels 15; Gaps 7;
QY 13 TSKYRFFITLLADYSSGSSFSNEIPILRQSTIPVSDAQPVLVELINQGXKTAIDY 72
DB 29 TKSSTSTFIOGRRLAFTQCTGCPILPST--ASSQWFFERFLNINDETVAVNV 85
QY 73 TTKYVAVYQADQSYELADPARGAFTLCTRTDSSTPFQSYKDERAG-EEQCLP 131
DB 86 TTVYVAVYADAVSYFEDTPAFAFLIPACTIKV--LYSQNIDKLSYVQKQKRWIE 143
QY 132 LGIQLQGVYALKRGGSTKQKRSILLQIMISFARFNPILMRKXQINSGSFEPD 191
DB 144 LGIPALSSAITNMVY--VDYSTALALVLQCTEMAFKYLIDQVSHSS--NFPYD 199
QY 192 XTMLELEFWSQSQSTQVQ--HSTDGVPANFKELAXKXNPVTLXWRX-VTASLALTL 246
DB 200 QAVTSJNNKRLSKQIQIDNRTGQGFENEVELINPDGRFSVYVNSAGVGNKILML 259
QY 247 FVCGERSSSDV 258
DB 260 YTKASVGSSEYDI 271
RESULF 15
RIPQ_GELONIN
AC P33186
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein gelonin precursor (rRNA N-glycosidase)
DE (EC 3.2.2.22).
GN GEL.
OC Gelonium multiflorum (Euphorbiaceae himalayana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Rosales; Malvales; Euphorbiales; Euphorbiaceae; Gelonium.
OX NCBI_taxonomy:3973;

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	FT	TURN	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	74
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FT ACT SITE 183 183 BY SIMILARITY.
 SQ SEQUENCE 289 AA; 31704 MW; 883D3E324288726 CRC64;
 Query Match 11.4%; Score 300; DB 1; Length 289;
 Best Local Similarity 31.4%; Pred. No. 7,66-22;
 Matches 85; Conservative 46; Mismatches 35; Indels 14; Gaps 9;

QY 13 TGEYRPFITLADYSSGSFEN---ETPLRQSTFVSDAQRVYVETLNQGXDTAA 69
 DB 33 TSSSYGVFISNFKALPFERKLDIPILR-STLRSS--QRYALHUNYVADETISVALDY 89
 QY 73 TKNVYVAKQAGOSYFLDA-PGAEHLFTGTROSSLPFGVSGYXDLERYAGH-POCI 130
 DB 90 TNYVWGTADGTSEFNEASTAEKAYVKNAR-KVLPFGSGNYERLQIAKXIRENT 148
 QY 131 PLGIKQIOSYKALRPGSGSTRKQARSILILQIMISEAAPNPILMKRXKINSKXSLD 190
 DB 149 ELGPDALDAITLTPYVANS--ASALNVLQISSEKAKRTFIEQIQKRVDE--TFL 204
 QY 191 DXYMLEETSGWGQSTQV--QSTGQVFNPNPRLAKXGNFVLAKNRYVIALATN 246
 DB 205 SLAISLSEMSALSQIQLASTNNQCFETPVLLVNAQGRVTLINVDAGVYVSNIALLL 264

RESULT 12
 RIPI-BRYDI STANDARD; PRT; 286 AA.
 AC P25339;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribosome-inactivating protein momordin II precursor (rRNA N-glycosidase) (EC 3.2.2.22).
 OS Momordica balsamina (Bitter melon) (Balsam pear).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Cucurbitales; Cucurbitaceae; Momordica.
 NCBI_TaxID=3672;
 RX [1] SEQUENCE FROM N.A.
 RC TISSUE=Seed
 RX MEDLINE=93027170; PubMed=1408771;
 RA Ortigao M.; Better M.;
 RT "Momordin II, a ribosome inactivating protein from Momordica balsamina, is homologous to other plant proteins."
 RL Nucleic Acids Res. 20:4662-4662(1992).
 CC -1- CATALYTIC ACTIVITY: Endolytic cleavage of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
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 CC EMBL: Z11175; CA48166.1;
 DR EMBL: S2560; S2560;
 DR EMBL: S2560; S2560;
 DR InterPro: IPR00161; RIF.1; RIF.
 DR Pfam: pf00161; RIF.1; RIF.
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN.
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal.
 KW 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 286 RIBOSOME-INACTIVATING PROTEIN MOMORDIN II.
 FT ACT SITE 181 181 BY SIMILARITY.
 SQ SEQUENCE 286 AA; 32031 MW; 3689PFLA6B52986 CRC64;

Query Match 10.9%; Score 287.5; DB 1; Length 286;
 Best Local Similarity 32.5%; Pred. No. 1,36-20;
 Matches 83; Conservative 49; Mismatches 102; Indels 21; Gaps 10;

QY 13 TGEYRPFITLADYSSGSFEN---ETPLRQSTFVSDAQRVYVETLNQGXDTAA 69
 DB 33 TKTATYKFL--EDFRATLPFSKHVYDIPILYST--ISDSRFLIDLSYVYETISVA 86
 QY 70 TKNVYVAKQAGOSYFLDA-PGAEHLFTGTROSSLPFGVSGYXDLERYAGH-R 127
 DB 87 IDVNTVYVAKNRYVYFNEASTAEKAYVKNAR-KVLPFGSGNYERLQIAKXIRENT 143
 QY 128 PLGIKQIOSYKALRPGSGSTRKQARSILILQIMISEAAPNPILMKRXKINSKXSLD 187
 DB 144 ENIDLALALSATITLTPYVANS--ASALNVLQISSEKAKRTFIEQIQKRVDE--TFL 199
 QY 188 DXYMLEETSGWGQSTQV--QSTGQVFNPNPRLAKXGNFVLAKNRYVIALATN 245
 DB 200 FEPALATISLSEMSALSQIQLASTNNQCFETPVLLVNAQGRVTLINVDAGVYVSNIALLL 259
 QY 246 LFGQGRSSSDVRY 260
 DB 260 LFL-NRBASTADENP 273

RESULT 13
 RIPI-BRYDI STANDARD; PRT; 290 AA.
 AC P3185; Q9S819;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase) (EC 3.2.2.22) (put).
 OS Bryonia dioica (Red bryonia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Cucurbitales; Cucurbitaceae; Bryonia.
 NCBI_TaxID=3652;
 RX [1] SEQUENCE FROM N.A.; AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RC TISSUE=Leaf;
 RX MEDLINE=97228081; PubMed=9115985;
 RA Gavril S.L.; Kneidauer W.; Kiet H.E.; Chang C.Y.Y.; Binspehr H.M.;
 RT "Molecular biological and preliminary structural analysis of recombinant bryodin I, a ribosome-inactivating protein from the plant Bryonia dioica."
 RL Biochemistry 36:3095-3103(1997).
 CC [2]
 CC SEQUENCE FROM N.A.
 RA Siegel C.B.;
 RT "Cloning and expression of a gene encoding bryodin I from Bryonia dioica."
 RL Patent number US541110. 30-JUL-1996.
 CC [3]
 CC SEQUENCE OF 24-66.
 RC TISSUE=Seed;
 RX MEDLINE=89326691; PubMed=2753596;
 RA Montecucchi P.C.; Lazzarini A.M.; Barbieri L.; Stirpe F.; Soria M.;
 RA Iapelli D.;
 RT "N-terminal sequence of some ribosome-inactivating proteins."
 RL Int. J. Pept. Protein Res. 33:263-267(1993).
 CC [4]
 CC SEQUENCE OF 24-43.
 RC TISSUE=Seed;
 RX MEDLINE=851812; PubMed=7849072;
 RA Siegel C.B.; Gavril S.L.; Chace D.; Wolfe E.A.; Misan B.;
 RA Montecucchi P.C.; Gavril S.L.;
 RT "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunokonjugates."

RESULT 7
AGGL_RICCO STANDARD; PRT: 564 AA.
AC P06750;
DT 01-JAN-1988 (Rel. 06, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Agglutinin precursor (RCM) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain].
OS Ricinus communis (Castor bean).
OC Spermatophyta; Euphorbiaceae; Stereophyta; Tracheophyta; Eudicotyledons; Magnoliopsida; Euphorbiales; Euphorbiaceae; Ricinus.
CX NCBI_TaxID:3989;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=6059449; PubMed=299130;
RA Roberts L.N., Lamb F.I., Pappin D.J.C., Lord J.M.;
RT "The primary sequence of Ricinus communis agglutinin. Comparison with ricin".
RL U. Biol. Chem. 260:15682-15686(1985).
RL [2]
RN [3]
RP SEQUENCE OF 303-564.
RX MEDLINE=60178723; PubMed=6768555;
RA Lin T.T.-S., Li S.S.-L.;
RT "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis".
RL Eur. J. Biochem. 105:453-459(1980).
CC -1- Specific activity: Endo-glycosylase of the N-glycosidic bond at one specific asparagine in the N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYR 2 RIP SUBFAMILY.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYR 2 RIP SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
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CC EMBL: M12089; AAA33869.1;
DR EMBL: A40366; AAB22564.1;
DR PIR: A24261; RLCASG.
DR HSSP: P02879; IIR6.
DR GlycoStatedB; P06750;
DR InterPro; IPR001574; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR SMART; SM00458; RCTN2.
DR PROSITE; PS00275; SHIGA_RICIN_1.
DR PROSITE; PS00275; SHIGA_RICIN_2.
KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; Signal.
FT SIGNAL 1 24
FT CHAIN 25 290 AGGLUTININ A CHAIN.
FT PROPEP 291 302 LINKER PEPTIDE.
FT CHAIN 303 564 AGGLUTININ B CHAIN.
FT DOMAIN 309 453 RICIN B-TYPE LECTIN 1.
FT DOMAIN 454 564 RICIN B-TYPE LECTIN 2.
FT REPEAT 319 361
FT REPEAT 362 401
FT REPEAT 402 437
FT REPEAT 405 437 1-GNMA.

FT REPEAT 450 485 2-ALPHA.
FT REPEAT 486 528 2-BETA.
FT REPEAT 529 564 2-ALPHA.
FT ACT SITE 200 208
FT DISULFID 282 306 INTERCHAIN (BY SIMILARITY).
FT DISULFID 322 341 BY SIMILARITY.
FT DISULFID 365 382 BY SIMILARITY.
FT DISULFID 453 466 BY SIMILARITY.
FT CARBOHYD 492 509 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLUCNA. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLUCNA. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLUCNA. . .) (POTENTIAL).
FT CARBOHYD 437 437 N-LINKED (GLUCNA. . .) (POTENTIAL).
FT CONFLICT 362 382 R -> D (IN REF. 2).
FT CONFLICT 374 374 R -> G (IN REF. 2).
FT CONFLICT 404 404 R -> T (IN REF. 2).
FT CONFLICT 552 552 F -> V (IN REF. 2).
SQ SEQUENCE 564 AA; 62851 MW; D455F2A2F609759 CRC64;
Query Match 41.9%; Score 1101; DB 1; Length 564;
Best Local Similarity 45.1%; Pred.No. 4.7e-100;
Matches 242; Conservative 81; Mismatched 193; Indels 20; Gaps 11;
QY 9 THOTTAKERYRITLADYVSSSS-FSETRPL-RQSTFVSDAQRFTVELNQKQKX 66
DB 37 TDAIVTXXVYVAVQADQSFAR-DAPRAE--THLFTGTRDRSSLPKSYVDLEY 94
QY 67 TDAIVTXXVYVAVQADQSFAR-DAPRAE--THLFTGTRDRSSLPKSYVDLEY 123
DB 95 TDAIVTAAVAVQACAGNAFFPHDQDEAEIHLFT-DVQNSFTAFAGVDRFEC 153
QY 124 AGRDDIPLIGIQLQGVYAL--RFGQSTKQASRIILHQMISEAARFPELIMEXQ 180
DB 154 GRENKILTFGLBEDIALYVYSTCTDPTLAFSPVCIQISEARFQYIGEMRT 213
QY 161 XINGKASTEDKXWLEETNSQGSQVQSTDEGFNNKXLAIXGFTLVKRVYA 240
DB 214 KLRNRRBARDPSVTLSSNKRSLALQSNQAFSLQDQRNKRNVYDLSILP 273
QY 241 SLAIMFVCGERSSDSVWMPVIRPVLD--DYTCASEPTVAIVGXGXVDRD 297
DB 274 IIALVYECAPPESSQ---FSLIFPVIRNADV-CMDEPIVAIVGNNGLCVDTG 328
QY 298 DFHDGNOQLMPKSNKNDNQLATIRRXITXISNSGLTTGVTAGVAVIPDCNVAB 357
DB 329 EEPNSPQLQPKSNNTDMQMLTKSTKSNKCLTKISKSPQGVYVNGSLTAVG 388
QY 358 AITQIYNGCTINRNSNIYVASSCTGTLTQGLDVLTCGHLAQNTPAPATYTG 417
DB 389 KTRQIKMNETINRSGULANRSGSTKLTYNIAVNSQMLPNTNTPPTLITG 448
QY 418 FPDICANNGSVWETCKSSQNKQXAAVYCGSIRPQKQNDCTGAGDSVNTV 477
DB 449 LYGMCICANGKVMLEDCSTSEKAO-QMALVADGSIHPQGRNDCLITDNIKGVKLL 507
QY 478 SCSSXSKQXRVVTEKATLNIKKXXXDVANQKLEKLIIVYACGEPQGMALV 533
DB 508 SCGPASSQKRWKNDQDTILNINGLVLDVRNDSKIKQIVHFRGNLQNLVLP 563
RESULT 8
NIGB_SAMVI STANDARD; PRT: 563 AA.
AC P3183; P3184; P33542;
DT 01-OCT-1993 (Rel. 27, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nigra-B precursor (Agglutinin V) (SNV) [Contains: Nigra b A chain (rRNA N-glycosidase) (EC 3.2.2.22); Nigra b B chain].
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Stereophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Eudicotyledons; core eudicots;


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Best Local Similarity: 91.8%, Pred. No. 8-9e-107, Indels 2, Gaps 1;
Matches 235; Conservative 0; Mismatches 15;

QY 1 YERLELVHTGTXEYFRFTLLADYVSSGFSNFIPLRGSTIPVSDAPFVLELVN 60
DB 1 YERLELVHTGTXEYFRFTLLADYVSSGFSNFIPLRGSTIPVSDAPFVLELVN 60
QY 61 QGSDXTDALIDVNNXYVAVQADQSYFLRDAFPGAEFTLFTGTRDSSLPFGXSYXD 120
DB 61 QGSDXTDALIDVNNXYVAVQADQSYFLRDAFPGAEFTLFTGTRDSSLPFGXSYXD 120
QY 121 ERYAGHRDQIPFGHDLQSVTALFPGSGSTRQASITLITOMISARRNPIIMKXQ 180
DB 121 ERYAGHRDQIPFGHDLQSVTALFPGSGSTRQASITLITOMISARRNPIIMKXQ 180
QY 119 ERYAGHRDQIPFGHDLQSVTALFPGSGSTRQASITLITOMISARRNPIIMKXQ 178
DB 119 ERYAGHRDQIPFGHDLQSVTALFPGSGSTRQASITLITOMISARRNPIIMKXQ 178
QY 181 XINSKASFLPDXVMELESTWQSGSTGVNPNPKLAIKXGNFVTLXVAVYIA 240
DB 181 XINSKASFLPDXVMELESTWQSGSTGVNPNPKLAIKXGNFVTLXVAVYIA 240
QY 179 YINSKASFLPDXVMELESTWQSGSTGVNPNPKLAIKXGNFVTLXVAVYIA 238
DB 179 YINSKASFLPDXVMELESTWQSGSTGVNPNPKLAIKXGNFVTLXVAVYIA 238
QY 241 SLALMTVCGERSSS 256
DB 241 SLALMTVCGERSSS 256
QY 239 SLALMTVCGERSSS 254
DB 239 SLALMTVCGERSSS 254

RESULT 5
ABRC ABRR STANDARD; PRT; 562 AA.
ID ABRC ABRR STANDARD; PRT; 562 AA.
AC P28590;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ABRC precursor (Contains: Abrcin-A chain (tRNA N-glycosidase))
DS ABRC 3.2.22; Abrcin-C B chain)
OS ABRC precursor (Contains: Abrcin-C B chain)
OC Pektinase (EC 3.2.22); Abrcin-C B chain; euglycote; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; core eudicots; Rosidae; eucroids I; Fabales; Fabaceae; Papilionales; Abrcin; Abrcin; NCBI_TaxID=3816;
RX NCBI_TaxID=3816;
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=9126697; PubMed=2050149;
RA MOD K.A., Lord J.M., Wawrzynczak E.J., Platak M.;
RT Preparation: genomic cloning, characterization and the expression of
RT the Abrcin B chain in Escherichia coli.
EL Eur J Biochem 187:329-33 (1999)
CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR IMPARTING PROTEIN
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OR 28 S RNA. THE
CC B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
CC BINDING OF ABRIN TO THE CELL MEMBRANES THAT PERCEIVES ENDOTOXIN.
CC -1- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF TWO DOMAINS, EACH DOMAIN
CC CONTAINS THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC CONTAINS A HOMOLOGOUS SUBDOMAIN (ALPHA, BETA, GAMMA).
CC -1- SIMILARITY: IN THE CATALYTIC SECTION, BELONGS TO THE RIBOSOME-
CC INACTIVATING PROTEIN FAMILY.
CC -1- SIMILARITY: Contains 2 ricin B-type lectin domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL, outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (see http://www.isdb-sib.ch/announce/
CC or send an email to license@isdb-sib.ch).
DR EMBL: X55667; CA39202.1; -
DR PIR: S16022; S16022.
DR HSSP: P1140; 1ABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RLP.

Query Match 43.3%; Score 1139; DB 1; Length 562;
Best Local Similarity: 46.0%; Pred. No. 1.1e-103;
Matches 242; Conservative 82; Mismatches 190; Indels 12; Gaps 9;

QY 9 TQGTGTXEYFRFTLLADYVSSGFSNFIPLRGSTIPVSDAPFVLELVNQGSDXTA 68
DB 9 TQGTGTXEYFRFTLLADYVSSGFSNFIPLRGSTIPVSDAPFVLELVNQGSDXTA 68
QY 43 TQGTGTXEYFRFTLLADYVSSGFSNFIPLRGSTIPVSDAPFVLELVNQGSDXTA 100
DB 43 TQGTGTXEYFRFTLLADYVSSGFSNFIPLRGSTIPVSDAPFVLELVNQGSDXTA 100
QY 69 AIDVTVXVAVQADQSYFLRDAFPGAEFTLFTGTRDSSLPFGXSYXDERYAGH-R 127
DB 69 AIDVTVXVAVQADQSYFLRDAFPGAEFTLFTGTRDSSLPFGXSYXDERYAGH-R 127
QY 101 GIDVTVXVAVQADQSYFLRDAFPGAEFTLFTGTRDSSLPFGXSYXDERYAGH-R 158
DB 101 GIDVTVXVAVQADQSYFLRDAFPGAEFTLFTGTRDSSLPFGXSYXDERYAGH-R 158
QY 128 DQIPDQIPFGHDLQSVTALFPGSGSTRQASITLITOMISARRNPIIMKXQINSK 187
DB 128 DQIPDQIPFGHDLQSVTALFPGSGSTRQASITLITOMISARRNPIIMKXQINSK 187
QY 159 ERYAGHRDQIPFGHDLQSVTALFPGSGSTRQASITLITOMISARRNPIIMKXQ 218
DB 159 ERYAGHRDQIPFGHDLQSVTALFPGSGSTRQASITLITOMISARRNPIIMKXQ 218
QY 219 ERYAGHRDQIPFGHDLQSVTALFPGSGSTRQASITLITOMISARRNPIIMKXQ 276
DB 219 ERYAGHRDQIPFGHDLQSVTALFPGSGSTRQASITLITOMISARRNPIIMKXQ 276
QY 247 FPGSGSTRQASITLITOMISARRNPIIMKXQINSK 305
DB 247 FPGSGSTRQASITLITOMISARRNPIIMKXQINSK 305
QY 279 FPGSGSTRQASITLITOMISARRNPIIMKXQINSK 334
DB 279 FPGSGSTRQASITLITOMISARRNPIIMKXQINSK 334
QY 306 QWESKNSNPNQMTIKEDTIRNSGCTTGYTGYVYIIPDQNTAVRBAITWQIX 365
DB 306 QWESKNSNPNQMTIKEDTIRNSGCTTGYTGYVYIIPDQNTAVRBAITWQIX 365
QY 335 IAKCKDLSENGKTLKSDKTKNSGCTTGYTGYVYIIPDQNTAVRBAITWQIX 394
DB 335 IAKCKDLSENGKTLKSDKTKNSGCTTGYTGYVYIIPDQNTAVRBAITWQIX 394
QY 366 NGTINPNSALVLAASGKTKTGYTGYVYIIPDQNTAVRBAITWQIX 425
DB 366 NGTINPNSALVLAASGKTKTGYTGYVYIIPDQNTAVRBAITWQIX 425
QY 395 NGTINPNSALVLAASGKTKTGYTGYVYIIPDQNTAVRBAITWQIX 454
DB 395 NGTINPNSALVLAASGKTKTGYTGYVYIIPDQNTAVRBAITWQIX 454
QY 426 KXGVSIVVTVKXSGQXVAVQADQSYFLRDAFPGAEFTLFTGTRDSSLPFGXSYXD 485
DB 426 KXGVSIVVTVKXSGQXVAVQADQSYFLRDAFPGAEFTLFTGTRDSSLPFGXSYXD 485
QY 455 QGSDXTDALIDVNNXYVAVQADQSYFLRDAFPGAEFTLFTGTRDSSLPFGXSYXD 513
DB 455 QGSDXTDALIDVNNXYVAVQADQSYFLRDAFPGAEFTLFTGTRDSSLPFGXSYXD 513
QY 486 QWESKNSNPNQMTIKEDTIRNSGCTTGYTGYVYIIPDQNTAVRBAITWQIX 531
DB 486 QWESKNSNPNQMTIKEDTIRNSGCTTGYTGYVYIIPDQNTAVRBAITWQIX 531
QY 514 QWESKNSNPNQMTIKEDTIRNSGCTTGYTGYVYIIPDQNTAVRBAITWQIX 559
DB 514 QWESKNSNPNQMTIKEDTIRNSGCTTGYTGYVYIIPDQNTAVRBAITWQIX 559

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	Query Match	45.3%;	Score 1190;	DB 1;	Length 528;
	Best Local Similarity	46.3%;	Pred. No. 86-109;		
	Matches 248;	Conservative	79;	Mismatches 177;	Indels 32;
				Gaps 10;	
Qy	9	PHDTGKRFPTLLRDYSSGSFNSRLPIRLQSTFVPSDAQRFVETLMDGSDXKA	68		
Dh	9	TEGATSSXKQIETALREHL-RGQ.IHD.PVLAPPT-FLGERKKIVLSELMSQSTSEV	66		
Qy	69	AIDVNNVYVAAGQAGQSPFLAPARAGAEHLFGTRBTRSSSLPQSGYDLEAYGH-R	127		
Dh	67	GIDVNNVYVAAPRGQSTFLHAPSSASDYLFLFGH-DQHSILPYGQYDLEAHQSR	124		
Qy	128	DOIRGICXILQSYXALRPGSTGQASLITLQMSLEAPFLPMLRHKQINSKX	167		
Dh	125	QQLPFGQLNRHSFSPSGQDMREKRLIVLIGVADHAFVLSNRVHSILQTH	164		
Qy	168	FLDPDYXMLEFSGSGQSGVQSGYDVFENRFXELAIXXGNPTLTXNVR-----	237		
Dh	165	PGDANMLSENNRMLSPGVQSYVQVTFPND-----VLTNLRNEPVVDSLH	234		
Qy	238	VTLALMLPFCRSPSSRWVFLYLRVADDTGCSL-EPVAVLQKXKQYDR	295		
Dh	235	PVALVLMPLFCPP-PPNNGS-----PLIRGLVEKSKCSNRVETLRIGDQACVDY	290		
Qy	296	DDPFDNDQIQAPSSSNNDNDQLTIRKPTLISNSGSLTYGTATGVYVIFDQNAV	355		
Dh	291	DNYHNGNRLIMMKCDRLRENDQLTKSPKISNSKRLTYGVAGDSVVAIDGTSNV	350		
Qy	356	RELTNQDQKQNTINPNSLTLAASGICKCTLTQTLDTLQGMALNAPLAPSVTI	415		
Dh	351	APATYWEIDQNTILNPFSALVLSAESSSGVGLTVQNMELMRGQRQNTISPPVSI	410		
Qy	416	YGRRLCMESNGSVWVETCKSSQDQXKXALYDSSLRPQKQDQCLTQGDSSVTYN	475		

Query Match	44.4%	Score 1165	DB 1	Length 254
411	SVSYDD	CMQAGQNSVMMADCDNSKKEQ	GMALYTDDGSRVQCTNRNCLGSRHCKSGSTLL	469
476	IVSYCSXXSXQXRMFVMEAL	LLILXXXXXXXXXVDVAAQPLKRIITPAGKQNNML	531	
470	LMGSCWMAQSRWFVKNQSDYSYSL	LYDDMMVDKSPDLSKQIILMPEYKQDNL	525	
DB				
411	SVSYDD	CMQAGQNSVMMADCDNSKKEQ	GMALYTDDGSRVQCTNRNCLGSRHCKSGSTLL	469
476	IVSYCSXXSXQXRMFVMEAL	LLILXXXXXXXXXVDVAAQPLKRIITPAGKQNNML	531	
470	LMGSCWMAQSRWFVKNQSDYSYSL	LYDDMMVDKSPDLSKQIILMPEYKQDNL	525	
RESULT 4				
MLA_VISUAL				
ID	MLA_VISUAL	STANDARD:	FT:	254 AA.
AC	P81446:			
DT	15-DEC-1998	(Rel. 37, Created)		
DT	15-DEC-1998	(Rel. 37, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Human glyceraldehyde 3-phosphate dehydrogenase (NAD+ specific) isoform 1 A chain (HGD)			
DE	Human glyceraldehyde 3-phosphate dehydrogenase (NAD+ specific) isoform 1 A chain (HGD)			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Vascularia; Viscum			
OC	Spermatophytes; Magnoliopsida; eudicotyledons; core eudicots; Viscum			
OX	NCBI_TaxID=3972;			
RS	Sequence			
RA	SRRLAN-Subsp. album;			
RA	MDLINE=97134581; PubMed=8960141;			
RA	Soler M.H., Stoeva S., Schwamborn C., Milheln S., Stiefel T., Voelter W.;			
RT	"Complete amino acid sequence of the A chain of mistletoe lectin I."			
RL	FEBS Lett. 399:153-157(1996).			
CC	-1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS BY REMOVING ADENINE FROM POSITION 4,24 OF 28 S RNA. THE B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY INTO THE CELL. OF THE A CHAIN, B CHAINS ARE ALSO RESPONSIBLE FOR CELL AGGLUTINATION (LECTIN ACTIVITY).			
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one specific adenosine on the 28S rRNA.			
CC	-1- SUBSTRATE: 28S rRNA and B chain.			
CC	-1- PHARMACOKINETIC: Due to its immunomodulatory effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid tumors.			
CC	-1- MISCELLANEOUS: TWO ISOPRFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA AND NON-GLYCOSYLATED FORM MLA.			
CC	-1- SIMILARITY: RELATED TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.			
DR	PIR: P0016; P00016.			
DR	HSSP: P0016; IABR.			
DR	InterPro: IPR001574; RIP.			
DR	Pfam: PF00161; RIF.			
DR	PRINTS: PR00396; SHIGARCTN.			
DR	PROSITE: PS00725; SHIGARCTN; FALSE_NEG.			
FM	Kabat database: Hydroxylase; Toxin; Repeat; Glycoprotein; Lectin.			
FM	Kabat database: Hydroxylase; Toxin; Repeat; Glycoprotein; Lectin.			
FT	CARBOHYD	112	112	
FT	VARIANT	15	15	
FT	VARIANT	66	66	
FT	VARIANT	112	112	
FT	VARIANT	116	116	
FT	VARIANT	133	134	
FT	VARIANT	140	140	
FT	VARIANT	140	140	
FT	VARIANT	151	151	
FT	VARIANT	179	179	
FT	VARIANT	184	184	
FT	VARIANT	190	190	
FT	VARIANT	218	218	
FT	VARIANT	223	224	
FT	VARIANT	234	234	
FT	VARIANT	234	234	
FT	VARIANT	254	254	
SEQUENCE	254 AA:	28478 MW;	538AF98DDE0FE67	CR664;

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us-09-601-667c-40.rtf

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CC		entry into the cell of the A chain; B chains are also responsible
CC		for cell aggregation (lectin activity). It binds to beta-D-
CC		galactose.
CC	-	SIMILARITY: Activity: Endoanalysis of the N-glycosidic bond at one
CC	-	specific asides on the 28S rRNA.
CC	-	DOMAIN: The b chain is composed of two domains, each domain
CC	-	consists of 3 homologous subdomains (alpha, beta, gamma).
CC	-	FM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE
CC	-	B-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
CC	-	FUNCTIONAL PROTEIN IN RIBONUCLEOPROTEIN COMPLEXES TO THE RIBOSOME-
CC	-	ANCHORING PROTEIN IN RIBONUCLEOPROTEIN COMPLEXES.
CC	-	SIMILARITY: Contains 2 rich b-type lectin domains.
CC	-	CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
CC	-	WITH THE SEQUENCE TRANSLATED FROM DATA (REF.1, REF.2 AND REF.3).
CC	-	DATABASE: NAME-Protein Spotlights;
CC	-	NOTA-tissue 31 of February 2003;
CC	-	WWW=http://www.expasy.org/spotlights/articles/spcl021.html".
CC	-	-----
CC	-	THE SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	-	entities requires a license agreement (See http://www.isdb.ch/aboutnse/
CC	-	or send an email to license@isdb.ch).
DR	EMBL:	X03119; CAZ62639.1; -
DR	EMBL:	X52908; CAZ67095.1; -
DR	EMBL:	X02389; CAZ6230.1; -
DR	EMBL:	A18892; CAA01058.1; -
DR	PIR:	A24041; ECSD.
DR	PDB:	2AKI; 31-JAN-94.
DR	PDB:	1PMP; 31-OCT-93.
DR	PDB:	1IFG; 14-JAN-98.
DR	PDB:	1IEF; 14-JAN-98.
DR	PDB:	1IFU; 14-JAN-98.
DR	PDB:	1RTG; 31-OCT-93.
DR	PDB:	1OHS; 16-JUN-97.
DR	PDB:	1OEF; 16-JUN-97.
DR	PDB:	1BEG; 02-FEB-98.
DR	PDB:	1BEG; 02-FEB-98.
DR	PDB:	11L3; 16-JAN-02.
DR	PDB:	11L4; 16-JAN-02.
DR	PDB:	11L9; 16-JAN-02.
DR	GlycoStitchDB:	p02879; -
DR	InterPro:	IPR001072; Ricin_B_lectin.
DR	InterPro:	IPR001574; RB.
DR	Fam:	PF00652; Ricin_B_lectin. 6.
DR	Fam:	PF00652; Ricin_B_lectin. 6.
DR	PRINTS:	PR00396; SHICARICIN.
DR	SMART:	SM00281; RICIN. 2.
DR	PROSITE:	PS00281; RICIN_B_LECTIN; 2.
KW	PROSITE:	PS00281; SHIGA_RICIN; 1.
KW	Plant defense; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;	
KM	Glycoprotein; Lectin; Signal; 3D-structure.	
FT	SIGNAL	1..35
FT	PEPTIDE	303..314
FT	CHAIN	315..576
FT	DOMAIN	321..448
FT	DOMAIN	451..575
FT	REPEAT	331..372
FT	REPEAT	374..414
FT	RSEST	417..445
FT	RSEST	417..445
FT	REPEAT	502..540
FT	REPEAT	543..570
FT	ACT SITE	212..212
FT	DISTPID	294..318
FT	DISTPID	334..353
	INTERCHAIN.	

[illegible]

RA Funatsu G., Kimura M., Funatsu M.,
 RA "Primary structure of Ala chain of ricin D.";
 RL Agric. Biol. Chem. 43:1221-1224(1979).
 RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.
 RX MEDLIN=90344223; PubMed=1368317.
 RX Kimura Y., Kusano H., Tada M., Takagi S., Funatsu G.,
 RT "Structural analyses of sugar chains of
 RT Agric. Biol. Chem. 54:157-162(1990).
 RN [7].
 RN MEDLINE=21480123; PubMed=1359634;
 RL Kunitake M., Kozlov O.V.,
 RL "Ricin", Kozlov O.V.,
 RL Toxicon 39:1723-1728(2001).
 RL [8].
 RX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=87155993; PubMed=5583917.
 RX Morcillo P., Villalencra J.E., Konzinger A.F., Ernst S.R., Katzin B.,
 RX Rutenber E., Moxey A.H., Hattin R., Roberts
 J Biol. Chem. 262:5396-5403(1987).
 RN [9].
 RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RX MEDLINE=91352004; PubMed=1891881;
 RX Katzin B.J., Collins E.C., Roberts J.D.,
 RX "Structure of ricin A-chain at 2.5 A.",
 RX Proteins 10:351-359(1991).
 RL [10].
 RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
 RX MEDLINE=91352005; PubMed=1891892;
 RX Rutenber E., Roberts J.D.,
 RT "Structure of ricin B-chain at 2.5-A resolution.",
 RT Proteins 10:360-369(1991).
 RL [11].
 RX X-RAY CRYSTALLOGRAPHY (3.8 ANGSTROMS) OF A-CHAIN.
 RX MEDLINE=91587000; PubMed=5903320.
 RX Weston S.A., Tucker A.D., Tatchell D.R., Debyatne D.J.,
 RA Paupit R.A.,
 RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.",
 RT J. Mol. Biol. 244:410-422(1994).
 RL [12].
 RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
 RX MEDLINE=96314222; PubMed=860513.
 RX Molins-Sydn M.C., Roberts J.D.,
 RT "Structure and activity of an active site substitution of ricin A
 RT chain".
 RL Biochemistry 35:11098-11103(1996).
 RL [13].
 RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RX MEDLINE=90117820; PubMed=1867850.
 RX Roberts J.D., Sydn M.C., Day P., Monzinger A.F., Pascel J.M.,
 RA "Structure-based identification of a ricin inhibitor",
 RT J. Mol. Biol. 266:1043-1049(1997).
 RL [14].
 RX MUTAGENESIS.
 RX MEDLINE=93165633; PubMed=1287657.
 RX Kim T., Roberts J.D.,
 RT "The active site residues of ricin A chain by
 RT mutagenesis and X-ray crystallography.",
 RT Protein Eng. 5:775-779(1992).
 RL [15].
 RX -1- FUNCTION: Ricin is highly toxic to animal cells and to a less
 RX extent to plant cells. The A chain is responsible for inhibiting
 RX protein synthesis through the catalytic inactivation of 60S
 RX ribosomal subunits. It acts as a glycosylase that removes a
 RX specific adenine residue from an exposed loop of ribosomal
 RX RNA. The modified ribosomes are unable to support protein
 RX synthesis. The A chain can inactivate a few thousand ribosomes
 RX per minute, thus inactivating them faster than the cell can make
 RX new ones. A single A-chain molecule can therefore kill an animal
 RX cell.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 9.17665 Seconds

Title: US-09-601-667C-40 (without alignments/sec
2736.539 Million cell updates/sec

Sequence: 1 YENKLVNTHQITKXETFR.....RRIITPATKPNQMWLPVX 534

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 127663 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127663

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1290	49.1	264	1 MIA_VISAL	Protein
2	1229.5	46.8	576	1 RICI_RICCO	Protein
3	1190	45.3	528	1 ABRP_ABRPP	Protein
4	1165	44.4	254	1 MIA_VISAL	Protein
5	1138	43.3	562	1 ABRP_ABRPP	Protein
6	1112.5	42.4	557	1 ABRP_ABRPP	Protein
7	1101	41.9	564	1 ABRP_ABRPP	Protein
8	1091	41.2	563	1 ABRP_ABRPP	Protein
9	1081	40.5	563	1 ABRP_ABRPP	Protein
10	1071	40.0	563	1 ABRP_ABRPP	Protein
11	1061	39.5	563	1 ABRP_ABRPP	Protein
12	1051	39.0	563	1 ABRP_ABRPP	Protein
13	1041	38.5	563	1 ABRP_ABRPP	Protein
14	1031	38.0	563	1 ABRP_ABRPP	Protein
15	1021	37.5	563	1 ABRP_ABRPP	Protein
16	1011	37.0	563	1 ABRP_ABRPP	Protein
17	1001	36.5	563	1 ABRP_ABRPP	Protein
18	991	36.0	563	1 ABRP_ABRPP	Protein
19	981	35.5	563	1 ABRP_ABRPP	Protein
20	971	35.0	563	1 ABRP_ABRPP	Protein
21	961	34.5	563	1 ABRP_ABRPP	Protein
22	951	34.0	563	1 ABRP_ABRPP	Protein
23	941	33.5	563	1 ABRP_ABRPP	Protein
24	931	33.0	563	1 ABRP_ABRPP	Protein
25	921	32.5	563	1 ABRP_ABRPP	Protein
26	911	32.0	563	1 ABRP_ABRPP	Protein
27	901	31.5	563	1 ABRP_ABRPP	Protein
28	891	31.0	563	1 ABRP_ABRPP	Protein
29	881	30.5	563	1 ABRP_ABRPP	Protein
30	871	30.0	563	1 ABRP_ABRPP	Protein
31	861	29.5	563	1 ABRP_ABRPP	Protein
32	851	29.0	563	1 ABRP_ABRPP	Protein
33	841	28.5	563	1 ABRP_ABRPP	Protein

ALIGNMENTS

RESULT	Query	Match	Length	DB ID	Description
1	US-09-601-667C-40	49.1	264	1 MIA_VISAL	Protein
2	US-09-601-667C-40	46.8	576	1 RICI_RICCO	Protein
3	US-09-601-667C-40	45.3	528	1 ABRP_ABRPP	Protein
4	US-09-601-667C-40	44.4	254	1 MIA_VISAL	Protein
5	US-09-601-667C-40	43.3	562	1 ABRP_ABRPP	Protein
6	US-09-601-667C-40	42.4	557	1 ABRP_ABRPP	Protein
7	US-09-601-667C-40	41.9	564	1 ABRP_ABRPP	Protein
8	US-09-601-667C-40	41.2	563	1 ABRP_ABRPP	Protein
9	US-09-601-667C-40	40.5	563	1 ABRP_ABRPP	Protein
10	US-09-601-667C-40	40.0	563	1 ABRP_ABRPP	Protein
11	US-09-601-667C-40	39.5	563	1 ABRP_ABRPP	Protein
12	US-09-601-667C-40	39.0	563	1 ABRP_ABRPP	Protein
13	US-09-601-667C-40	38.5	563	1 ABRP_ABRPP	Protein
14	US-09-601-667C-40	38.0	563	1 ABRP_ABRPP	Protein
15	US-09-601-667C-40	37.5	563	1 ABRP_ABRPP	Protein
16	US-09-601-667C-40	37.0	563	1 ABRP_ABRPP	Protein
17	US-09-601-667C-40	36.5	563	1 ABRP_ABRPP	Protein
18	US-09-601-667C-40	36.0	563	1 ABRP_ABRPP	Protein
19	US-09-601-667C-40	35.5	563	1 ABRP_ABRPP	Protein
20	US-09-601-667C-40	35.0	563	1 ABRP_ABRPP	Protein
21	US-09-601-667C-40	34.5	563	1 ABRP_ABRPP	Protein
22	US-09-601-667C-40	34.0	563	1 ABRP_ABRPP	Protein
23	US-09-601-667C-40	33.5	563	1 ABRP_ABRPP	Protein
24	US-09-601-667C-40	33.0	563	1 ABRP_ABRPP	Protein
25	US-09-601-667C-40	32.5	563	1 ABRP_ABRPP	Protein
26	US-09-601-667C-40	32.0	563	1 ABRP_ABRPP	Protein
27	US-09-601-667C-40	31.5	563	1 ABRP_ABRPP	Protein
28	US-09-601-667C-40	31.0	563	1 ABRP_ABRPP	Protein
29	US-09-601-667C-40	30.5	563	1 ABRP_ABRPP	Protein
30	US-09-601-667C-40	30.0	563	1 ABRP_ABRPP	Protein
31	US-09-601-667C-40	29.5	563	1 ABRP_ABRPP	Protein
32	US-09-601-667C-40	29.0	563	1 ABRP_ABRPP	Protein
33	US-09-601-667C-40	28.5	563	1 ABRP_ABRPP	Protein

A/Reference number: A36274; PMID:90256790; PMID:2341400
 A/Molecule type: DNA
 A/Residues: 1-233; 'T', '235-246', 'M', '248-289' <CHO>
 A/Cross-references: GB:J05434; MID:9170534; PIND:AAA34206.1; PID:9170533
 R:Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
 A/Title: Site 24, 42-51, 1994
 A/Abstract: The complete sequence of the gene encoding trichosanthin.
 A/Reference number: J01093; PMID:94271611; PMID:8003348
 A/Accession: J01093
 A/Molecule type: DNA
 A/Residues: 1-72; 'V', '74-90', 'S', '92-233', 'T', '235-267', 'D', '269-289' <ZHE>
 A/Cross-references: GB:S70176; MID:9547148; PIND:AB31048.1; PID:9547149
 R:Collins, E.J.; Robertus, J.D.; Lopresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwar
 J. Biol. Chem. 265, 8665-8669, 1990
 A/Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abor
 A/Reference number: A36273; PMID:90256789; PMID:2341399
 A/Accession: A36273
 A/Molecule type: protein
 A/Residues: 1-247 <TOY>
 R:Wang, Y.; Zhao, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
 Pure Appl. Chem. 58, 789-798, 1986
 A/Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application
 A/Reference number: J00003
 A/Accession: J00003
 A/Molecule type: protein
 A/Residues: 24-56; 'L', '58-59', 'I', '61-71', 'I', '73-81', '85-86', 'L', '88-92', 'DAGLEPRNVL', '93-142', 'GV'
 A/Experimental source: tuber
 R:Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
 Submitted to the Brookhaven Protein Data Bank, July 1994
 A/Reference number: A67092; PDB:1MRX
 R:Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
 Submitted to the Brookhaven Protein Data Bank, July 1994
 A/Reference number: A67092; PDB:1MRX
 A/Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24
 R:Xiong, J.P.; Xia, Z.X.; Wang, Y.
 Submitted to the Brookhaven Protein Data Bank, December 1994
 A/Reference number: A67111; PDB:1TCS
 A/Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27
 R:Xiong, J.P.; Xia, Z.X.; Wang, Y.
 Nat. Struct. Biol. 1, 695-700, 1994
 A/Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re
 A/Reference number: A67112; PDB:1TCS
 A/Contents: annotation; X-ray crystallography, 1.7 angstroms
 A/Comment: Alpha-trichosanthin has been used to induce abortions.
 A/Genetics:
 A:Gene: tcs
 C:Function:
 A:Description: Hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA ther
 C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 C/Keywords: abortifacient; glycosidase; hydrolase; root; toxin
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-27/Domain: trichosanthin alpha #status experimental <NMR>
 F:27-266/Domain: rRNA N-glycosidase homology
 F:271-289/Domain: carboxy-terminal homology #status predicted <CTP>
 F:93,183,186/Active site: Tyr, Glu, Arg #status predicted

Query Match 11.5%; Score 301; DB 1; Length 289;
 Best Local Similarity 34.6%; Pred. No. 2,4e-21;
 Matches 83; Conservative 50; Mismatches 93; Indels 14; Gaps 9;

DB 13 TXKXFFITLLRDYVSSGSFNSNEILRQSTIPVSDQRFVLEITNQGXSXTAIDV 72
 DB 33 TSSSTGVFISNRKALPERKCDIPLRL-STLPGS-QRYALHLINVADETIVADIV 89
 QY 73 TXKXVYVQAGOSYETADA-PRGAFTHLTGTTTRDSSLEPGSXYLERNVAG-NDQI 130
 DB 90 TNYIMGRADGTSYFNEASATEAKYVFDAMF-KVTLPSGNVRLQIAAGKIKEMI 148
 QY 131 PLGIXOLIOSVVALRXPGGSTRKQARSLILQIMISEARFNPILMRKXINSXSFLP 190
 DB 149 PLGLPALDSAITTLFTYNNNS--ASALMWLIQSTSEARVYKFIQOIGKRVDK--TFLP 204

QY 191 DXYMELEPTSMQOOSTVOV--HSTQGVNPKRLAIXGNFTLXNVX--VIASLAINL 246
 DB 205 SLATISLNSWALSRSKQIQAISTNQCETFPVVLNNQKQSVITTVADAGVTSINALL 264
 BESTIT 15
 J00393 - Mongolian snake-gourd
 C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
 A/Accession: J00393; P0163
 R:Toyokawa, S.; Takeda, T.; Kato, Y.; Nakabayashi, K.; Ogihara, Y.
 Chem. Pharm. Bull. 39, 1244-1249, 1991
 A/Title: The complete amino acid sequence of an abortifacient protein, karasurin.
 A/Reference number: J00393; PMID:92005921; PMID:1914000
 A/Accession: J00393
 A/Molecule type: protein
 A/Residues: 1-247 <TOY>
 A/Note: a sequence which lacks Ala-247 is also shown in this publication
 C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 C/Keywords: abortifacient; glycosidase; hydrolase; root; toxin
 F:1-23/Domain: signal sequence #status predicted <SIG>

Query Match 11.4%; Score 300; DB 2; Length 247;
 Best Local Similarity 35.4%; Pred. No. 2,4e-21;
 Matches 85; Conservative 46; Mismatches 95; Indels 14; Gaps 9;

QY 13 TXKXFFITLLRDYVSSGSFNSNEILRQSTIPVSDQRFVLEITNQGXSXTAIDV 72
 DB 10 TSSSTGVFISNRKALPERKCDIPLRL-STLPGS-QRYALHLINVADETIVADIV 66
 QY 73 TXKXVYVQAGOSYETADA-PRGAFTHLTGTTTRDSSLEPGSXYLERNVAG-NDQI 130
 DB 67 TNYIMGRADGTSYFNEASATEAKYVFDAMF-KVTLPSGNVRLQIAAGKIKEMI 125
 QY 131 PLGIXOLIOSVVALRXPGGSTRKQARSLILQIMISEARFNPILMRKXINSXSFLP 190
 DB 126 PLGLPALDSAITTLFTYNNNS--ASALMWLIQSTSEARVYKFIQOIGKRVDK--TFLP 181
 QY 191 DXYMELEPTSMQOOSTVOV--HSTQGVNPKRLAIXGNFTLXNVX--VIASLAINL 246
 DB 182 SLATISLNSWALSRSKQIQAISTNQCETFPVVLNNQKQSVITTVADAGVTSINALL 241
 Search completed: December 11, 2003, 13:55:47
 Job time: 16.5989 secs

A/Residues: 1-69, 'PS', 72-209, 'N', 211-241, 243-250, 'V', 252-263 <NA>
 A/Experimental source: seed
 C/Superfamily: ricin; rRNA N-glycosidase homology
 C/Keywords: duplication; glycoprotein; glycosidase; hydrolase
 F:1-263/Product: ricin B chain B #status experimental <CH>
 F:17-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40; residue repeats
 F:20-59, 63-80, 151-164, 190-207/Duplicate bonds: #status predicted
 F:59, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match

Best Local Similarity 59.2%; Pred. No. 4,58-72;
 Matches 154; Conservative 32; Mismatches 72; Indels 2; Gaps 2;

QY 275 CSASEPTVRIIVGRKXKXVYVADDDPHDQIQIIMPESKSNDDPVOIWTIKEDYTIIRNSQC 334
 DB 4 GNDPEPTVIVGRKXKXVYVADDDPHDQIQIIMPESKSNDDPVOIWTIKEDYTIIRNSQC 63
 QY 335 LTTGYTATVGRKXKXVYVADDDPHDQIQIIMPESKSNDDPVOIWTIKEDYTIIRNSQC 394
 DB 64 LTTGYTATVGRKXKXVYVADDDPHDQIQIIMPESKSNDDPVOIWTIKEDYTIIRNSQC 123
 QY 395 DYTLAGQWLAGNDTAREVITVGFEDICMESKXSVVETCSQXQXQXQXQXQXQXQXQXQXQX 454
 DB 124 IVASQGLPTNTPPTVITVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLVGLV 182
 QY 455 PKQNDQCTLRGRDSVSTVIVGSCXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 513
 DB 183 PKQNDQCTLRGRDSVSTVIVGSCXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 242
 QY 514 LKRIITVATGKX 573
 DB 243 LKRIITVATGKX 262

RESULT 12

C/Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
 C/Accession: C39761, S14471
 R/Svensen, G.; Mathiesen, A.; Sundan, A.
 J. Biol. Chem. 266, 6848-6852, 1991
 A/Title: Direct molecular cloning and expression of two distinct abrin A-chains.
 A/Reference number: A39761; PMID:91201329; PMID:2016300
 A/Accession: C39761, S14471
 A/Residues: 1-251 <ENV>
 A/Molecular type: RNA
 A/Keywords: abrin; ricin; rRNA N-glycosidase; hydrolase; toxin
 C/Keywords: duplication; glycosidase; hydrolase; toxin
 F:1-251/Product: abrin (clone 7.2) chain A #status predicted <CH>
 F:7-246/Duplicate bonds: rRNA N-glycosidase homology <RNS>
 F:74, 113, 195, 196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:164, 167/Active site: Glu, Arg #status predicted

Query Match 16.9%; Score 443; DB 2; Length 251;
 Best Local Similarity 43.6%; Pred. No. 3,16-35;
 Matches 106; Conservative 34; Mismatches 97; Indels 6; Gaps 5;

QY 9 TGGTGGKX 68
 DB 9 TGGTGGKX 66
 QY 63 AIDVTKXVYVAGQDQSYFADARQKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 127

DB 67 GIDVTNNVAVRAGQSYFADARQKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 124
 QY 128 DOIFGTGXKX 187
 DB 125 EQLSISQALTAISLISGASNDKARLITVILQMSKXKXKXKXKXKXKXKXKXKXKXKXKX 184
 QY 188 FLEEDYVLETSNGQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQST 246
 DB 189 FLEEDYVLETSNGQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQST 244
 QY 247 FVC 249
 DB 245 FVC 247

RESULT 13

C/Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
 C/Accession: J05032
 R/Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
 J. Biol. Chem. 266, 1485-1489, 1991
 A/Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and
 A/Reference number: J05032; PMID:9108848; PMID:8951169
 A/Accession: J05032
 A/Keywords: karasurin-B; karasurin-B; karasurin-B; karasurin-B; karasurin-B
 C/Keywords: karasurin-B; karasurin-B; karasurin-B; karasurin-B; karasurin-B
 F:1-243/Product: karasurin-B (clone 1.1) chain B #status predicted <CH>
 F:1-243/Duplicate bonds: rRNA N-glycosidase homology <RNS>

Query Match

Best Local Similarity 35.4%; Pred. No. 1,58-21;
 Matches 85; Conservative 46; Mismatches 95; Indels 14; Gaps 9;

QY 13 TGGTGGKX 72
 DB 10 TGGTGGKX 66
 QY 73 TGGTGGKX 130
 DB 67 TGGTGGKX 125
 QY 133 FLGKX 190
 DB 132 FLGKX 181
 QY 191 DVTWLETSNGQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQST 246
 DB 192 DVTWLETSNGQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQSTQYQST 241

RESULT 14

C/Date: 30-Sep-1998 #sequence_revision 26-Jan-1996 #text_change 23-Mar-2001
 C/Accession: J05066, A36274, G10993, A36273, J05003
 R/Schwartz, P.C.; Yung, M.H.; Zhu, R.H.; Ho, M.K.K.; Ng, T.B.; Yeung, H.W.
 Gene 97, 267-272, 1991
 A/Title: Cloning of trichosanthin cDNA and its expression in *Escherichia coli*.
 A/Reference number: J05066; PMID:19932971
 A/Accession: J05066, A36274, G10993, A36273, J05003
 A/Residues: 1-268 <CH>
 A/Keywords: trichosanthin; trichosanthin; trichosanthin; trichosanthin; trichosanthin
 C/Keywords: trichosanthin; trichosanthin; trichosanthin; trichosanthin; trichosanthin
 F:1-268/Product: trichosanthin (clone 1.1) chain B #status predicted <CH>
 F:1-268/Duplicate bonds: rRNA N-glycosidase homology <RNS>

QY 9 TGGTGGKX 68
 DB 9 TGGTGGKX 66
 QY 63 AIDVTKXVYVAGQDQSYFADARQKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 127

Oy	66	XTALADIVNNKYVVAQAGCGEYFLDARFAGATGTHLPGTGRDSRLSPFGXGYDLEERNA	121
Db	37	VSFNLTASDYEPEFLRALQGEVLTALNHADLPVLNPS-QVDSNMFVLPVLTIPMSQD	95
Oy	8	VTHQTKGE-YRRFTLTALVDESSSPFN-EFLRQSLTPVSGARQFVRLTQKXGS	65
Db	37	VSFNLTASDYEPEFLRALQGEVLTALNHADLPVLNPS-QVDSNMFVLPVLTIPMSQD	95

	Query Match	Best Local Similarity	Score	Seq. ID	Length
	33.44%	35.44%	851	21	570
	Matches	Conservative	79	Mismatches	220
				Indels	36
Qy	8	VTHTQTQKE-YRRITLLEDEYVSSSSSSN-EFLIKSGITIPYSDAQRPIYLVELINQAGDS	65		
Dy	37	VSNINLTADYTPRRLQALDEKYLSTHITAPDEVLAINES-QVSSNRKSTIPYIPINPSGDT	95		
Qy	66	XPLADYVKKVYVYVQAGQSGEYTLNDARCARLHPLGTGTRDSR.PKSGXYDLELYAG	122		
Dy	96	VTLALDYVNLVYVAFSSNKRKYPSSGTAVORDNLPVDTQEE-ELNTGNTSLERQV	155		
Qy	126	H-RDQITPLGIXDILQGVAALEK---PGSGTSPKQALSRILLNQTMSAARBNPLIMKRRQK	181		

154	FGVYVIFPGKSLDQAKISLSTVTTTADIDKFKLARGVLVIVQWSEARPRVETLRLTIS	218
Qy	182 INSGSFLPDPXYMLLETSMWQSTQVQHS-IDGVFNNNKXLAIXXGAFVTLANRVY--	238
Db	214 ITDASSETPLMLTSMNNKMSMSSEIQQAQDGI-FAGVGLDHERNNISLEVYNRELEF	272
Qy	239 IASLALMLVCGEGRPESS-----DVRWPLVIREPVAD--DVTCSASFPVIRVGRX	285
Db	214 LVTYVNLITGCAPIVPTSSISNNALDAQ-----ITKRFPRQGEYEVKQSVETRLISGMG	330
Qy	320 NAYEDPDDEHGMQCLAPKESKNDPMQLTISADTITNSNCSLTITGTAGYTMIF	342
Db	331 LCVDIRKGHYIDNPQALF--GNECHQALMFRFDITRLAKCL-----ITSSVWLI	383
Qy	350 DCKTVEEATIMQWANGIINPRNLTVALASGIGKTIITVQNTDLYTLGGKGLAGNDR	409
Db	384 DCKVPEEATIKKVVSLDGIITNHSGLVTLPAQABCFSLSTNNIHAQGWTVG-DYE	442
Qy	410 PREVTIYGRDLCWESNKS--VVTETCSQXQXQXKMLVGDGSI-RPKQNDQCLTXR	467
Db	443 PLATFIYGRKQKCLRENENNFVLEDCVNLNRPVQ--EMALYGDGSIIRFNSNRSLVTSB	507
Qy	468 DSVSTVINTVINSXKXQXQXRVETEXAIIINLKXXXXXVYVQANPLRLRIIYPATKPN	527
Db	502 HEPSLVLILKCS-GSGNQQRVFNNTGTSINPNKMLMDVQSDVSLKRIILIRYTGNNR	560
Qy	528 QMTL 531	
Db	561 QQHI 564	

C.Date: 31-Mar-1990 #seqno _sequence_ revision 31-Mar-1990 #text_change 20-Aug-1999
C.Accession: S06330 #JC5381
R./adin, B.I., Murray, E.E., Halling, A.C.; Halling, K.C.; Tlakaetene, N.; Le
Plant, M.O. Biol. 9, 287-295, 1987
A.Title: Characterization of a cDNA encoding ricin B, a hybrid ricin-Richins c
A.Reference number: S06330
A.Accession: S06330
A.Status: not compared with conceptual translation
A.Molecule type: mRNA
A.SeaDate: 1-263-LDND
A.Protein: 263-LDND.MW:6521, NID:G169714, RIDN:AA63306.1, PID:G169715
A.Protein: 7; P:Enzyme: 3.1.1.15
A.Biochem. Biophys. Acta 911, 191-200, 1987
A.Title: The cDNA sequence of the B-chain of ricin E isolated from
A.Reference number: JC5381; NID: 87210186; PMID:3801493
A.Accession: JC5381
A.Molecule type: Protein

F/200.253.361.401.402/Binding site: carbohydrate (Asp) (covariant) #status predicted
 F/247-269.286-305.329-346.417-430.456-473/Disulfide bonds: #status predicted
 F/288.312/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted
 F/500.521/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted

Query March 43.38; Score 1137; DB 2; Length 528;
 Best Local Similarity 46.08; Pred. No. 2.7e-102;

Matches 242; Conservative 83; Mismatches 189; Indels 12; Gaps 9;

9 THQTTKXEFRTFLMDYSSGSFENIPILKOSTIPYSDAQRFVLELTVQKXSTX 68
 9 TKGISQYKQFTEALNQL-TGALHDIIVLPPT-TVERKRYIVELNSRESIEV 66
 69 AIDVNTXVYVAQNDQSYFLDAPAGAEHLFTGTRNRSGLPKSGXYDLERYAGH-R 127
 67 GIDVNAVYVAFASQSYFLADPAPASVFLFPT-ORVSLRPSYGLDELMHQR 124
 128 DQPLATKQILOSVALRPGSGTRKONSILILICMISEAEPFLMKXQKINSXS 187
 125 KETGLQALHRIEPLSGANDERKATLIVIGNSBAKAYVLSNKGVSIRGIA 184
 188 FLDPXMLELSTMGQOSTQVQSTDPGVNPKRLAIXGNFTLXAN-RVYLSALML 246
 185 FQDPKMLSLNNMNLSCGVQSVQDFPNNVLLSIRQPVVSDLSHPTVYALML 244
 247 FVCGEPSSDVRWPLVIRPLADDTVCAS-BPTVRLVGRKXGVYADDPHDQNI 305
 245 FVCGP-PHAKQS--FLILRSIVSKICSGKRIETVLRGKNCQVDYDGHNGRI 300
 306 QLPFSKNDPQNLWKIKEDTIRNSGCLTGYTGYVYVFPDCTAPEATIQIWX 365
 301 IAWKCDLEENLWIKSDTIRSGKLTLEGAGVGMVYDCTSNVAALATWEIMD 360
 366 NGTITPNSMLVLAASGKIKITLVQTLTYTLQQMLAGNDAPRPVITVFPDQNES 425
 361 NGTITPNSMLVLAASGKIKITLVQTLTYTLQQMLAGNDAPRPVITVFPDQNES 420
 426 KNGSVVETKSSQKQXKMLVGDGSIIRKQNDQCLXGRQSVTYINIVSCSXKX 485
 421 QGSVVLADCNKKKQ-QMLVTDGSIRESVQNTNCLISDKRGQSPVILWAGSNWAS 479
 486 QGVFTNEKAILMLKXXXXXVDVQAPFLARLIIYPTKQNGMML 531
 480 QGVFTNDGSIRESVQNTNCLISDKRGQSPVILWAGSNWAS 525

RESULT 8

S32430
 abrin-b precursor - Indian licorice (fragment)

N/Contains: rRNA N-glycosidase (BC 3.2.2.22)

C/Species: Abrus precatorius (Indian licorice)

C/Date: 30-Sep-1993 #sequence revision 01-Aug-1997 #ext_change 20-Aug-1999

C/Accession: S32430, UCL399

R/Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.

J. Mol. Biol. 229, 263-267, 1993

Article: Primary structure of three distinct isoforms determined by cDNA sequencing.

N/Accession: S32431, S32429, M01D:91313798, F01D:842113

A/Molecule type: mRNA

A/Residues: 1-557 <HDS>

A/Cross-references: GB:M98345; NID:G166296; P1DN:AAA32625.1; PID:G166297

BioSci. Biotechnol. Biochem. 57, 166-169, 1993

Article: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic

A/Accession: UCL399

A/Residues: 260-281/D'281-290, N', 292-349, 'PQ', 352-377, N', 379-425, N', 427, 'D', 429-430

A/Experimental source: seed

C/Superfamily: ricin; rRNA N-glycosidase homology

C/Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F

F/1-250/Product: abrin-b chain A #status predicted <ACH>

F/7-245/Domain: rRNA N-glycosidase homology <RNG>

F/260-527/Product: abrin-b chain B #status experimental <RCH>
 F/282-324.325-365.368-406.413-448.452-491.494-527/Region: 40-residue repeats
 F/1/Modified site: pyroglutamate carboxylic acid (Glu) #status predicted
 F/74.113.194.195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F/110.360.400/Binding site: carbohydrate (Asp) (covariant) #status predicted
 F/163.166/Active site: Glu, Arg #status predicted
 F/246-269.286-304.328-345.416-439.455-472/Disulfide bonds: #status predicted
 F/287.311/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted
 F/499.520/Binding site: N-acetylglactosamine (Asp, Asn) #status predicted

Query March 42.48; Score 112.5; DB 2; Length 527;
 Best Local Similarity 45.44; Pred. No. 6.4e-100;

Matches 239; Conservative 83; Mismatches 191; Indels 13; Gaps 10;

9 THQTTKXEFRTFLMDYSSGSFENIPILKOSTIPYSDAQRFVLELTVQKXSTX 68
 9 TKGISQYKQFTEALNQL-TGALHDIIVLPPT-TVERKRYIVELNSRESIEV 66
 69 AIDVNTXVYVAQNDQSYFLDAPAGAEHLFTGTRNRSGLPKSGXYDLERYAGH-R 127
 67 GIDVNAVYVAFASQSYFLADPAPASVFLFPT-ORVSLRPSYGLDELMHQR 124
 128 DQPLATKQILOSVALRPGSGTRKONSILILICMISEAEPFLMKXQKINSXS 187
 125 KETGLQALHRIEPLSGANDERKATLIVIGNSBAKAYVLSNKGVSIRGIA 184
 188 FLDPXMLELSTMGQOSTQVQSTDPGVNPKRLAIXGNFTLXAN-RVYLSALML 246
 185 FQDPKMLSLNNMNLSCGVQSVQDFPNNVLLSIRQPVVSDLSHPTVYALML 244
 247 FVCGEPSSDVRWPLVIRPLADDTVCAS-BPTVRLVGRKXGVYADDPHDQNI 305
 245 FVCGP-PHAKQS--FLILRSIVSKICSGKRIETVLRGKNCQVDYDGHNGRI 300
 306 QLPFSKNDPQNLWKIKEDTIRNSGCLTGYTGYVYVFPDCTAPEATIQIWX 365
 301 IAWKCDLEENLWIKSDTIRSGKLTLEGAGVGMVYDCTSNVAALATWEIMD 360
 366 NGTITPNSMLVLAASGKIKITLVQTLTYTLQQMLAGNDAPRPVITVFPDQNES 425
 361 NGTITPNSMLVLAASGKIKITLVQTLTYTLQQMLAGNDAPRPVITVFPDQNES 420
 426 KNGSVVETKSSQKQXKMLVGDGSIIRKQNDQCLXGRQSVTYINIVSCSXKX 485
 421 QGSVVLADCNKKKQ-QMLVTDGSIRESVQNTNCLISDKRGQSPVILWAGSNWAS 479
 486 QGVFTNEKAILMLKXXXXXVDVQAPFLARLIIYPTKQNGMML 531
 480 QGVFTNDGSIRESVQNTNCLISDKRGQSPVILWAGSNWAS 524

RESULT 9

R1CSAG
 agglutinin precursor - castor bean

N/Contains: rRNA N-glycosidase (BC 3.2.2.22)

C/Species: Ricinus communis (castor bean)

C/Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #ext_change 16-Jul-1999

C/Accession: M24261, A24210

R/Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.

J. Mol. Biol. 229, 263-267, 1993

Article: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.

N/Accession: A24261, M01D:86059449, F01D:2999130

A/Molecule type: mRNA

A/Residues: 1-564 <RCH>

A/Cross-references: GB:M12089; NID:G169700; P1DN:AAA33869.1; PID:G169701

BioSci. Biotechnol. Biochem. 57, 166-169, 1993

Article: The complete amino acid sequences of the B-chains of the Ricinus communis agglutinin

A/Accession: A24210

A/Residues: 260-281/D'281-290, N', 292-349, 'PQ', 352-377, N', 379-425, N', 427, 'D', 429-430

A/Experimental source: seed

C/Superfamily: ricin; rRNA N-glycosidase homology

C/Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F

F/1-250/Product: abrin-b chain A #status predicted <ACH>

F/7-245/Domain: rRNA N-glycosidase homology <RNG>

PD0018
 mistletoe lectin I A chain - Viscum album (fragment)
 C/Species: Viscum album
 C/Accession: U01018
 C/Date: 19-Mar-1997 #sequence, revision 10-Jul-1998 #text, change 26-Aug-1999
 R/Author: S. J. Krugger, R. J. M. H. J. A. J. Stoeva, S. J. Betzel, C. J. Voelter, W. J. R. Biochem. Biophys. Res. Commun. 247: 362-372, 1998
 A/Title: Primary structure and molecular modelling of mistletoe lectin I from Viscum album
 A/Reference number: PD0018; MIM:380823; PMID:9642133
 A/Accession: PD0018
 A/Molecule type: protein
 A/Residues: 1-254 <ESC>
 C/Superfamily: ricin; RNA N-glycosidase homology
 F/7-246/Domain: RNA N-glycosidase homology <RNG>

Query Match 44.4%; Score 1165; DB 2; Length 254;
 Best Local Similarity 91.8%; Pred. No. 1,96-105;

Matches 235; Conservative 0; Mismatches 19; Indels 2; Gaps 1;

QY	1	YERILRATVHTGKEXYERFLLADYSSGSFSENEPLRQSTPRSNQSPFVETM	60
DB	1	YERILRATVHTGKEXYERFLLADYSSGSFSENEPLRQSTPRSNQSPFVETM	60
QY	61	QGNDSKTAIDVYKVVAAVQADQSYFLRDPGAEHLFTGTRDRSLPEFGSYDL	120
DB	61	QGNDSKTAIDVYKVVAAVQADQSYFLRDPGAEHLFTGTRDRSLPEFGSYDL	120
QY	121	ERYAGHDQIPGLIKOILQSYALKEKFGSTRKQASILLIQMTSARNPILMEXRQ	180
DB	121	ERYAGHDQIPGLIKOILQSYALKEKFGSTRKQASILLIQMTSARNPILMEXRQ	180
QY	181	ERYAGHDQIPGLIKOILQSYALKEKFGSTRKQASILLIQMTSARNPILMEXRQ	240
DB	181	ERYAGHDQIPGLIKOILQSYALKEKFGSTRKQASILLIQMTSARNPILMEXRQ	240
QY	241	SLAIMEFCGERPSS 256	256
DB	241	SLAIMEFCGERPSS 256	256

RESULT 6

S16022
 abrin-c precursor - Indian jicorice

N/Contains: RNA N-glycosidase (EC 3.2.2.22)

C/Species: Abrus precatorius (Indian jicorice)

C/Date: 19-Mar-1997 #sequence, revision 19-Mar-1997 #text, change 20-Aug-1999

R/Author: K.A. J. Lord, J.M. J. Nawzynek, E.C. J. Platak, M. J. Wood, J. Biochem. 198: 723-732, 1991

A/Title: Precursor: genomic cloning, characterization and the expression of the A-chain

A/Reference number: S16022; MIM:3126957; PMID:2050149

A/Accession: S16022

A/Molecule type: protein

A/Residues: 1-562 <MOO>

C/Superfamily: ricin; RNA N-glycosidase homology

F/7-246/Domain: RNA N-glycosidase homology <RNG>

F/3-283/Product: abrin-c chain A #status predicted <RCH>

F/3-283/Product: abrin-c chain A #status predicted <RCH>

F/3-283/Product: abrin-c chain A #status predicted <RCH>

F/3-283/Product: abrin-c chain A #status predicted <RCH>

F/3-283/Product: abrin-c chain A #status predicted <RCH>

F/3-283/Product: abrin-c chain A #status predicted <RCH>

F/3-283/Product: abrin-c chain A #status predicted <RCH>

F/3-283/Product: abrin-c chain A #status predicted <RCH>

F/3-283/Product: abrin-c chain A #status predicted <RCH>

F/3-283/Product: abrin-c chain A #status predicted <RCH>

Best Local Similarity 46.0%; Pred. No. 2,36-102;
 Matches 242; Conservative 82; Mismatches 190; Indels 12; Gaps 9;

QY	9	THQTKGKEXYERFLLADYSSGSFSENEPLRQSTPRSNQSPFVETM	60
DB	9	THQTKGKEXYERFLLADYSSGSFSENEPLRQSTPRSNQSPFVETM	60
QY	43	TGATGQSYKQFELMQLTGLLHIDIPVLDPTTWERNRYVALSNERSEIEY	100
DB	43	TGATGQSYKQFELMQLTGLLHIDIPVLDPTTWERNRYVALSNERSEIEY	100
QY	69	AIDVYKVVAAVQADQSYFLRDPGAEHLFTGTRDRSLPEFGSYDL	127
DB	69	AIDVYKVVAAVQADQSYFLRDPGAEHLFTGTRDRSLPEFGSYDL	127
QY	101	GLDTHAIVAYKASQSTFLMDASITLPLPGLQRIELRFDQSGULRKHQRT	158
DB	101	GLDTHAIVAYKASQSTFLMDASITLPLPGLQRIELRFDQSGULRKHQRT	158
QY	128	DOIPGLIKOILQSYALKEKFGSTRKQASILLIQMTSARNPILMEXRQ	187
DB	128	DOIPGLIKOILQSYALKEKFGSTRKQASILLIQMTSARNPILMEXRQ	187
QY	159	ERYAGHDQIPGLIKOILQSYALKEKFGSTRKQASILLIQMTSARNPILMEXRQ	218
DB	159	ERYAGHDQIPGLIKOILQSYALKEKFGSTRKQASILLIQMTSARNPILMEXRQ	218
QY	188	FPLPXYMLELSTWQSGQSYFLRDPGAEHLFTGTRDRSLPEFGSYDL	246
DB	188	FPLPXYMLELSTWQSGQSYFLRDPGAEHLFTGTRDRSLPEFGSYDL	246
QY	219	FQDPKPMALSTENNDISGQVQVDFPNNVILSINQFVYVDSLHPVAVLALM	278
DB	219	FQDPKPMALSTENNDISGQVQVDFPNNVILSINQFVYVDSLHPVAVLALM	278
QY	247	FCGERPSSSDVMPVLPVADVYKAS-EPTVAVKXKXVYVDDDFDQNOI	305
DB	247	FCGERPSSSDVMPVLPVADVYKAS-EPTVAVKXKXVYVDDDFDQNOI	305
QY	279	FVQNP-FHAKQS--PLLIRSVESKICSRKRYEYVAGDQCVYDQYHNGRI	334
DB	279	FVQNP-FHAKQS--PLLIRSVESKICSRKRYEYVAGDQCVYDQYHNGRI	334
QY	306	GLPSPSPNDPQMLTKEDTISNSGSLTYGQVYVDDDFDQNOI	365
DB	306	GLPSPSPNDPQMLTKEDTISNSGSLTYGQVYVDDDFDQNOI	365
QY	335	IMKCDLBNQVLTKEKTIISNGKCLTSGYAFQNVVILDCRAVLEATYMEID	394
DB	335	IMKCDLBNQVLTKEKTIISNGKCLTSGYAFQNVVILDCRAVLEATYMEID	394
QY	366	NOTIIPRSNIVLAASGKLTITVQTLVQCGMLANDTAPREYTYGPRDLCS	425
DB	366	NOTIIPRSNIVLAASGKLTITVQTLVQCGMLANDTAPREYTYGPRDLCS	425
QY	395	NOTIIPRSNIVLAASGKLTITVQTLVQCGMLANDTAPREYTYGPRDLCS	454
DB	395	NOTIIPRSNIVLAASGKLTITVQTLVQCGMLANDTAPREYTYGPRDLCS	454
QY	426	NXGVSIVETKSSQXKXVYVDDDFDQNOI	485
DB	426	NXGVSIVETKSSQXKXVYVDDDFDQNOI	485
QY	455	QSNVVLADCKNKKED-QALVYDQSGVYVDDDFDQNOI	513
DB	455	QSNVVLADCKNKKED-QALVYDQSGVYVDDDFDQNOI	513
QY	486	QPMVFNEXALINKKXKXVYVDDDFDQNOI	531
DB	486	QPMVFNEXALINKKXKXVYVDDDFDQNOI	531
QY	514	QPMVFNEXALINKKXKXVYVDDDFDQNOI	559
DB	514	QPMVFNEXALINKKXKXVYVDDDFDQNOI	559

RESULT 7

S32431
 abrin-d precursor - Indian jicorice (fragment)

N/Contains: RNA N-glycosidase (EC 3.2.2.22)

C/Species: Abrus precatorius (Indian jicorice)

C/Date: 19-Mar-1997 #sequence, revision 01-Aug-1997 #text, change 01-Aug-1997

R/Author: C.H. J. Lee, M.C. J. Lee, T.C. J. Lin, J.Y. J. Mol. Biol. 229: 263-267, 1993

A/Title: Primary structure of three distinct isoforms determined by cDNA sequencing

A/Reference number: S32431; MIM:3133798; PMID:842133

A/Accession: S32431

A/Molecule type: protein

A/Residues: 1-528 <HUN>

C/Superfamily: ricin; RNA N-glycosidase homology

F/7-246/Domain: RNA N-glycosidase homology <RNG>

F/3-283/Product: abrin-d chain A #status predicted <RCH>

F/3-283/Product: abrin-d chain A #status predicted <RCH>

F/3-283/Product: abrin-d chain A #status predicted <RCH>

F/3-283/Product: abrin-d chain A #status predicted <RCH>

F/3-283/Product: abrin-d chain A #status predicted <RCH>

F/3-283/Product: abrin-d chain A #status predicted <RCH>

F/3-283/Product: abrin-d chain A #status predicted <RCH>

F/3-283/Product: abrin-d chain A #status predicted <RCH>

F/3-283/Product: abrin-d chain A #status predicted <RCH>

F/3-283/Product: abrin-d chain A #status predicted <RCH>

Db 340 GEFHNNALIGLPGKSNIDNDQMLTKRNTIRSNKLTITVYSGPVYWIYDKTAT 399
 Qy 357 EATIQIWKXGIIINPRLVLAASSGIGKTTLTGTLDTLQOQMIAGNDTAREVTY 416
 Db 400 DATPQIWDNGIINPRLVLAASSGIGKTTLTGTLDTLQOQMIAGNDTAREVTY 459
 Qy 417 GFDLCWESKSGYVETCSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 476
 Db 460 GFDLCWESKSGYVETCSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 518
 Qy 477 VSCSXXSXQXVETCSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 533
 Db 519 LSCGASQGRWPFQNDGFIINYSGLVLDVAADPSLKKIITVPLHDPDQIWL 575

RESULT 4

PROTEIN

A:Name: A precursor - Indian licitins (fragment)
 A:Accession: S24133
 A:Residues: 262-297, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 <CHB>
 C:Species: Abrus precatorius (Indian licitins)
 C:Date: 31-Dec-1993 #sequence revision 01-Aug-1997 #next change 16-Jul-1999
 C:Accession: S32429, J02021, A39761, J01398, S14472, S24133, S74110, S74111
 R:Hum, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
 J. Mol. Biol. 229, 263-267, 1993

A:Title: Primary structure of three distinct isobabins determined by cDNA sequencing, CD
 A:Reference number: S2429, PMID:9132798, PMID:8421313
 A:Accession: S2429
 A:Residues: 1-201, 203-251 <FUN>
 A:Molecule type: rRNA
 A:Cross-references: GB:098344; NID:5166294; PID:AAA3262.1; PID:5166295
 A:Note: The coding region for the sequence shown is preceded by an ATG codon
 A:Note: Residues 1-8 were derived from the synthesized primer
 R:Funatsu, G.; Taguchi, Y.; Kamemoto, M.; Yanaka, M.
 Agric. Biol. Chem. 52, 1095-1097, 1988

A:Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from
 A:Reference number: J0202
 A:Accession: S2429
 A:Residues: 1-201, 203-251 <FUN>
 A:Molecule type: protein
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 R:Funatsu, G.; Taguchi, Y.; Kamemoto, M.; Yanaka, M.
 J. Biol. Chem. 266, 6848-6852, 1991

A:Title: Direct molecular cloning and expression of two distinct abrin A-chains.
 A:Reference number: A39761; PMID:9120139, PMID:2016300
 A:Accession: A39761
 A:Residues: 1-201, 203-251 <FUN>
 A:Molecule type: rRNA
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 R:Funatsu, G.; Taguchi, Y.; Kamemoto, M.; Yanaka, M.
 J. Biol. Chem. 266, 6848-6852, 1991

A:Title: The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic
 A:Reference number: J01398; PMID:91569023, PMID:7763422
 A:Accession: J01398
 A:Residues: 1-201, 203-251 <FUN>
 A:Molecule type: protein
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 R:Funatsu, G.; Taguchi, Y.; Kamemoto, M.; Yanaka, M.
 J. Biol. Chem. 266, 6848-6852, 1991

A:Title: The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic
 A:Reference number: S14471
 A:Accession: S14471
 A:Residues: 1-201, 203-251 <FUN>
 A:Molecule type: protein
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 R:Funatsu, G.; Taguchi, Y.; Kamemoto, M.; Yanaka, M.
 J. Biol. Chem. 266, 6848-6852, 1991

A:Title: The complete primary structure of abrin-a B chain.
 A:Reference number: S24133; PMID:92371656, PMID:1505674

A:Accession: S24133
 A:Molecule type: protein
 A:Residues: 262-297, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 <CHB>
 R:Lin, S.H.; Chow, L.P.; Chen, Y.L.; Lin, Y.C.; Chen, J.K.; Lin, J.Y.
 Eur. J. Biochem. 240, 564-569, 1996
 A:Title: Probing the domain structure of abrin-a by tryptic digestion.
 A:Reference number: S74110; PMID:9700945; PMID:865605
 A:Accession: S74110
 A:Residues: 89-108, 154-172 <LIN>
 A:Molecule type: protein
 A:Experimental source: seed

A:Residues: 262-276, 'X', 278-280, 328-348, 369-388, 399-418 <LIN>
 A:Experimental source: seed
 A:Comment: Abirin-a is more toxic than ricin. The toxin consists of an A chain, which is
 containing receptors on the cell surface. The A and B chains are linked by a single disul-
 fide bond. The B chain is a glycoprotein with a molecular weight of 26 kDa. The A chain is a
 polypeptide with a molecular weight of 26 kDa. The B chain is a glycoprotein with a molecu-
 lar weight of 26 kDa. The A chain is a polypeptide with a molecular weight of 26 kDa. The B
 chain is a glycoprotein with a molecular weight of 26 kDa. The A chain is a polypeptide with
 a molecular weight of 26 kDa. The B chain is a glycoprotein with a molecular weight of 26 kDa.
 F:261-528/Product: abrin-a chain B #status experimental <CHB>
 F:1283-325, 326-366, 369-407, 414-449, 453-492, 495-528/Region: 40-residue repeats
 F:1/Modified site: pyrrolidone carboxylic acid (Glu) #status experimental
 F:174,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:164,167/Active site: Glu, Arg #status predicted
 F:247-269, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted
 F:289,311/Binding site: N-acetylglucosamine (Asp, Asn) #status experimental
 F:500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 45.3%; Score 1190; DB 1; Length 528;
 Best Local Similarity 46.3%; Pred. No. 1.9e-107;
 Matches 248; Conservative 79; Mismatches 177; Indels 32; Gaps 10;

Qy 9 TRQTKKRYFTLLADYSSSSSSNELLRLRSTTVSPDQFVETLWQXGXSTX 68
 9 TRQTKKRYFTLLADYSSSSSSNELLRLRSTTVSPDQFVETLWQXGXSTX 68
 Db 186 TRQTKKRYFTLLADYSSSSSSNELLRLRSTTVSPDQFVETLWQXGXSTX 68
 Qy 69 AIDYKXVYVAAQAGQSVYVPRVAVPVDVDTGSAS-EEYVAVIGXGXGVDR 295
 69 AIDYKXVYVAAQAGQSVYVPRVAVPVDVDTGSAS-EEYVAVIGXGXGVDR 295
 Db 67 GIDYVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 124
 Qy 128 DQIFADIGVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 167
 128 DQIFADIGVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 167
 Db 125 QDIFADIGVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 164
 125 QDIFADIGVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 164
 Qy 188 FIDYKXVYVAAQAGQSVYVPRVAVPVDVDTGSAS-EEYVAVIGXGXGVDR 295
 188 FIDYKXVYVAAQAGQSVYVPRVAVPVDVDTGSAS-EEYVAVIGXGXGVDR 295
 Db 186 FIDYKXVYVAAQAGQSVYVPRVAVPVDVDTGSAS-EEYVAVIGXGXGVDR 295
 186 FIDYKXVYVAAQAGQSVYVPRVAVPVDVDTGSAS-EEYVAVIGXGXGVDR 295
 Qy 238 -VLSIAALMFVCGRRSSSVYVPRVAVPVDVDTGSAS-EEYVAVIGXGXGVDR 295
 238 -VLSIAALMFVCGRRSSSVYVPRVAVPVDVDTGSAS-EEYVAVIGXGXGVDR 295
 Db 235 FIDYKXVYVAAQAGQSVYVPRVAVPVDVDTGSAS-EEYVAVIGXGXGVDR 295
 235 FIDYKXVYVAAQAGQSVYVPRVAVPVDVDTGSAS-EEYVAVIGXGXGVDR 295
 Qy 296 DDEFDHGNQGLWPKSKNDNDQMLTKRNTIRSNKLTITVYSGPVYWIYDKTAT 399
 296 DDEFDHGNQGLWPKSKNDNDQMLTKRNTIRSNKLTITVYSGPVYWIYDKTAT 399
 Db 291 DDEFDHGNQGLWPKSKNDNDQMLTKRNTIRSNKLTITVYSGPVYWIYDKTAT 399
 291 DDEFDHGNQGLWPKSKNDNDQMLTKRNTIRSNKLTITVYSGPVYWIYDKTAT 399
 Qy 356 EATIQIWKXGIIINPRLVLAASSGIGKTTLTGTLDTLQOQMIAGNDTAREVTY 416
 356 EATIQIWKXGIIINPRLVLAASSGIGKTTLTGTLDTLQOQMIAGNDTAREVTY 416
 Db 351 EATIQIWKXGIIINPRLVLAASSGIGKTTLTGTLDTLQOQMIAGNDTAREVTY 416
 351 EATIQIWKXGIIINPRLVLAASSGIGKTTLTGTLDTLQOQMIAGNDTAREVTY 416
 Qy 416 GFDLCWESKSGYVETCSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 475
 416 GFDLCWESKSGYVETCSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 475
 Db 411 GFDLCWESKSGYVETCSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 475
 411 GFDLCWESKSGYVETCSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 475
 Qy 476 VSCSXXSXQXVETCSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 531
 476 VSCSXXSXQXVETCSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 531
 Db 470 VSCSXXSXQXVETCSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 525
 470 VSCSXXSXQXVETCSQXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 525

RESULT 5

A:Molecule type: protein
A:Residues: 1-265 <SD>
C:Superfamily: ricin/ RNA N-glycosidase homology
C:Keywords: glycoprotein
F:61,96,136/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 48.7%; Score 1279.5; DB 2; Length 265;
Best Local Similarity 92.0%; Pred. No. 1,5e-116;
Matches 243; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

OY 271 DDTGASAEPTVRIWKGXGVYRDDPDHDCNOIAMPSSKNDPNOIATIKEDTIS 330
DB 1 DDVTCASAEPTVRIWKGXGVYRDDPDHDCNOIAMPSSKNDPNOIATIKEDTIS 60

OY 331 NGSCITVGTAGYVWIFDGNARVBEATITWQIWNKGTIPRSMVLAASSGKGTILT 390
DB 61 NGSCITVGTAGYVWIFDGNARVBEATITWQIWNKGTIPRSMVLAASSGKGTILT 120

OY 391 VQIDITLGGQMLAGNDTAPREVTIYGRDLCEMSKNSGVVETCKSSQNXWALYGD 450
DB 121 VQIDITLGGQMLAGNDTAPREVTIYGRDLCEMSKNSGVVETCKSSQNXWALYGD 180

OY 451 GSIRPKNDQCLTGPDSVTYINVSQXKXGPMFTNKAIAKXXHXHADA 510
DB 181 GSIRPKNDQCLTGPDSVTYINVSQXKXGPMFTNKAIAKXXHXHADA 240

OY 511 NPKLRITIIIPATNGKPKQMW-LPV 533
DB 241 NPKLRITIIIPATNGKPKQMW-LPV 264

RESULT 3
R:CDSD
ricin D precursor - castor bean
N:Contains: RNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C>Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #ext. change 16-Jul-1999
C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13: 8019-8033, 1985
A>Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A:Reference number: A24041; MUID:86067214; PMID:2999712
A:Accession: A24041
A:Molecule type: DNA
A:Residues: 1-576 <RNA>
A:Accession: A24041; MUID:86067214; PMID:2999712
R:Teague, J.W.; Roberts, L.N.
Plant Mol. Biol. 18: 515-525, 1992
A>Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
A:Reference number: S20513; MUID:92163016; PMID:1371405
A:Accession: S20513
A:Molecule type: DNA
A:Residues: 1-576 <RNA>
A:Accession: A24614; MUID:85179479; PMID:3838723
R:Teague, J.W.; Roberts, L.N.
Eur. J. Biochem. 148: 265-270, 1985
A>Title: Nucleotide sequence of cloned cDNA coding for prepro-ricin.
A:Reference number: A24614; MUID:85179479; PMID:3838723
A:Accession: A24614
A:Molecule type: mRNA
A:Residues: 12-75/'D', 77-550/'R', 552-576 <LMA>
R:Koshitake, S.; Funatsu, G.; Funatsu, M.
J. Biol. Chem. 262: 1267-1274, 1987
A>Title: Isolation and sequences of peptic peptides, and the complete sequence of the ch
A:Accession: A03372
A:Molecule type: protein
A:Residues: 36-97/'Q', 99-109/'S', 111-269/'D', 272-283/'V', 285-288,290-302 <YOS>
A>Note: this paper cites the others in the series providing experimental details for the
R:Ataki, T.; Funatsu, G.
FEBS Lett. 191, 121-124, 1985
A>Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A:Reference number: A24010
A:Accession: A24010
A:Molecule type: protein
A:Residues: 315-383/'P', 386-576 <ASA>
R:Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A>Title: Primary structure of Ala chain of ricin D.
A:Reference number: A03374
A:Accession: A03374
A:Molecule type: protein
A:Residues: 36-97/'Q', 99-109/'S', 111-269/'D', 272-283/'V', 285-288,290-302 <YOS>
A>Note: this paper, one of a series, summarizes the experimental details for the deter
R:Ready, M.P.; Kim, Y.; Robertus, J.D.
Proteins 10, 270-278, 1991
A>Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism
A:Reference number: A48237; MUID:91352006; PMID:1881883
A:Contents: annotation, active site
R:Robertus, J.D.
Proteins 10, 260-269, 1991
A>Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A:Reference number: A48238; MUID:91352005; PMID:1881882
A:Contents: annotation, X-ray crystallography, 2.5 angstroms
R:Robertus, J.D.; Collins, E.C.; Robertus, J.D.
Proteins 10, 251-259, 1991
A>Title: Structure of ricin A-chain at 2.5 angstroms.
A:Reference number: A48239; MUID:91352004; PMID:1881881
A:Contents: annotation, X-ray crystallography, 2.5 angstroms
C:Comment: The functional molecule is a disulfide-linked dimer of A and B chains, whic
C:Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal sub
C:Comment: This protein is cytotoxic and very poisonous to animals.
C:Superfamily: ricin/ RNA N-glycosidase homology
C:Species: Ricinus communis (castor bean)
C>Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #ext. change 16-Jul-1999
C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13: 8019-8033, 1985
A>Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A:Reference number: A24041; MUID:86067214; PMID:2999712
A:Accession: A24041
A:Molecule type: DNA
A:Residues: 1-576 <RNA>
A:Accession: A24041; MUID:86067214; PMID:2999712
R:Teague, J.W.; Roberts, L.N.
Plant Mol. Biol. 18: 515-525, 1992
A>Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
A:Reference number: S20513; MUID:92163016; PMID:1371405
A:Accession: S20513
A:Molecule type: DNA
A:Residues: 1-576 <RNA>
A:Accession: A24614; MUID:85179479; PMID:3838723
R:Teague, J.W.; Roberts, L.N.
Eur. J. Biochem. 148: 265-270, 1985
A>Title: Nucleotide sequence of cloned cDNA coding for prepro-ricin.
A:Reference number: A24614; MUID:85179479; PMID:3838723
A:Accession: A24614
A:Molecule type: mRNA
A:Residues: 12-75/'D', 77-550/'R', 552-576 <LMA>
R:Koshitake, S.; Funatsu, G.; Funatsu, M.
J. Biol. Chem. 262: 1267-1274, 1987
A>Title: Isolation and sequences of peptic peptides, and the complete sequence of the ch
A:Accession: A03372
A:Molecule type: protein
A:Residues: 36-97/'Q', 99-109/'S', 111-269/'D', 272-283/'V', 285-288,290-302 <YOS>
A>Note: this paper cites the others in the series providing experimental details for the
R:Ataki, T.; Funatsu, G.
FEBS Lett. 191, 121-124, 1985
A>Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

Thu Dec 11 16:09:57 2003

us-09-601-667c-40.rpt

Page 1

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18 / Search time 16.5989 seconds
(without alignments)
3093.817 Million cell updates/sec

Title: US-09-601-667c-40

Reflect score: 2626

Sequence: 1 KERRLRVHTQTGKVEFR.....RRILLYPATGKPNQWMLPYV 534

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1290	49.1	264	2	PD0019
2	1279.5	48.7	265	2	JM0090
3	1229.5	46.8	576	1	RLCSD
4	1190	45.3	528	1	TLISA
5	1165	44.4	254	2	PD0018
6	1155	43.3	362	2	SL6022
7	1137	42.4	528	2	SL2434
8	1113.5	42.4	570	2	RLCSD
9	1101	41.9	564	1	RLCSD
10	851	32.4	570	2	SL6022
11	822	31.3	263	2	S06230
12	443	16.9	251	2	C39761
13	302	11.5	247	2	JC5032
14	301	11.5	289	1	RLZ77
15	300	11.4	247	2	JM0093
16	300	11.4	289	2	JC5066
17	287.5	11.0	245	2	UC4840
18	287.5	11.0	286	2	S25560
19	280.2	10.7	386	2	UC4335
20	273.5	10.4	336	2	UC4335
21	254	9.7	278	2	S23613
22	253.5	9.7	286	1	RLP033
23	244.5	9.3	277	2	S22494
24	239.5	9.1	250	2	JM0108
25	233.5	8.9	278	2	A39817
26	191.5	7.3	261	2	JEO401
27	189	7.2	313	2	S17757
28	184	6.9	313	2	S28421
29	172.5	6.6	106	2	B39761

30	168	6.4	253	2	S28539	rRNA N-glycosidase
31	166	6.3	253	2	S28542	rRNA N-glycosidase
32	162	6.2	253	2	S29931	rRNA N-glycosidase
33	162	6.2	283	2	S05205	rRNA N-glycosidase
34	159	6.1	253	2	S28541	rRNA N-glycosidase
35	157	6.0	232	1	RLQ032	rRNA N-glycosidase
36	150	5.7	272	2	UC4811	betavuligin - beet
37	150	5.7	272	2	UC4811	betavuligin - beet
38	138.4	5.4	253	2	AS5923	rRNA N-glycosidase
39	138.4	5.4	253	2	AS5923	rRNA N-glycosidase
40	131	5.0	253	2	S17232	rRNA N-glycosidase
41	125.5	4.8	377	2	JC7515	rRNA N-glycosidase
42	123.5	4.7	289	2	T12573	rRNA N-glycosidase
43	120	4.6	281	2	B38664	30K ribosome inact
44	118.5	4.5	477	1	J50589	endo-1,4-beta-ylase
45	115.5	4.4	383	2	T34603	xylosidase A - strep

ALIGNMENTS

RESULT 1
mistletoe lectin I B chain - Viscum album (fragment)
C/Species: Viscum album
C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #ext_change 07-May-1999
C/Accession: PD0019
R./Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W.
Biochem. Biophys. Res. Commun. 247, 367-372, 1998
A./Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum al
A./Reference number: PD0018; NCBI:68108123; PMID:9642133
A./Accession: PD0019
X./Accession: E226, PDB:1PSC
A./Residues: 1-264, protein
C./Superfamily: lectin, rRNA N-glycosidase homology
Query Match 49.1%, Score 1290, DB 2, Length 264,
Best Local Similarity 92.4%, Pred. No. 1, 4e-117,
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 271 DDVTCASPTVAIVGKXGVYDRODDPHDGNQIQLPKSKNDPQWMLTIRKXTRR 330
DB 1 DDVTCASPTVAIVGKXGVYDRODDPHDGNQIQLPKSKNDPQWMLTIRKXTRR 60
QY 331 NQSCITVTGTAQVYVWIPDQVNHATINQWKGITINPNSLTVLAASGIGKTTTL 390
DB 61 NQSCITVTGTAQVYVWIPDQVNHATINQWKGITINPNSLTVLAASGIGKTTTL 120
QY 391 VQVLDVTCGQWAGNTPARFVITIGRDLCKESNGSWYETCSGKXQKXALVAG 450
DB 121 VQVLDVTCGQWAGNTPARFVITIGRDLCKESNGSWYETCSGKXQKXALVAG 180
QY 451 GSIRPQNDQCLTGRDSVTVNTVSCSXXKQWVFTKXALINLKKXXXXVAVQA 510
DB 181 GSIRPQNDQCLTGRDSVTVNTVSCSXXKQWVFTKXALINLKKXXXXVAVQA 240
QY 511 NPKRILIIIPATGKPNQWMLPY 533
DB 241 NPKRILIIIPATGKPNQWMLPY 263
RESULT 2
Jm0090 - European mistletoe
N./Alternate names: ML-I
C/Species: Viscum album (European mistletoe)
C/Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #ext_change 19-May-2000
R./Accession: JM0090
X./Accession: N1, Stoeva, S.; Voelter, W.
Biochem. Biophys. Res. Commun. 246, 566-601, 1998
A./Title: Complete amino acid sequence of the B chain of mistletoe lectin I.
A./Reference number: JM0090; NCBI:9828575; PMID:9610256
A./Accession: JM0090

LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-338-793D-61

Query Match
Best Local Similarity 30.5%; Score 396; DB 2; Length 267;
Best Local Similarity 40.2%; Pred. No. 1,9e-33;
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

9 THQTGDEYFRTLLRDYSSGS-FSNEIFPL-RGSIPTVSADQRFVVELINQGDGI 66
13 TGAIVQSYTNFIRAVGRGLTGADVREHIFVLPVRVGLPIN-QRIIVELSNHAEISV 70
67 TAAIDVTNAYVAYQAGDSYFLR-DAPRGAE--THLFTGTRDSSSLPFGSYTDLERY 123
71 TLAIDVTNAYVAYQAGDSYFLR-DAPRGAE--THLFTGTRDSSSLPFGSYTDLERY 129
124 AGH-RDQIPGIEQLQSVNLY--FGSTRQANSITLITOMISPAAPFPIIMRYR 179
130 ASHARNEILNGFLEAHSALYYSVGQQLPLASPTICIMISEAARFQYIBERN 189
180 QDINSSEFLPDWMLLETSMQGSYOVCHSTDCVFNPFALISTGNVTSNRSYI 239
190 TRIRYRRASAPPSVITLNSWGLSTALQSNQAFASPIQLQRNRSKSYIVSILI 249
240 ASALMLFVCGERSS 255
250 PITALMYRCAPRPS 265

DB

US-08-839-765-1
Sequence 1. Application US/08839765
Patent No. 6146631

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.

APPLICANT: Studzika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:

INDRESS: Andrews, Hald & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago

STATE: Illinois
COUNTRY: USA

ZIP: 60661
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

OS/2 2.11, Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
FIRM: Canac M.
REGISTERED NUMBER: 2,318
REFERENCE/DOCKET NUMBER: 11022US09/200-70.F3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein

US-08-839-765-1
Query Match
Best Local Similarity 30.5%; Score 396; DB 3; Length 267;
Best Local Similarity 40.2%; Pred. No. 1,9e-33;
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

9 THQTGDEYFRTLLRDYSSGS-FSNEIFPL-RGSIPTVSADQRFVVELINQGDGI 66
13 TGAIVQSYTNFIRAVGRGLTGADVREHIFVLPVRVGLPIN-QRIIVELSNHAEISV 70
67 TAAIDVTNAYVAYQAGDSYFLR-DAPRGAE--THLFTGTRDSSSLPFGSYTDLERY 123
71 TLAIDVTNAYVAYQAGDSYFLR-DAPRGAE--THLFTGTRDSSSLPFGSYTDLERY 129
124 AGH-RDQIPGIEQLQSVNLY--FGSTRQANSITLITOMISPAAPFPIIMRYR 179
130 ASHARNEILNGFLEAHSALYYSVGQQLPLASPTICIMISEAARFQYIBERN 189
180 QDINSSEFLPDWMLLETSMQGSYOVCHSTDCVFNPFALISTGNVTSNRSYI 239
190 TRIRYRRASAPPSVITLNSWGLSTALQSNQAFASPIQLQRNRSKSYIVSILI 249
240 ASALMLFVCGERSS 255
250 PITALMYRCAPRPS 265

DB
US-08-839-765-1
Sequence 1. Application US/08839765
Patent No. 6146631

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.

APPLICANT: Studzika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:

INDRESS: Andrews, Hald & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago

STATE: Illinois
COUNTRY: USA

ZIP: 60661
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

OS/2 2.11, Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

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Page 7

DB 13 TGAATVQSYTNFRAVGRGLTGGADVREHIFVLPWRVGLPIN--ORFLVELSHNAELSV 70
QY 67 TTAIDVTAAVVAQADQSYFLR-DARQAR--TTLFTGTDRSSLPFTQSYTDLERY 123
DB 71 TTAIDVTAAVVAQADQSYFLR-DARQAR--TTLFTGTDRSSLPFTQSYTDLERY 129
QY 124 RGH-HQPGICBOLIOVSNAIR--FGSTRQAQASILLIOMISPAAPNFIIMRYR 179
DB 130 RGH-HQPGICBOLIOVSNAIR--FGSTRQAQASILLIOMISPAAPNFIIMRYR 189
QY 180 QDINSGBFLPDVWMLLETWQSQSTQVCHSTQVFNPFRLAISTQNVTLANRSVI 239
DB 190 TRINVRKSAADPSVITLNSWGLSTAYIGSNQASAPFTQLQRNNGKFSYDVSI 249
QY 240 ASLAIMLVGGERPSS 255
DB 250 PTLNMYRKNCPRESS 265

RESULT 13
US-08-646-360-1
Sequence 1, Application US/08646360
Patent No. 5837491

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
INVENTOR: Better, Marc D.
TITLE OF INVENTION: Immunocytins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 13-MAY-1996
CLASSIFICATION: 350
PRIOR APPLICATION DATA:
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: PCT/US94/05348
PRIOR APPLICATION DATA:
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 08/064,691
PRIOR APPLICATION DATA:
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/988,430
PRIOR APPLICATION DATA:
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/901,707

ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70, P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-1
Query Match 30.5%; Score 396; DB 2; Length 267;
Best Local Similarity 40.2%; Pct. No. 1.9e-35;
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;
QY 9 TQRTDDEYRFTLLADVSSGS-PSNEPLI-RQSTPVSQKQRFVLELWQADSI 66
DB 13 TGAATVQSYTNFRAVGRGLTGGADVREHIFVLPWRVGLPIN--ORFLVELSHNAELSV 70
QY 67 TTAIDVTAAVVAQADQSYFLR-DARQAR--TTLFTGTDRSSLPFTQSYTDLERY 123
DB 71 TTAIDVTAAVVAQADQSYFLR-DARQAR--TTLFTGTDRSSLPFTQSYTDLERY 129
QY 124 RGH-HQPGICBOLIOVSNAIR--FGSTRQAQASILLIOMISPAAPNFIIMRYR 179
DB 130 RGH-HQPGICBOLIOVSNAIR--FGSTRQAQASILLIOMISPAAPNFIIMRYR 189
QY 180 QDINSGBFLPDVWMLLETWQSQSTQVCHSTQVFNPFRLAISTQNVTLANRSVI 239
DB 190 TRINVRKSAADPSVITLNSWGLSTAYIGSNQASAPFTQLQRNNGKFSYDVSI 249
QY 240 ASLAIMLVGGERPSS 255
DB 250 PTLNMYRKNCPRESS 265

RESULT 14
US-08-338-793D-61
Sequence 61, Application US/08338793D
Patent No. 5840521

GENERAL INFORMATION:
APPLICANT: Barton, Peter Thomas
INVENTOR: Barton, Peter Thomas
TITLE OF INVENTION: VECTOR
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DAREY CUSHMAN
ADDRESS: INTELLECTUAL PROPERTY GROUP OF
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C. 20005
COUNTRY: U.S.A.
ZIP: 20005-3118

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word or ASCII editors
CURRENT APPLICATION DATA:
FILING DATE: 08-NOV-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: 07/84,081
APPLICATION NUMBER: 9104017.0
FILING DATE: 26-Feb-91
APPLICATION NUMBER: 9109188-4
FILING DATE: 29-Apr-91
ATTORNEY/AGENT INFORMATION:
NAME: Kohls, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 202-661-3000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-661-3000
TELEFAX: 202-661-3044
TELEX: 671467 CUSH
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:

Thu Dec 11 16:09:51 2003

us-09-601-667c-38.ra1

Page 6

US-08-488-113B-1
Sequence 1, Application US/08488113B
Patent No. 5,445,639
GENERAL INFORMATION:
APPLICANT: Bettef, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
CLASSIFICATION: 520
FILING DATE: 07-JUN-1995
PRIORITY NUMBER: 18
PRIORITY DATE: 18-APR-1995
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIORITY NUMBER: 18
PRIORITY DATE: 18-APR-1995
APPLICATION DATA:
FILING DATE: 12-MAY-1993
PRIORITY NUMBER: 07/988,430
FILING DATE: 09-DEC-1992
PRIORITY NUMBER: 07/901,707
PRIORITY DATE: 19-JUN-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70-P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
FAX: 312/707-8889
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-1
Query Match
Best Local Similarity 40.2%, P-Val 1.9e-33, Indels 12, Gaps 8,
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;
Cy 9 THQTGDEYFFETLLRDYSSGS-FSNEPPL-ROSTIPVSDAORFVLTNOCOSI 66
Db 13 TAGATVOSYTFNFAVAGSLTADVRHPIPLNRYGLPIN--ORFVLSHAEISLV 70
Cy 67 TAAIDVNAVYVAVQADOSTFLR-DARGAR--THLFGTTRDSSSPTGSTDYERY 123
Db 71 TLADVNAVAVGAGSALFPHDQCDARLTHLFT-DVQKRTFAGGNDRLDGL 129
Cy 124 AGH-POIRIEHQIOLSVSAIKY--FGSFRQARSLILCMISAPAPYILMYR 179
Db 130 AGNLRNIELGNGFLERALSALVYTSQGLPFLANSFICICMISAPAPYILMYR 189

US-08-477-484B-1
Sequence 1, Application US/08477484B
Patent No. 5,755,639
GENERAL INFORMATION:
APPLICANT: Bettef, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
CLASSIFICATION: 520
FILING DATE: 07-JUN-1995
PRIORITY NUMBER: 18
PRIORITY DATE: 18-APR-1995
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION DATA:
APPLICATION NUMBER: US 06/064,691
FILING DATE: 12-MAY-1993
PRIORITY NUMBER: 09-DEC-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIORITY NUMBER: 07/901,707
PRIORITY DATE: 19-JUN-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70-P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
FAX: 312/707-8889
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-1
Query Match
Best Local Similarity 30.5%, Score 396, DB 1, Length 267,
P-Val 1.9e-33, Indels 12, Gaps 8,
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;
Cy 9 THQTGDEYFFETLLRDYSSGS-FSNEPPL-ROSTIPVSDAORFVLTNOCOSI 66
Db 13 TAGATVOSYTFNFAVAGSLTADVRHPIPLNRYGLPIN--ORFVLSHAEISLV 70
Cy 67 TAAIDVNAVYVAVQADOSTFLR-DARGAR--THLFGTTRDSSSPTGSTDYERY 123
Db 71 TLADVNAVAVGAGSALFPHDQCDARLTHLFT-DVQKRTFAGGNDRLDGL 129
Cy 124 AGH-POIRIEHQIOLSVSAIKY--FGSFRQARSLILCMISAPAPYILMYR 179
Db 130 AGNLRNIELGNGFLERALSALVYTSQGLPFLANSFICICMISAPAPYILMYR 189

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us-09-601-667c-38.ra1

Page 5

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US-08-218-303-16
; Sequence 16, Application US/08218303
; Patent No. 5547867
; GENERAL INFORMATION:
; APPLICANT: Kera, Bhupendra V.
; APPLICANT: Hockney, Robert C.
; APPLICANT: Johnson, John E.
; TITLE OF INVENTION: IMMUNIZATION PROCESS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/218,303
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/841,533
; FILING DATE: 26-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerkulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PKR/3893/94908/MW
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELETYPE: 202-861-3000
; INFORMATION FOR SEQ ID NO. 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-218-303-16

Query Match 30.5%; Score 396; DB 1; Length 267;
Best Local Similarity 40.2%; Pred. No. 1,9e-33;
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

QY 9 THGTGDEYFRFTLLADYSSGS-FSNEIPL-ROSTIPVSDQRFVLEWTQGGDI 66
DB 13 TAGATVQSYTNFPAVAGLTTAGDVREHLPVLPVRGGLIN--QRFITLSEHMAISV 70
QY 67 TLAIDTVNAVVAVOAGDSQFPLR-DARQAR--THLFTGTDRSSLPFTSYTDLERY 123
DB 71 TLAIDTVNAVVAVOAGDSQFPLR-DARQAR--THLFTGTDRSSLPFTSYTDLERY 129
QY 124 ASH-ROQPLGIBOLIOSVSLR--FGSTRKQASILLIOMISAPAPNPILMAYR 179
DB 130 KQNRNENIELGNGPLERASLVLYSTGCTQLPLASFLICOMISAPAPNPILMAYR 189
QY 180 QDINSQSEFLPDVWMLSTSWQSGSTQVGHSTQVNNPRLAISTGNFTLVANVSYI 239
DB 190 THIVNRKAPDSVYTLLENMNGSLTAIGESVQAGAPSPQLQRRNSKFSYDVSIIL 249
QY 240 ASLAINLFCGGRPS 255
DB 250 PTLNIVYRCAPPS 265
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US-08-425-336-1
; Sequence 1, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studinka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; PROTEINS
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/425,336
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION NUMBER: 07/501,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Weyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-0440
; TELEFAX: 312/474-0448
; TELETYPE: 312/474-0448
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-336-1

Query Match 30.5%; Score 396; DB 1; Length 267;
Best Local Similarity 40.2%; Pred. No. 1,9e-33;
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;

QY 9 THGTGDEYFRFTLLADYSSGS-FSNEIPL-ROSTIPVSDQRFVLEWTQGGDI 66
DB 13 TAGATVQSYTNFPAVAGLTTAGDVREHLPVLPVRGGLIN--QRFITLSEHMAISV 70
QY 67 TLAIDTVNAVVAVOAGDSQFPLR-DARQAR--THLFTGTDRSSLPFTSYTDLERY 123
DB 71 TLAIDTVNAVVAVOAGDSQFPLR-DARQAR--THLFTGTDRSSLPFTSYTDLERY 129
QY 124 ASH-ROQPLGIBOLIOSVSLR--FGSTRKQASILLIOMISAPAPNPILMAYR 179
DB 130 KQNRNENIELGNGPLERASLVLYSTGCTQLPLASFLICOMISAPAPNPILMAYR 189
QY 180 QDINSQSEFLPDVWMLSTSWQSGSTQVGHSTQVNNPRLAISTGNFTLVANVSYI 239
DB 190 THIVNRKAPDSVYTLLENMNGSLTAIGESVQAGAPSPQLQRRNSKFSYDVSIIL 249
QY 240 ASLAINLFCGGRPS 255
DB 250 PTLNIVYRCAPPS 265
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Page 4

APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 04-NOV-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-901-707-1

Query Match 30.5%; Score 396; DB 1; Length 267;
Best Local Similarity 40.2%; Pred. No. 1,9e-33;
Matches 103; Conservative 45; Mismatches 56; Indels 12; Gaps 8;
QY 9 THQTGDEYFRFTLADYVSSGS-FSNEIFLL-RGSTIPVSDAQRFLVNLNQSDSI 66
DB 13 TGAIVYOSTNFRIRAVRGHILTAADVREIPVLPFRVGLPIN--QRFILVLSHMAISV 70
QY 67 TTAIDVTNAYVYVAGQSDSYFLR-DAPRGAE--THLFTGTDRSSLPFTGSTDYERY 123
DB 71 TLAADVTAAYVYVAGQSDSYFLR-DAPRGAE--THLFTGTDRSSLPFTGSTDYERY 129
QY 124 AGH-RDPIGLAIEGLIQGVVALRY---PGSSTQAQSEIILITOMISEAARFNIMRY 179
DB 130 AGNLRNIEILANGPILBEAISALVYVSTGCTOLPTLANSEFICIMISEAARFNIMRY 189
QY 180 QDINSGEFLPDWYMLETSTMGQSTOVQSTGVDGVPNNFRLAISTGNVFLTANVSATY 239
DB 190 TRIRYRNSADPSVITLSEMSGRSLTAQENQGAFASTPQLORNGSRFSYDVSIIL 249
QY 240 ASIAIMLVYCGRRPS 255
DB 250 FTLAMVYCAFPSS 265

RESULT 8
US-07-988-430-1
Sequence 1, Application US/07988430
Patent No. 5416202
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.

APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19-JUN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-988-430-1

Query Match 30.5%; Score 396; DB 1; Length 267;
Best Local Similarity 40.2%; Pred. No. 1,9e-33;
Matches 103; Conservative 45; Mismatches 56; Indels 12; Gaps 8;
QY 9 THQTGDEYFRFTLADYVSSGS-FSNEIFLL-RGSTIPVSDAQRFLVNLNQSDSI 66
DB 13 TGAIVYOSTNFRIRAVRGHILTAADVREIPVLPFRVGLPIN--QRFILVLSHMAISV 70
QY 67 TTAIDVTNAYVYVAGQSDSYFLR-DAPRGAE--THLFTGTDRSSLPFTGSTDYERY 123
DB 71 TLAADVTAAYVYVAGQSDSYFLR-DAPRGAE--THLFTGTDRSSLPFTGSTDYERY 129
QY 124 AGH-RDPIGLAIEGLIQGVVALRY---PGSSTQAQSEIILITOMISEAARFNIMRY 179
DB 130 AGNLRNIEILANGPILBEAISALVYVSTGCTOLPTLANSEFICIMISEAARFNIMRY 189
QY 180 QDINSGEFLPDWYMLETSTMGQSTOVQSTGVDGVPNNFRLAISTGNVFLTANVSATY 239
DB 190 TRIRYRNSADPSVITLSEMSGRSLTAQENQGAFASTPQLORNGSRFSYDVSIIL 249
QY 240 ASIAIMLVYCGRRPS 255
DB 250 FTLAMVYCAFPSS 265

RESULT 9

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US-08-378-761A-71
/ Sequence 71, Application US/08378761A
/ Patent No. 5635344
/ GENERAL INFORMATION:
/ APPLICANT: WALSH, TERENCE A
/ APPLICANT: HEY, TIMOTHY D
/ TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
/ TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
/ NUMBER OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
/ NUMBER OF INVENTION: USING
/ CORRESPONDENCE ADDRESS: 81
/ ADDRESS: ANDREA T. BORUCKI
/ STREET: 9330 ZIONSVILLE ROAD
/ CITY: INDIANAPOLIS
/ STATE: IN
/ COUNTRY: US
/ ZIP: 46268
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ CURRENT APPLICATION DATA: Patent in Release #1.0, Version #1.25
/ FILING DATE: 26-JAN-1995
/ APPLICATION NUMBER: 435
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BORUCKI, ANDREA T
/ REGISTRATION NUMBER: 33651
/ REFERENCE/DOCKET NUMBER: 382728
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (317) 337-4846
/ INFORMATION FOR SEQ ID NO: 71:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 250 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-378-761A-71

Query Match
35.9%; Score 466.5; DB 1; Length 250;
Best Local Similarity 43.1%; Pred. No. 76-41;
Matches 109; Conservative 37; Mismatches 80; Indels 27; Gaps 7;

QY 9 TQCTGDEYFRTLLADYVSSGSFSENEIPRLRGSTIPVSDAGRFVLVELINQGGDSTTA 68
DB 9 TEGATISQKQIFALREKL-RGGLIHIDIPVLPDPT-TLQERNRYITVELSNQDSEIEV 66
QY 69 AIDVTNAYVAYVADQSYFLRDAFPGAEETHLTCTTRDSSLPFTGSYTLERKAYGH-R 127
DB 67 GIDVTNAYVAYVAYRAGQSYFLRDAFSSASDYLTGT--DQHSIPYGTIGDLERNAHQSR 124
QY 128 DQPIGLIGLOISVSLRYPGSGSTRQARSILILQIMSEARFPIIMRWKQDINSGES 187
DB 125 QQIPLGQALTHGISFRSGSNDEKARKTILVILQNVADKARFYISNKNVYSIGDTGA 184
QY 188 FLPMWVMELETSGQOSTQVGHSTQVFNPRFLAISGNFVTLSNVS----- 237
DB 185 FQPDAMKSLLENW-DNRAGVQESVQDTFPGQ-----VLTINIRNEPVIVDSLSH 233
QY 238 -VIASLAIWLFPVC 249
DB 234 PTVAVALMLLFPVC 246

US-08-485-286-71
/ Sequence 1, Application US/08485286
/ Patent No. 5646026
/ Patent No. 5646026
/ GENERAL INFORMATION:
/ APPLICANT: Bernhardt, Susan L.
/ APPLICANT: Better, Marc D.

US-09-601-667c-38.ra1
/ APPLICANT: WALSH, TERENCE A
/ APPLICANT: HEY, TIMOTHY D
/ TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
/ TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
/ NUMBER OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
/ NUMBER OF INVENTION: USING
/ CORRESPONDENCE ADDRESS: 81
/ ADDRESS: ANDREA T. BORUCKI
/ STREET: 9330 ZIONSVILLE ROAD
/ CITY: INDIANAPOLIS
/ STATE: IN
/ COUNTRY: US
/ ZIP: 46268
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ CURRENT APPLICATION DATA: Patent in Release #1.0, Version #1.25
/ FILING DATE: 26-JAN-1995
/ APPLICATION NUMBER: 435
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BORUCKI, ANDREA T
/ REGISTRATION NUMBER: 33651
/ REFERENCE/DOCKET NUMBER: 382728
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (317) 337-4846
/ INFORMATION FOR SEQ ID NO: 71:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 250 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-485-286-71

Query Match
35.9%; Score 466.5; DB 1; Length 250;
Best Local Similarity 43.1%; Pred. No. 76-41;
Matches 109; Conservative 37; Mismatches 80; Indels 27; Gaps 7;

QY 9 TQCTGDEYFRTLLADYVSSGSFSENEIPRLRGSTIPVSDAGRFVLVELINQGGDSTTA 68
DB 9 TEGATISQKQIFALREKL-RGGLIHIDIPVLPDPT-TLQERNRYITVELSNQDSEIEV 66
QY 69 AIDVTNAYVAYVADQSYFLRDAFPGAEETHLTCTTRDSSLPFTGSYTLERKAYGH-R 127
DB 67 GIDVTNAYVAYVAYRAGQSYFLRDAFSSASDYLTGT--DQHSIPYGTIGDLERNAHQSR 124
QY 128 DQPIGLIGLOISVSLRYPGSGSTRQARSILILQIMSEARFPIIMRWKQDINSGES 187
DB 125 QQIPLGQALTHGISFRSGSNDEKARKTILVILQNVADKARFYISNKNVYSIGDTGA 184
QY 188 FLPMWVMELETSGQOSTQVGHSTQVFNPRFLAISGNFVTLSNVS----- 237
DB 185 FQPDAMKSLLENW-DNRAGVQESVQDTFPGQ-----VLTINIRNEPVIVDSLSH 233
QY 238 -VIASLAIWLFPVC 249
DB 234 PTVAVALMLLFPVC 246
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RESULT 2
US-08-776-059-31
/ Sequence 31, Application US/087760598
/ Patent No. 6271368
/ GENERAL INFORMATION:
/ APPLICANT: LENTZEN, Hans
/ APPLICANT: ECK, Jurgen
/ APPLICANT: AXEL, Axel
/ APPLICANT: BAUR, Axel
/ APPLICANT: ZINKE, Holger
/ TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
/ FILE REFERENCE: 674503-2003
/ CURRENT APPLICATION NUMBER: US/08/776, 0598
/ CURRENT FILING DATE: 1999-06-19
/ EARLIER APPLICATION NUMBER: PCT/EP96/02273
/ EARLIER FILING DATE: 1996-06-25
/ EARLIER APPLICATION NUMBER: 95109949.8
/ EARLIER FILING DATE: 1995-06-26
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 31
/ LENGTH: 253
/ TYPE: PRT
/ ORGANISM: Viscum album

US-08-776-059-31
Query Match          90.4%; Score 1174; DB 3; Length 253;
Best Local Similarity 91.7%; Pred. No. 4,7e-115;
Matches 233; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

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DB 2 YERILRWHTGDEPRFRLILNDVSSGSFNEIPILRGSTIPVSDAQFVLEYN 61
QY 61 QGDSITPAIDVYNAVVAQADDSYFLRDPAGAEHTLFTGTRRDSALPFGSYTDL 120
DB 62 QGDSITPAIDVYNAVVAQADDSYFLRDPAGAEHTLFTGTRRDSALPFGSYTDL 119
QY 121 ERYAGHDQIPVIGBOLIQSVSALRPGSGTAAQASILLIQMISAPARNPILMRARQ 180
DB 120 ERYAGHDQIPVIGBOLIQSVSALRPGSGTAAQASILLIQMISAPARNPILMRARQ 179
QY 181 DINGSGRFPDMWLETFSSQSGTQSGTQSGTQSGTQSGTQSGTQSGTQSGTQSGT 240
DB 180 YINSGASFPDVMWLETFSSQSGTQSGTQSGTQSGTQSGTQSGTQSGTQSGTQSGT 239
QY 241 SLAIVLPGCGRPS 254
DB 240 SLAIVLPGCGRPS 253

RESULT 3
US-08-776-059-39
/ Sequence 39, Application US/087760598
/ Patent No. 6271368
/ GENERAL INFORMATION:
/ APPLICANT: LENTZEN, Hans
/ APPLICANT: ECK, Jurgen
/ APPLICANT: AXEL, Axel
/ APPLICANT: BAUR, Axel
/ APPLICANT: ZINKE, Holger
/ TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
/ FILE REFERENCE: 674503-2003
/ CURRENT APPLICATION NUMBER: US/08/776, 0598
/ CURRENT FILING DATE: 1999-06-19
/ EARLIER APPLICATION NUMBER: PCT/EP96/02273
/ EARLIER FILING DATE: 1996-06-25
/ EARLIER APPLICATION NUMBER: 95109949.8
/ EARLIER FILING DATE: 1995-06-26
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 39
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Viscum album

US-08-776-059-39
Query Match          83.8%; Score 1089; DB 3; Length 235;
Best Local Similarity 92.0%; Pred. No. 3.4e-106;
Matches 218; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 18 FPIITLADVYSSGSFNEIPILRGSTIPVSDAQFVLEYNQGSITPAIDVYNAVY 77
DB 1 FPIITLADVYSSGSFNEIPILRGSTIPVSDAQFVLEYNQGSITPAIDVYNAVY 60
QY 78 VAVQADDSYFLRDPAGAEHTLFTGTRRDSALPFGSYTDLERYAGHDQIPVIGBOL 137
DB 61 VAVQADDSYFLRDPAGAEHTLFTGTRRDSALPFGSYTDLERYAGHDQIPVIGBOL 118
QY 138 IQSVSALRPGSGTAAQASILLIQMISAPARNPILMRARQDINGSGRFPDMWLETF 197
DB 119 IQSVSALRPGSGTAAQASILLIQMISAPARNPILMRARQDINGSGRFPDMWLETF 178
QY 198 ETSWQSGSTQVGHSTQGVNPPRLAISTGNPVILSNVSYSLAIVLPGCGRPS 254
DB 179 ETSWQSGSTQVGHSTQGVNPPRLAISTGNPVILSNVSYSLAIVLPGCGRPS 235

RESULT 4
US-09-538-873-3
/ Sequence 3, Application US/09538873
/ Patent No. 6566500
/ GENERAL INFORMATION:
/ APPLICANT: VITETTA, EILEEN S.
/ APPLICANT: GHEITE, VICTOR F.
/ APPLICANT: SHALISHAW, JOAN
/ APPLICANT: BALDWIN, ROXANA G.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
/ FILE REFERENCE: USPD 603
/ CURRENT APPLICATION NUMBER: US/09/538, 873
/ CURRENT FILING DATE: 2000-03-30
/ EARLIER APPLICATION NUMBER: 60/126, 826
/ EARLIER FILING DATE: 1999-03-30
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ TYPE: PRT
/ ORGANISM: Abinus precatorius

US-09-538-873-3
Query Match          36.5%; Score 474; DB 4; Length 251;
Best Local Similarity 43.1%; Pred. No. 1.1e-41;
Matches 109; Conservative 37; Mismatches 81; Indels 26; Gaps 6;

QY 9 THQTDGKFRPFIITLADVYSSGSFNEIPILRGSTIPVSDAQFVLEYNQGSITPAIDVYNAVY 68
DB 9 THQTDGKFRPFIITLADVYSSGSFNEIPILRGSTIPVSDAQFVLEYNQGSITPAIDVYNAVY 66
QY 69 AIDVYNAVVAQADDSYFLRDPAGAEHTLFTGTRRDSALPFGSYTDLERYAGH-R 127
DB 67 AIDVYNAVVAQADDSYFLRDPAGAEHTLFTGTRRDSALPFGSYTDLERYAGH-R 124
QY 128 DQIILGIBOLIQSVSALRPGSGTAAQASILLIQMISAPARNPILMRARQDINGSGS 187
DB 125 DQIILGIBOLIQSVSALRPGSGTAAQASILLIQMISAPARNPILMRARQDINGSGS 184
QY 188 FIPDMWLETFSSQSGTQSGTQSGTQSGTQSGTQSGTQSGTQSGTQSGTQSGT 237
DB 185 FIPDMWLETFSSQSGTQSGTQSGTQSGTQSGTQSGTQSGTQSGTQSGTQSGT 234
QY 238 -VLSAIVLPGCGRPS 249
DB 235 FTVAVLALMFLVC 247

RESULT 5
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Thu Dec 11 16:09:51 2003

us-09-601-667c-38.ra1

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18 / Search time 8.86328 seconds
(without alignments)

1222.073 Million cell updates/sec

Title: US-09-601-667C-38

Prefix score: 1232

Sequence: 1 YERLKLRYHTQTDYFRFP.....SYLASLALTEFVCGRRPSS 256

Scoring table: BLOSUM62

Gapop 10.0, Gapept 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: /cgn2_6/prodata/1/aa/5A.COMB.pep.*

2: /cgn2_6/prodata/1/aa/5B.COMB.pep.*

3: /cgn2_6/prodata/1/aa/6A.COMB.pep.*

4: /cgn2_6/prodata/1/aa/6B.COMB.pep.*

5: /cgn2_6/prodata/1/aa/6C.COMB.pep.*

6: /cgn2_6/prodata/1/aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1188	91.5	564	3	US-08-776-059-35
2	1178	90.4	253	3	US-08-776-059-31
3	1174	90.4	253	3	US-08-776-059-31
4	474	32.8	225	4	US-08-477-484B-6
5	466.5	35.9	250	4	US-08-482-721-71
6	466.5	35.9	250	4	US-08-482-721-71
7	396	30.5	287	1	US-07-988-430-1
8	396	30.5	287	1	US-07-988-430-1
9	396	30.5	287	1	US-08-218-303-16
10	396	30.5	287	1	US-08-425-336-1
11	396	30.5	287	1	US-08-488-1138-1
12	396	30.5	287	1	US-08-477-484B-1
13	396	30.5	287	2	US-08-646-360-1
14	396	30.5	287	2	US-08-938-7930-61
15	396	30.5	287	3	US-08-439-765-1
16	396	30.5	287	3	US-08-439-765-1
17	396	30.5	287	4	US-08-439-765-1
18	396	30.5	287	4	US-08-439-765-1
19	396	30.5	287	5	US-08-439-765-1
20	396	30.5	287	5	US-08-439-765-1
21	396	30.5	287	5	US-08-439-765-1
22	396	30.5	287	5	US-08-439-765-1
23	396	30.5	287	5	US-08-439-765-1
24	396	30.5	287	5	US-08-439-765-1
25	396	30.5	287	5	US-08-439-765-1
26	396	30.5	287	5	US-08-439-765-1
27	396	30.5	287	5	US-08-439-765-1
28	396	30.5	287	5	US-08-439-765-1
29	396	30.5	287	5	US-08-439-765-1
30	396	30.5	287	5	US-08-439-765-1
31	396	30.5	287	5	US-08-439-765-1
32	396	30.5	287	5	US-08-439-765-1
33	396	30.5	287	5	US-08-439-765-1
34	396	30.5	287	5	US-08-439-765-1
35	396	30.5	287	5	US-08-439-765-1
36	396	30.5	287	5	US-08-439-765-1
37	396	30.5	287	5	US-08-439-765-1
38	396	30.5	287	5	US-08-439-765-1
39	396	30.5	287	5	US-08-439-765-1
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42	396	30.5	287	5	US-08-439-765-1
43	396	30.5	287	5	US-08-439-765-1
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ALIGNMENTS

28	329	25.3	267	1	US-08-176-761A-74	Sequence 74, Appl
29	329	25.3	267	1	US-08-485-286-74	Sequence 74, Appl
30	327	25.2	247	1	US-08-488-1138-6	Sequence 6, Appl
31	327	25.2	247	1	US-08-477-484B-6	Sequence 6, Appl
32	327	25.2	247	2	US-08-646-360-6	Sequence 6, Appl
33	327	25.2	247	3	US-08-938-765-6	Sequence 6, Appl
34	327	25.2	247	3	US-08-136-389-6	Sequence 6, Appl
35	327	25.2	247	3	US-07-935-889-6	Sequence 6, Appl
36	327	25.2	247	3	US-08-439-765-6	Sequence 6, Appl
37	322	24.8	289	1	US-08-182-327-4	Sequence 4, Appl
38	322	24.8	289	2	US-08-482-320-4	Sequence 4, Appl
39	322	24.8	289	3	US-08-483-502-4	Sequence 4, Appl
40	322	24.8	289	4	US-09-726-651A-4	Sequence 4, Appl
41	322	24.8	289	4	US-08-483-502-4	Sequence 4, Appl
42	314	24.2	263	1	US-07-901-707-4	Sequence 4, Appl
43	314	24.2	263	1	US-07-988-430-4	Sequence 4, Appl
44	314	24.2	263	1	US-08-425-336-4	Sequence 4, Appl
45	314	24.2	263	1	US-08-488-1138-4	Sequence 4, Appl

RESULT 1

US-08-776-059-35

Sequence 35, Application US/0876059B

Patent No. 6271368

GENERAL INFORMATION:

APPLICANT: LENTZEN, Hans

APPLICANT: ECK, Jürgen

APPLICANT: BARK, Axel

APPLICANT: BARK, Axel

TITLE OF INVENTION: RECOMBINANT KISTLETOR LECTIN (RML)

CURRENT APPLICATION NUMBER: US/08/776, 059B

EARLIER FILING DATE: 1999-06-19

EARLIER FILING DATE: 1996-06-25

EARLIER APPLICATION NUMBER: 95109949.8

NUMBER OF SEQ ID NOS: 56

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 35

TYPE: PEP

ORGANISM: Viscum album

US-08-776-059-35

Query Match

Best local similarity 91.5%; Score 1188; DB 3; Length 564;

Matches 227; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

Qy	1	YERLKLRYHTQTDYFRFP	111	LDYVSSGFSNRPILKOSTIPVSDAKQFVYVLN	60
Db	34	YERLKLRYHTQTDYFRFP	111	LDYVSSGFSNRPILKOSTIPVSDAKQFVYVLN	93
Qy	121	ERYAGHNDQIPGIEDIQSVSLAYGSGTAPQASIIILIQMSKALFPIVWYRQ	180		
Db	152	ERYAGHNDQIPGIEDIQSVSLAYGSGTAPQASIIILIQMSKALFPIVWYRQ	211		
Qy	181	DINSGSFLPDVYKLELFTSGKSTOVCHSDVFNPFRLAISTGPFYLSNRSVYA	240		
Db	212	YINSGASLFDVYKLELFTSGKSTOVCHSDVFNPFRLAISTGPFYLSNRSVYA	271		
Qy	241	SLATLVCGRRPSS 256			
Db	272	SLATLVCGRRPSS 287			

Thu Dec 11 16:09:52 2003

us-09-601-667c-38.rapb

Page 7

Query Match 22.7%; Score 294.5; DB 12; Length 251;
Best Local Similarity 34.4%; Pred. No. 7.2e-23;
Matches 87; Conservative 36; Mismatches 109; Indels 21; Gaps 7;
US-10-127-890-102

Query 8 VTHQGTGDEYFRFTLLADY---VSSGSSNENFLRQSTIPVSDARFVLEINQGD 64
DB 5 VSPSTGATYTVVNFLEIRYKLEKPSGNSHGLPLKRC--DQKCFVLAINDMQ 62
DB 63 LAELIDVTSYVVGQVNRSTYFDAPDAVAGLFRNTIKTR--LHFGSYPSLGEK 120
DB 125 GHNDQPLGIGIOL---IOSVALRYPGSGTRQAQASILLIOMISGAAR---NPLMR 177
DB 121 ARRTDLDGIEPLIGIKEDENAIKNTKTELASSLLVYQVSEARFTIENDIRN 180
DB 178 YRDINGSGSLPDMVYLELTSWQOOSTQVQHS--TDGFNNPFLAISTGNVTLNVR 236
DB 181 PQGRIR-----PANNITSLNWKGLSFQIRTSQAGNFSBAVELEBRANKKYVTVAD 234
DB 237 SVTASLAIMLFCV 249
DB 235 QVERKIALKFCV 247

RESULT 15
US-10-127-890-102
Sequence 102, Application US/10/12/7890
Publication 102, US/09/01/6196A1
GENERAL INFORMATION
APPLICANT: Bertel, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois

FILING DATE: 23-APR-2002
CLASSIFICATION: <Unknown>
PRIORITY INFORMATION:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
FILING DATE: 07/901,707
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-127-890-111

COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT RELEASE DATE: US/10/12/7890
FILING DATE: 23-APR-2002
CLASSIFICATION: <Unknown>
PRIORITY INFORMATION:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
FILING DATE: 07/901,707
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-10-127-890-102

Query Match 22.4%; Score 290.5; DB 12; Length 251;
Best Local Similarity 34.0%; Pred. No. 1.9e-22;
Matches 86; Conservative 37; Mismatches 109; Indels 21; Gaps 7;
US-10-127-890-102

Query 8 VTHQGTGDEYFRFTLLADY---VSSGSSNENFLRQSTIPVSDARFVLEINQGD 64
DB 5 VSPSTGATYTVVNFLEIRYKLEKPSGNSHGLPLKRC--DQKCFVLAINDMQ 62
DB 63 LAELIDVTSYVVGQVNRSTYFDAPDAVAGLFRNTIKTR--LHFGSYPSLGEK 120
DB 125 GHNDQPLGIGIOL---IOSVALRYPGSGTRQAQASILLIOMISGAAR---NPLMR 177
DB 121 ARRTDLDGIEPLIGIKEDENAIKNTKTELASSLLVYQVSEARFTIENDIRN 180
DB 178 YRDINGSGSLPDMVYLELTSWQOOSTQVQHS--TDGFNNPFLAISTGNVTLNVR 236
DB 181 PQGRIR-----PANNITSLNWKGLSFQIRTSQAGNFSBAVELEBRANKKYVTVAD 234
DB 237 SVTASLAIMLFCV 249
DB 235 QVERKIALKFCV 247

Search completed: December 11, 2003, 14:48:51
Job time: 16.4973 secs

Thu Dec 11 16:09:52 2003

us-09-601-667c-38.rapb

TYPE: amino acid
; DOPO: 1184
; MOLEWT: 1184
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-127-890-4

Query Match 24.2%; Score 314; DB 12; Length 263;
Best Local Similarity 35.0%; Pred. No. 6,6e-25;
Matches 85; Conservative 49; Mismatches 89; Indels 20; Gaps 9;

QY 13 TUDERFTTLADYSSGSFNS--EPLRQSTIPVDAQFVYVLELNGQDSI 69
DB 10 TACTIKFI--EDPRATIPSHRYDILFIST--ISDRKFIIDLIDISYAEHISVA 63
QY 70 IDPTNAYVAYVAYQADQSYFLDAPRGAETLFTGTDRSSLEPTGSGYDLERYAGH--R 127
DB 64 IDVTNAYVAYVAYTRDVSYPFESPEPVAIVLTKIR--KITLPTGYNEMLTQ--AAKIR 120
QY 128 DOIPLGIGIOLIOSVALRYPGSGSTRAPKSEILILQWISBAKFPILMYRQDINSSES 187
DB 121 EMTDGLPALSALTTFYMAQSAFSA--LVLITQTEAKAFKXIERHAKTV--ATN 176
QY 188 FLDPWYMLLETSMNGQSTQV--QASTDGVFNNPFLAISTGVPVLSNVSASTAIAM 245
DB 177 FRENALITSLNQSALSKQIFLAQNGSGFRRPVDLITGERQVATNDDVYKNIK 236
QY 246 LPV 248
DB 237 LLL 239

RESULT 12
US-09-792-793A-34
; Sequence 34; Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; INVENTOR: McDaniel, John R.
; APPLICANT: McDaniel, John R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Bryonia dioica
US-09-792-793A-34

Query Match 23.4%; Score 303.5; DB 10; Length 247;
Best Local Similarity 33.2%; Pred. No. 7,8e-24;
Matches 82; Conservative 50; Mismatches 98; Indels 17; Gaps 8;
QY 7 RVHQQTGDEYFRTTLADYSSGSFNSNEIPLRQSTIPVDAQFVYVLELNGQDSI 66
DB 5 RLSGATT--TSYGVFIRNLRALPYERKYNIPIILRS--ISGSRFTLHLNVADETI 60
QY 67 TLAIDTNAAYVAYVAYQADQSYFLDAPRGAETLFTGTDRSSLEPTGSGYDLERYAGH 126
DB 61 SVADVATNVTIMGLDGVSYFPRBASATEAKAFVCKAKKVTLPYSGNVERLTQAAK 120
QY 127 -RDQIPLGIGIOLIOSVALRYPGSGSTRAPKSEILILQWISBAKFPILMYRQDINS- 184
DB 121 IRENIPGLPALDSALTTLVYTSASASA--LVLIOSTASARVFT---EQQIKR 174
QY 185 -GSEFLDPWYMLLETSMNGQSTQV--HSTDGVFNNPFLAISTGVPVLSN--VRSVI 239
DB 175 VKRTPLSLATISLNNMSLSKQIQIASINQGSFESVVLIDGNMQRVSLTNASRYVT 234
QY 240 ASIAIML 246
DB 237 LLL 239

US-10-127-890-4
; Sequence 111; Application US/10127890
; Publication No. US20030166156A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; INVENTOR: Carroll, Stephen F.
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESS: McAdams, Heid & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER readable form:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890

DB 235 SWIALML 241

RESULT 13
US-10-375-209A-34
; Sequence 34; Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; INVENTOR: McDaniel, John R.
; APPLICANT: McDaniel, John R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; FILE REFERENCE: 25020-601S
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Bryonia dioica
US-10-375-209A-34

Query Match 23.4%; Score 303.5; DB 12; Length 247;
Best Local Similarity 33.2%; Pred. No. 7,8e-24;
Matches 82; Conservative 50; Mismatches 98; Indels 17; Gaps 8;

QY 7 RVHQQTGDEYFRTTLADYSSGSFNSNEIPLRQSTIPVDAQFVYVLELNGQDSI 66
DB 5 RLSGATT--TSYGVFIRNLRALPYERKYNIPIILRS--ISGSRFTLHLNVADETI 60
QY 67 TLAIDTNAAYVAYVAYQADQSYFLDAPRGAETLFTGTDRSSLEPTGSGYDLERYAGH 126
DB 61 SVADVATNVTIMGLDGVSYFPRBASATEAKAFVCKAKKVTLPYSGNVERLTQAAK 120
QY 127 -RDQIPLGIGIOLIOSVALRYPGSGSTRAPKSEILILQWISBAKFPILMYRQDINS- 184
DB 121 IRENIPGLPALDSALTTLVYTSASASA--LVLIOSTASARVFT---EQQIKR 174
QY 185 -GSEFLDPWYMLLETSMNGQSTQV--HSTDGVFNNPFLAISTGVPVLSN--VRSVI 239
DB 175 VKRTPLSLATISLNNMSLSKQIQIASINQGSFESVVLIDGNMQRVSLTNASRYVT 234
QY 240 ASIAIML 246
DB 235 SWIALML 241

US-10-127-890-111
; Sequence 111; Application US/10127890
; Publication No. US20030166156A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; INVENTOR: Carroll, Stephen F.
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESS: McAdams, Heid & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER readable form:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6
 US-10-127-890-6

Query Match 25.2%; Score 327; DB 12; Length 247;
 Best Local Similarity 36.0%; Pred. No. 2.5e-26;
 Matches 87; Conservative 52; Mismatches 85; Indels 18; Gaps 10;

QY 13 TDEYFRFTLLRDVYSSGFSFNEIPILROSTIPVSDAQRVVELTNGQDSITAAIDV 72
 DB 10 TSSSYGVFISNLKRALPRKXKYDIPILR--SDPQS--QRYALHTLNTVADETTISVAIDV 66
 QY 73 TNAVVAQAQDQSYFRLDA--PRGAEHLFTGTDRASLPFTGSYTDLERYAGH-RDQI 130
 DB 67 TNYITMGVRAQDQSYFPRNASTATKAYVFDKMR-KVTLPSGNTVRLQTPAAKIRENI 125
 QY 131 PLGIBOLIOSVSALEPYGSGTQAQASIIILICMISEAPRMLIKRYODIUS--GESP 188
 DB 126 PLGIPALDSALITLTFYVANSASA--LWVLQSTSEAAHYKEI----EQIGKRVDTF 179
 QY 189 LPEWYMLELFTSMQGSQTVQ--HSTGVFNNPFLAISTGNFVLSNRS--VIASLAI 244
 DB 180 LPSLAIISLNSWSALSKQIQIASTNNOQFETPVVLLNMQNRFVITNDAVGVTSNIAL 239
 QY 245 ML 246
 DB 240 IL 241

RESULT 10

US-10-280-679B-4
 Sequence 4, Application US/10280679B
 Publication No. US20030150019A1

GENERAL INFORMATION:
 APPLICANT: LargeScale Biology Corporation
 TITLE OF INVENTION: A Novel Method for Producing Recombinant Proteins
 FILE REFERENCE: USBC-0108-1803
 CURRENT APPLICATION NUMBER: US/10/280,679B

PRIOR APPLICATION DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: 09/557,941
 PRIOR FILING DATE: 2000-04-24
 PRIOR APPLICATION NUMBER: 08/484,341
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 07/923,692
 PRIOR FILING DATE: 1992-07-31
 PRIOR APPLICATION NUMBER: 07/600,244
 PRIOR FILING DATE: 1990-10-22
 PRIOR APPLICATION NUMBER: 07/641,617
 PRIOR FILING DATE: 1991-01-16
 PRIOR APPLICATION NUMBER: 07/737,899
 PRIOR FILING DATE: 1991-07-26
 PRIOR APPLICATION NUMBER: 07/739,143
 PRIOR FILING DATE: 1991-08-01
 PRIOR APPLICATION NUMBER: 07/310,881
 PRIOR FILING DATE: 1989-02-17
 PRIOR APPLICATION NUMBER: 07/160,766
 PRIOR FILING DATE: 1988-02-26
 PRIOR APPLICATION NUMBER: 07/160,771
 PRIOR FILING DATE: 1988-02-26
 PUBLICATION DATE: 2003-01-09
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 4
 LENGTH: 289
 TYPE: PRT
 ORGANISM: Chinese cucumber protein alpha-trichosanthin
 US-10-280-679B-4

Query Match 24.8%; Score 322; DB 12; Length 289;
 Best Local Similarity 36.0%; Pred. No. 1.1e-25;
 Matches 87; Conservative 51; Mismatches 36; Indels 18; Gaps 10;

QY 13 TDEYFRFTLLRDVYSSGFSFNEIPILROSTIPVSDAQRVVELTNGQDSITAAIDV 72
 DB 33 TSSSYGVFISNLKRALPRKXKYDIPILR--SDPQS--QRYALHTLNTVADETTISVAIDV 69
 QY 73 TNAVVAQAQDQSYFRLDA--PRGAEHLFTGTDRASLPFTGSYTDLERYAGH-RDQI 130
 DB 90 TNYITMGVRAQDQSYFPRNASTATKAYVFDKMR-KVTLPSGNTVRLQTPAAKIRENI 148
 QY 131 PLGIBOLIOSVSALEPYGSGTQAQASIIILICMISEAPRMLIKRYODIUS--GESP 188
 DB 149 PLGIPALDSALITLTFYVANSASA--LWVLQSTSEAAHYKEI----EQIGKRVDTF 202
 QY 189 LPEWYMLELFTSMQGSQTVQ--HSTGVFNNPFLAISTGNFVLSNRS--VIASLAI 244
 DB 203 LPSLAIISLNSWSALSKQIQIASTNNOQFETPVVLLNMQNRFVITNDAVGVTSNIAL 262
 QY 245 ML 246
 DB 263 IL 264

RESULT 11

US-10-127-890-4
 Sequence 4, Application US/10127890
 Publication No. US2003016196A1

GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 Stuchlik, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McGraw-Hill, Inc.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/10/127,890
 FILING DATE: 23-APR-2002
 CLASSIFICATION DATA: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/05/646,360
 FILING DATE: 13-MAY-1996
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993/7/988,430
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-DEC-1992
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70-P4
 TELEPHONE: 312/707-8883
 TELEFAX: 312/707-9155

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 263 amino acids

Thu Dec 11 16:09:52 2003

us-09-601-667c-38.rapb

Page 4

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QY      240 ASLAIMLFVCGERPSS 255
      .      :|:|:|
Db      285 PIALMVYRCAPPPSS 300
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RESULT 7
US-09-792-793A-39
? Sequence 39, Application US/09792793A
? Patent No. US20020168370A1
? GENERAL INFORMATION:
? APPLICANT: McDonald, John R.
? INVENTOR: Cozzinis, Philip
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND DISORDERS
? TITLE OF INVENTION: OTHER INVENTIONARY CONDITIONS AND DISORDERS
? FILE REFERENCE: 45020-601D
? CURRENT APPLICATION NUMBER: US/09/792,793A
? NUMBER OF SEQ ID NOS: 33
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO: 3

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ORGANISM: *Trichosanthea kirilowii*
US-09-792-793A-39

Query Match	25.3%;	Score 329;	DB 10;	Length 247;
Best Local Similarity	36.4%;	Pred. No. 1.5e-26;		
Matches 88;	Conservative 52;	Mismatches 84;	Indels 18;	Gaps 10;

QY	1	TGGEYFHTLRLRYVSSSSSSNEI	PILRQSTIVPMARQVVEVNEQOOSTAIDV	72
Dy	10	TSSSGVAFISINLRALNNERLDIPLR	SSLPSS--GRYALILNMYADETISALDV	66
Dy	1	TNNVYVQAQNGSTFLDA--PRGAETHLFTGTRNRSLEPTGSIYDERVAGH	RDQI	135
Dy	67	YNNHNGRQSTIFEPNNSALREAKYVKNAR	KVTLISNREIDRYPKGITHETI	120
QY	131	PLQICIGSVSALAPRGSGSRQARSLIL	IQWISAPAEFLIRPRQDGS--GSEF	188
Dy	126	FILDLALDASLITTLFFYNNANSASA	--LMLVQSSTPAARVTF--EQQGRKVDKTF	179
QY	189	LEPMHMLLETGNSQOSTOV--HSDGVNPPRFLATGTENPVL	SWNS--VTALAI	244
Dy	180	LPGLAIIISLNSMSALSKQIOI	ASTNNQESPVLINRQREVTITVDAGVTSNIAL	239
QY	245	ML	246	
Dy	240	LT	241	

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RESULT 8
US-10-375-209A-39
Sequence 39, Application US/10375209A
Publication No. US2003025421A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
INVENTOR: Cossins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND DISORDERS
FILE REFERENCE: US 2002-02-24
CURRENT APPLICATION NUMBER: US/10/375,209A
CURRENT FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentr Ver. 2.0
SEQ ID NO 39
LENGTH: 247
TYPE: PRT
ORGANISM: Trichosantheus kilowooli
US-10-375-209A-39

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Query Match	25.3%;	Score 329;	DB 12;	Length 247;
Best Local Similarity	36.4%;	Pred. No. 1.5e-26;		
Matches 88;	Conservative 52;	Mismatches 84;	Indels 18;	Gaps 10;

QY 13 TGEFFEFFILLRQVSSSSSSNEI FILLROSTIPVSPARQVLEWITQOQSDITAIAY 72
Dd 10 TSSSGVAFISNIRKALPERKRDIPILR SLPSS -ORVALHITVADREISVAID 66
QY 73 TAAVVAVNAQSDQSYFLDRA -PQAEFTHLFTGTRDSSLEFFQSYTDLERVACH -RDOJ 136
Dd 67 TAVIIMQKQVOTDYPFNEBAREAKRYQDQMR -KTLFISQNBELQKQKQKQEN 122
QY 131 PGLIOTIIOGVALRARPQSGRRQKRSILLLIOWISAAKRNPLIMRWPOINS -DESS 188
Dd 126 FLGLPGLDASITTLFTFYNNANSASA -LWMLQSTISBAKRYKE-----DOJQKQVWKTF 176
QY 189 LPMWMELETWQOQSTOVV -HSQDQVNNPFRALISTONEVITSNVS -VIASLAI 244
Dd 180 LPSLAIISLSPNSWALSKOIOIASTNNQOSESFVLLINQORQVITTVDAQVTSNIAL 235
QY 245 ML 246
Dd 240 LL 241

RESULT 3
 US-10-127-890-6
 Sequence 6, Application US/10127890
 Publication No. US20030166196A1
 GENERAL INFORMATION:
 APPLICANT: Bettey, Marc D.
 Inventor: Bettey, Marc D.
 Stroika, Stephen P.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 Proteins
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: IBM PC DOS/MS-DOS
 SOFTWARE RELEASE: Microsoft Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/127, 890
 FILING DATE: 23-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/646, 360
 FILING DATE: 13-May-1996
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-May-1994
 APPLICATION NUMBER: US 08/064, 691
 FILING DATE: 12-May-1993/7,988, 430
 APPLICATION NUMBER: US 07/901, 707
 FILING DATE: 19-Jun-1992/7,982, 182
 APPLICATION NUMBER: US 07/787, 567
 FILING DATE: 04-Nov-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70, P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 247 amino acids

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Page 3

Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;
QY 9 THQGTGEYFREFITLADYVSSGS-FSNEIPL-RGSTITPVSADQRFVLELWQODSI 66
DB 13 TAGATVQSYTNFIRAVGRGLTGADVHHEIPYLPNVEGLPILN--GRFIVELSNHAEISV 70
QY 67 TAAIDVTNAYVVAQAGDSIFLR-DAPKAAE--THLFTGTDRSSLPFGSTIDLEKY 123
DB 71 TAAIDVTNAYVVAQAGDSIFLR-DAPKAAE--THLFTGTDRSSLPFGSTIDLEKY 129
QY 124 AGH-RDQIPGIBOLIOSVSLRY--PGSTRQAQASITLILQWISBAAPNPILMYR 179
DB 130 AGH-RDQIPGIBOLIOSVSLRY--PGSTRQAQASITLILQWISBAAPNPILMYR 189
QY 180 QDINSGESFLPDWYMLEETISWQGSQVQVHSTGVFNNPFLAISTGNFTLSNVSAT 239
DB 190 TRLRNRSAPDPVSITLNSWRLSTAIQESNCAFPASPIQLOHNSKRSFVDSVILI 249
QY 240 ASIAITMFLVCGERRSS 255
DB 250 PIIAMVYRCAPPPSS 265

RESULT 5
US-10-127-890-1
Sequence 1, Application US/10127890
Publication No. US20030166136A1
GENERAL INFORMATION
APPLICANT: Chynoll, Stephen F.
INVENTOR: Shudnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Xcandrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 2002-05-21
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/777-9158
TELEFAX: 312/777-9158
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-127-890-1
Query Match
Best Local Similarity 40.2%; Pred. No. 1,35-33;
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;
QY 9 THQGTGEYFREFITLADYVSSGS-FSNEIPL-RGSTITPVSADQRFVLELWQODSI 66
DB 13 TAGATVQSYTNFIRAVGRGLTGADVHHEIPYLPNVEGLPILN--GRFIVELSNHAEISV 70
QY 67 TAAIDVTNAYVVAQAGDSIFLR-DAPKAAE--THLFTGTDRSSLPFGSTIDLEKY 123
DB 71 TAAIDVTNAYVVAQAGDSIFLR-DAPKAAE--THLFTGTDRSSLPFGSTIDLEKY 129
QY 124 AGH-RDQIPGIBOLIOSVSLRY--PGSTRQAQASITLILQWISBAAPNPILMYR 179
DB 130 AGH-RDQIPGIBOLIOSVSLRY--PGSTRQAQASITLILQWISBAAPNPILMYR 189
QY 180 QDINSGESFLPDWYMLEETISWQGSQVQVHSTGVFNNPFLAISTGNFTLSNVSAT 239
DB 190 TRLRNRSAPDPVSITLNSWRLSTAIQESNCAFPASPIQLOHNSKRSFVDSVILI 249
QY 240 ASIAITMFLVCGERRSS 255
DB 250 PIIAMVYRCAPPPSS 265

RESULT 6
US-10-083-336A-1
Sequence 1, Application US/10083336A
Publication No. US20030181659A1
GENERAL INFORMATION
APPLICANT: Mark A
INVENTOR: Mark A
APPLICANT: Byrne, Michael P
APPLICANT: Mannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P6745200 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 576
TYPE: PPT
ORGANISM: Ricinus communis
US-10-083-336A-1
Query Match
Best Local Similarity 30.5%; Score 396; DB 12; Length 576;
Best Local Similarity 40.2%; Pred. No. 4,1e-33;
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;
QY 9 THQGTGEYFREFITLADYVSSGS-FSNEIPL-RGSTITPVSADQRFVLELWQODSI 66
DB 13 TAGATVQSYTNFIRAVGRGLTGADVHHEIPYLPNVEGLPILN--GRFIVELSNHAEISV 105
QY 67 TAAIDVTNAYVVAQAGDSIFLR-DAPKAAE--THLFTGTDRSSLPFGSTIDLEKY 123
DB 106 TAAIDVTNAYVVAQAGDSIFLR-DAPKAAE--THLFTGTDRSSLPFGSTIDLEKY 164
QY 124 AGH-RDQIPGIBOLIOSVSLRY--PGSTRQAQASITLILQWISBAAPNPILMYR 179
DB 165 AGH-RDQIPGIBOLIOSVSLRY--PGSTRQAQASITLILQWISBAAPNPILMYR 224
QY 180 QDINSGESFLPDWYMLEETISWQGSQVQVHSTGVFNNPFLAISTGNFTLSNVSAT 239
DB 225 TRIVYRSAPDPVSITLNSWRLSTAIQESNCAFPASPIQLOHNSKRSFVDSVILI 264

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QY 121 ERVAGHRDIPGTEGIGTSGVSAALRYPGSTRAQASIIILIKMISPAAPFPIIARRQ 180
DB 119 ERVAGHRDIPGTEGIGTSGVSAALRYPGSTRAQASIIILIKMISPAAPFPIIARRQ 178
QY 181 DINSGBELPDYVWMLLETSGGQSTVOYQSTIDGVNPNPFLAISTGNFVTLNVSQVIA 240
DB 179 YINSGBELPDYVWMLLETSGGQSTVOYQSTIDGVNPNPFLAISTGNFVTLNVSQVIA 238
QY 241 SLAIMEFVCGERP 254
DB 239 SLAIMEFVCGERP 252

RESULT 2
US-09-347-064-2
Sequence 2, Application US/09347064A
Patent No. US20020045208A1

GENERAL INFORMATION:
APPLICANT: Beck, Jürgen
APPLICANT: Schmidt, Arno
APPLICANT: Zinke, Holger
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-inactivating Proteins of the mistletoe viscum
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347, 064A
EARLIER FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
SEQ ID NO 2
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-2

Query Match 90.1%; Score 1170; DB 9; Length 252;
Best Local Similarity 91.7%; Pred. No. 8, 8e-116;
Matches 232; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 YERILRVTHOTTGDEFRFIIILADYVSSGSSNVEPIILROSTTIVSDAQRVYELRN 60
DB 2 YERILRVTHOTTGDEFRFIIILADYVSSGSSNVEPIILROSTTIVSDAQRVYELRN 61
QY 61 OGGSITAIIDVTNAYVVAOAGQSYFLRDAFGAETHLFGTTRDSI.PPTGSYTDI 120
DB 62 OGGSITAIIDVTNAYVVAOAGQSYFLRDAFGAETHLFGTTRDSI.PPTGSYTDI 119
QY 121 ERVAGHRDIPGTEGIGTSGVSAALRYPGSTRAQASIIILIKMISPAAPFPIIARRQ 180
DB 120 ERVAGHRDIPGTEGIGTSGVSAALRYPGSTRAQASIIILIKMISPAAPFPIIARRQ 179
QY 181 DINSGBELPDYVWMLLETSGGQSTVOYQSTIDGVNPNPFLAISTGNFVTLNVSQVIA 240
DB 180 YINSGBELPDYVWMLLETSGGQSTVOYQSTIDGVNPNPFLAISTGNFVTLNVSQVIA 239
QY 241 SLAIMEFVCGERP 253
DB 240 SLAIMEFVCGERP 252

RESULT 3
US-10-282-935-3
Sequence 1, Application US/10282935
Patent No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.

QY 9 THOTGDEFRFIIILADYVSSGSSNVEPIILROSTTIVSDAQRVYELRN 60
DB 9 THOTGDEFRFIIILADYVSSGSSNVEPIILROSTTIVSDAQRVYELRN 61
QY 69 AIDVTNAYVVAOAGQSYFLRDAFGAETHLFGTTRDSI.PPTGSYTDIERYAGH-R 127
DB 67 GIDVTNAYVVAOAGQSYFLRDAFGAETHLFGTTRDSI.PPTGSYTDIERYAGH-R 124
QY 128 DQIPGIGTSGVSAALRYPGSTRAQASIIILIKMISPAAPFPIIARRQ 187
DB 125 DQIPGIGTSGVSAALRYPGSTRAQASIIILIKMISPAAPFPIIARRQ 184
QY 188 FLDPYVWMLLETSGGQSTVOYQSTIDGVNPNPFLAISTGNFVTLNVSQVIA 240
DB 186 FQDPAAMISLENNMDLSRGVQSYVOTFPNG-----VTLINRREYIVDSLSH 234
QY 238 -VIAIAIMLFVC 249
DB 235 PIVAVIALMLFVC 247

US-10-282-935-3
Sequence 1, Application US/10282935
Patent No. US20030143193A1

GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACIOUS COMPOUNDS
FILE REFERENCE: US/10/282, 935
CURRENT APPLICATION NUMBER: US/10/282, 935
EARLIER FILING DATE: 2002-10-29
EARLIER APPLICATION NUMBER: 09/538, 873
EARLIER FILING DATE: 2000-03-30
EARLIER APPLICATION NUMBER: 60/126, 826
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
SEQ ID NO 2
TYPE: PRT
ORGANISM: Abirus precatorius
US-10-282-935-3

Query Match 36.5%; Score 474; DB 12; Length 251;
Best Local Similarity 49.1%; Pred. No. 6, 5e-42;
Matches 109; Conservative 37; Mismatches 81; Indels 26; Gaps 6;
QY 9 THOTGDEFRFIIILADYVSSGSSNVEPIILROSTTIVSDAQRVYELRN 60
DB 9 THOTGDEFRFIIILADYVSSGSSNVEPIILROSTTIVSDAQRVYELRN 61
QY 69 AIDVTNAYVVAOAGQSYFLRDAFGAETHLFGTTRDSI.PPTGSYTDIERYAGH-R 127
DB 67 GIDVTNAYVVAOAGQSYFLRDAFGAETHLFGTTRDSI.PPTGSYTDIERYAGH-R 124
QY 128 DQIPGIGTSGVSAALRYPGSTRAQASIIILIKMISPAAPFPIIARRQ 187
DB 125 DQIPGIGTSGVSAALRYPGSTRAQASIIILIKMISPAAPFPIIARRQ 184
QY 188 FLDPYVWMLLETSGGQSTVOYQSTIDGVNPNPFLAISTGNFVTLNVSQVIA 240
DB 186 FQDPAAMISLENNMDLSRGVQSYVOTFPNG-----VTLINRREYIVDSLSH 234
QY 238 -VIAIAIMLFVC 249
DB 235 PIVAVIALMLFVC 247

RESULT 4
US-10-282-935-1
Sequence 1, Application US/10282935
Patent No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACIOUS COMPOUNDS
FILE REFERENCE: US/10/282, 935
CURRENT APPLICATION NUMBER: US/10/282, 935
EARLIER FILING DATE: 2002-10-29
EARLIER APPLICATION NUMBER: 09/538, 873
EARLIER FILING DATE: 2000-03-30
EARLIER APPLICATION NUMBER: 60/126, 826
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
SEQ ID NO 2
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-282-935-1

Query Match 30.5%; Score 396; DB 12; Length 267;
Best Local Similarity 40.2%; Pred. No. 1, 3e-33;

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Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 14:01:14 ; Search time 16.4973 Seconds
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Title: US-09-601-667C-38
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Sequence: 1 YERILRLVHTQGTGDEYFRF.....SVTASIALMLFVCGERSSS 256

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications A1:
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Result Query #
No. Score Match Length DB ID Description

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3	1170	90.1	252	9	US-10-127-890-1	Sequence 3, Appl1
4	336	30.5	257	12	US-10-127-890-1	Sequence 1, Appl1
5	336	30.5	257	12	US-10-127-890-1	Sequence 1, Appl1
6	336	30.5	257	12	US-10-127-890-1	Sequence 1, Appl1
7	339	25.3	247	10	US-09-792-793A-39	Sequence 39, Appl1
8	339	25.3	247	12	US-10-375-209A-39	Sequence 6, Appl1
9	337	25.2	247	12	US-10-127-890-6	Sequence 4, Appl1
10	332	24.8	289	12	US-10-280-679B-4	Sequence 4, Appl1
11	314	24.2	263	10	US-10-127-890-4	Sequence 4, Appl1
12	303.5	23.4	247	12	US-10-375-209A-34	Sequence 34, Appl1
13	303.5	23.4	247	12	US-10-375-209A-34	Sequence 11, Appl1
14	293.7	22.7	231	12	US-10-127-890-111	Sequence 102, Appl1
15	290.5	22.4	231	12	US-10-127-890-102	Sequence 102, Appl1

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16 285 22.0 251 12 US-10-127-890-7 Sequence 7, Appl1

17 285.5 22.0 251 12 US-10-127-890-101 Sequence 101, Appl1

18 285.5 22.0 251 12 US-10-127-890-110 Sequence 110, Appl1

19 284.5 21.9 251 12 US-10-127-890-99 Sequence 99, Appl1

20 282.5 21.7 251 12 US-10-127-890-100 Sequence 100, Appl1

21 282.5 21.7 251 12 US-10-127-890-105 Sequence 105, Appl1

22 282.5 21.7 251 12 US-10-127-890-106 Sequence 106, Appl1

23 282.5 21.7 251 12 US-10-127-890-107 Sequence 107, Appl1

24 282.5 21.7 251 12 US-10-127-890-108 Sequence 108, Appl1

25 282.5 21.7 251 12 US-10-127-890-109 Sequence 109, Appl1

26 282.5 21.7 251 12 US-10-127-890-110 Sequence 110, Appl1

27 281.5 21.7 251 12 US-10-127-890-2 Sequence 2, Appl1

28 281.5 21.7 251 12 US-10-127-890-103 Sequence 103, Appl1

29 281.5 21.7 251 12 US-10-127-890-106 Sequence 106, Appl1

30 281.5 21.7 251 12 US-10-127-890-108 Sequence 108, Appl1

31 281.5 21.7 251 12 US-10-127-890-109 Sequence 109, Appl1

32 281.5 21.7 251 12 US-10-127-890-110 Sequence 110, Appl1

33 280.5 21.6 251 12 US-10-127-890-105 Sequence 105, Appl1

34 280.5 21.6 251 12 US-10-127-890-106 Sequence 106, Appl1

35 278.5 21.4 251 12 US-10-127-890-107 Sequence 107, Appl1

36 278.5 21.4 251 12 US-09-765-527-259 Sequence 259, Appl1

37 278.5 21.4 309 9 US-09-765-527-253 Sequence 253, Appl1

38 278.5 21.4 332 9 US-09-765-527-251 Sequence 251, Appl1

39 268.5 20.7 185 12 US-10-083-336A-9 Sequence 9, Appl1

40 260 20.0 188 12 US-10-083-336A-4 Sequence 4, Appl1

41 260 20.0 188 12 US-10-083-336A-8 Sequence 8, Appl1

42 260 20.0 189 12 US-10-083-336A-6 Sequence 6, Appl1

43 260 20.0 190 12 US-10-083-336A-11 Sequence 11, Appl1

44 247.5 19.1 250 12 US-09-792-793A-36 Sequence 36, Appl1

45 247.5 19.1 250 12 US-10-127-890-8 Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-09-347-064-8
Sequence 8, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: SCA, Quigen
INVENTOR: SCA, Quigen
APPLICANT: SCA, Quigen
TITLE OF INVENTION: Recombinant Fusion Proteins of the miltelce Visum
TITLE OF INVENTION: Ribosome Inactivating Proteins of the miltelce Visum
FILE REFERENCE: 09282-5
CURRENT FILING DATE: US/09/347, 064A
EARLIER FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: SE 97 10 0012.0
NUMBER OF SEQ. IDS: 197-01-02
SOFTWARE: PatentIn Ver. 2.1
SEQ. ID NO 8
LENGTH: 252
TYPE: PRT
ORIGIN: Visum album
US-09-347-064-8
Query Match 90.4%; Score 1174; DB 9; Length 252;
Best Local Similarity 91.7%; Pctg. No. 3,36-116;
Matches 231; Conservative 1; Mismatches 12; Indels 2; Gaps 1;
1 YERILRLVHTQGTGDEYFRFILLADYSSGSFENRILPLRGSTIPUSPAGFVLYELN 60
DB 1 YERILRLVHTQGTGDEYFRFILLADYSSGSFENRILPLRGSTIPUSPAGFVLYELN 60
CY 1 YERILRLVHTQGTGDEYFRFILLADYSSGSFENRILPLRGSTIPUSPAGFVLYELN 60
CY 61 CQGDSDIRALIDVNAVVAQADDSYFRLDPAGAFHFLFTGTRRSLAPFGSYTDL 120
DB 61 CQGDSDIRALIDVNAVVAQADDSYFRLDPAGAFHFLFTGTRRSLAPFGSYTDL 120

Thu Dec 11 16:09:51 2003

us-09-601-667c-38.rag

Page 10

FT	Misc-difference	141	/label= Asp, Glu
FT	Misc-difference	141	/label= Ser, Thr
FT	Misc-difference	145	/label=
FT	Misc-difference	145	/label= Phe, Tyr
FT	Misc-difference	152	/label= Thr, Ala
FT	Misc-difference	157	/label= Ala, Tyr
FT	Misc-difference	150	/label= Tyr, Asp
FT	Misc-difference	168	/label= Ala, Glu
FT	Misc-difference	191	/label= Val, Met
FT	Misc-difference	219	/label= Val, Phe
FT	Misc-difference	224	/label= Pro, Ser
FT	Misc-difference	225	/label= Pro, Ser
FT	Misc-difference	232	/label= Thr, Ser
FT	Misc-difference	236	/label= Asp, Ser
FT	Misc-difference	236	/label= Asp, Ser
XX	DE19604210-41.		
XX	12-AUG-1999.		
XX	03-FEB-1998;	98DE-1004210.	
XX	03-FEB-1998;	98DE-1004210.	
XX	(BIOS-) BIOSYN ARZNEIMITTEL GMBH.		
XX	Morris P, Stiefel T, Voelter W, Welters P;		
XX	WPI; 1999-445335/38.		
DR	Preparation of mistletoe lectin in heterologous systems,		
PT	particularly for use as anticancer agents and immunostimulants		
XX	Claim 41; Page 39; 76pp; German.		
XX	This invention describes a novel mistletoe lectin (I) and its fragments		
XX	CC which have antitumor and immunostimulatory activity. The A-chain (MLA)		
XX	CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of		
XX	CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and its		
XX	CC lymphokine-producing macrophages, so stimulate immunity. (I) and its		
XX	CC fragments are used to treat immunosuppressed cells (particularly		
XX	CC cancer) and if the lectin is modified, the length of the		
XX	CC immune response, particularly to a co-administered antigen		
XX	CC (tumor-associated, bacterial or viral). The method allows production of		
XX	CC mistletoe lectin, and its individual chains, in many different isoforms		
XX	CC and on a large scale, at any time of the year. Recombinant products are		
XX	CC free from toxins present in natural mistletoe extracts. This sequence		
XX	CC represents a consensus sequence of the mistletoe lectin A chain (MLA)		
XX	CC described in the invention.		
XX	Sequence	255 AA;	
OY	Query Match	90.2%; Score 1171.5; DB 20; Length 255;	
OY	Best Local Similarity	91.8%; Pred. No. 1.5e-113;	
OY	Matches 235; Conservativity	0; Mismatches 20; Indels 1; Gaps 1	
DB	1 YERLHNTHTGCTGTXEFPFILLTDVSSGSPNEPLAGSTPIPDAGAFVULBN	60	
DB	1 YERLHNTHTGCTGTXEFPFILLTDVSSGSPNEPLAGSTPIPDAGAFVULBN	60	
OY	61 QGQDSIDTADVTAAVYVYVQADQSYELNDPFGCAETLPTGTRDSSGLPFGSYTL	120	
OY	61 QGQDSKTXALDVTXKVAVYVQADQSYELNDPFGCAETLPTGTRDSSGLPFGSYTL	120	
DB	61 QGQDSKTXALDVTXKVAVYVQADQSYELNDPFGCAETLPTGTRDSSGLPFGSYTL	120	

```

Qy 12 BEVAGHROIPJGIEBOJOSVSLMYFGOSTRAOASTILLIOMISAAFRNILLMRRO 180
Db 120 EKHGKSTPFGJLJLQJLXKXKXGOSTRAOASTILLIOMISAAFRNILLMRKQ 179
Qy 181 HINGKSTPDMWJLZELMSGOGOSTOHSSTOQVNNPRLALSTQVNTTLANRESVTA 240
Db 180 XHNGKXSTLZPDYMLZELMSGOGOSTOHSSTOQVNNPRLALXKXGFTLANRKAFTA 239
Qy 241 STALMLFYCGERPSSS 236
Db 240 STALMLFYCGERPSSS 235

```

XX Mistletoe lectin A chain MIA consensus protein sequence 2.
 XX
 XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KW ribosome; 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform.
 XX
 XX viscum album.
 OS
 FH Key Location/Qualifiers
 FH MISC-difference 15 /label= Asp, Glu
 FT MISC-difference 63 /label= Gly, Gln
 FT MISC-difference 66 /label= Ile, Val
 FT MISC-difference 75 /label= Leu, Ala
 FT MISC-difference 107 /label= Asp, Arg, none
 FT MISC-difference 113 /label= Asn, Thr
 FT MISC-difference 117 /label= Ala, Tyr
 FT MISC-difference 130 /label= Pro, Thr
 FT MISC-difference 133 /label= Asp, Glu
 FT MISC-difference 141 /label= Ser, Thr
 FT MISC-difference 145 /label= Phe, Tyr
 FT MISC-difference 152 /label= Thr, Ala
 FT MISC-difference 177 /label= Ala, Tyr
 FT MISC-difference 190 /label= Tyr, Asp
 FT MISC-difference 185 /label= Ala, Glu
 FT MISC-difference 191 /label= Val, Met
 FT MISC-difference 219 /label= Ile, Phe
 FT MISC-difference 224 /label= Phe, Ser
 FT MISC-difference 225 /label= Pro, Thr
 FT MISC-difference 232 /label= Thr, Ser
 FT MISC-difference 236 /label= Asp, Ser
 FT
 PN DE19804210-A1.
 XX
 XX 12-AUG-1999.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIOS-) BIOSYN ARANIMITTEL GMBH.
 XX
 XX Morris P, Sciefel T, Voelter W, Welters P.
 PI
 XX WPI; 1999-44535/38.
 DR
 XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 5; Page 30; 78pp; German.
 PS
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)

CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly of
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC (I) in a recombinant form, and its use in many different isoforms
 CC and on a large scale at any stage of chain elongation. Products are
 CC free from toxins present in natural mistletoe extract. (I) is
 CC described in the invention.
 XX
 XX Sequence 255 AA;
 SQ
 Query Match 90.24; Score 1171.5; DB 20; Length 255;
 Best Local Similarity 91.84; Pred. No. 1.5e-113;
 Matches 235; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
 QY 1 VERLRARPTHTQGTGKPRFTILRRVYSSGSPNRIELARQSTIVSDAQRVYVLEIN 60
 DB 1 VERLRARPTHTQGTGKPRFTILRRVYSSGSPNRIELARQSTIVSDAQRVYVLEIN 60
 QY 61 QGQDSITRAIDVNAVYVAVQKQDQYFLDAPRQAEITLFTGTDRSSIPPTGSYTDL 120
 DB 61 QGQDSITRAIDVNAVYVAVQKQDQYFLDAPRQAEITLFTGTDRSSIPPTGSYTDL 120
 QY 121 ERVAGRDQIPIGIEOLISVALRPGGSTRQARSLILTIOWISEARPNFIIMRYRQ 180
 DB 121 ERVAGRDQIPIGIEOLISVALRPGGSTRQARSLILTIOWISEARPNFIIMRYRQ 180
 QY 181 DINGSGSTLPPMMLFETSGQOSTQVORSTQVFNPRFALSTQNFVTLSSNRYVLA 240
 DB 181 DINGSGSTLPPMMLFETSGQOSTQVORSTQVFNPRFALSTQNFVTLSSNRYVLA 240
 QY 180 XINGKSLPDXMLELTSWQOSTQVQSTSDQVFNKXRLIXKGFILNRYVLA 239
 DB 241 SLAIIMFVCGERSSS 256
 DB 240 SLAIIMFVCGERSSS 255
 RESULT 15
 XN123977
 ID XN123977 standard; protein; 255 AA.
 AC XN123977;
 XX
 XX 18-OCT-1999 (first entry)
 DT
 DE Mistletoe lectin A chain MIA consensus protein sequence 3.
 XX
 XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KW ribosome; 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform.
 XX
 XX viscum album.
 OS
 FH Key Location/Qualifiers
 FH MISC-difference 15 /label= Asp, Glu
 FT MISC-difference 63 /label= Gly, Gln
 FT MISC-difference 66 /label= Ile, Val
 FT MISC-difference 75 /label= Leu, Ala
 FT MISC-difference 107 /label= Asp, Arg, none
 FT MISC-difference 113 /label= Asn, Thr
 FT MISC-difference 117 /label= Ala, Tyr
 FT MISC-difference 130 /label= Pro, Thr
 FT MISC-difference 141 /label= Ser, Thr
 FT MISC-difference 145 /label= Phe, Tyr
 FT MISC-difference 152 /label= Thr, Ala
 FT MISC-difference 177 /label= Ala, Tyr
 FT MISC-difference 190 /label= Tyr, Asp
 FT MISC-difference 185 /label= Ala, Glu
 FT MISC-difference 191 /label= Val, Met
 FT MISC-difference 219 /label= Ile, Phe
 FT MISC-difference 224 /label= Phe, Ser
 FT MISC-difference 225 /label= Pro, Thr
 FT MISC-difference 232 /label= Thr, Ser
 FT MISC-difference 236 /label= Asp, Ser
 FT

Db 2 YERILAVYHTQGTGERFPIITLADYVSSGSFSENFILRQSTIPVSDAQFVLELTN 61
 QY 61 QGQDSITPAIDVTNAVVAVYAGDQSYFLRDPAGAEHLPTGTTRDRSSLPFTGSYTDL 120
 Db 62 QGQDSITPAIDVTNLVVAVYAGDQSYFLRDPAGAEHLPTGTT--RSSLPFTGSYPL 119
 QY 121 ERYAGHRDQIPGIGIOLQSVSALRYPGQSTPAQASITLILQMTSEKAEFPIIMRYRQ 180
 Db 120 ERYAGHRDQIPGIGIDLIQSVLALRPQSGSTPAQASITLILQMTSEKAEFPIIMRYRQ 179
 QY 181 DINSSESLPDMYMLLETRSGQSTQVQHSIDQVFNPFILISTGNFVTSNRSVIA 240
 Db 180 YINSASLPDPMYMLLETRSGQSTQVQHSIDQVFNPFILISTGNFVTSNRSVIA 239
 QY 241 SLAIIMLVCGERS 254
 Db 240 SLAIIMLVCGERS 253

RESULT 13

AAV25971 ID AAV25971 standard; protein; 255 AA.

AAV25971;

18-OCT-1999 (first entry)

Mistletoe lectin A chain MIA consensus protein sequence 1.

Mistletoe, lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

lymphokine-producing macrophage; uncontrolled cell growth; treatment;

cancer; cytotoxicity; antigen; isoform.

viscum album.

Key

Misc-difference 15 Location/Qualifiers

FT /label= Asp, Glu

FT /label= Gly, Glu

FT /label= Ile, Val

FT /label= Leu, Ala

FT /label= Asp, Arg or none

FT /label= Asp, Thr

FT /label= Pro, Thr

FT /label= Asp, Glu

FT /label= Ser, Thr

FT /label= Phe, Tyr

FT /label= Thr, Ala

FT /label= Ala, Tyr

FT /label= Tyr, Asp

FT /label= Ala, Glu

FT /label= Val, Met

FT /label= Ile, Phe

FT /label= Pro, Ser

FT /label= Pro, Thr

FT Misc-difference 232 /label= Thr, Ser
 FT Misc-difference 236 /label= Asp, Ser
 PN DE19804210-A1.
 FD 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 PA (Bios-) BIOSYN AFZNEIMITTEL GMBH.
 PI Morris P, Stiefel T, Voelter W, Welters P.
 XX WPI; 1999-44535/38.
 DR Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX Claim 2; Page 27; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered method of production of
 CC (immune-activated) and its individual chains in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a consensus sequence of the mistletoe lectin A chain (MIA)
 CC described in the invention.

SO Sequence 255 AA;

Query Match 90.2%; Score 1171.5; DB 20; Length 255;

Best Local Similarity 91.8%; From NCBI 128-113; Gaps 1;

Matches 235; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 YERILAVYHTQGTGERFPIITLADYVSSGSFSENFILRQSTIPVSDAQFVLELTN 60

Db 1 QGQDSITPAIDVTNAVVAVYAGDQSYFLRDPAGAEHLPTGTTRDRSSLPFTGSYTDL 120

QY 61 QGQDSITPAIDVTNAVVAVYAGDQSYFLRDPAGAEHLPTGTTRDRSSLPFTGSYTDL 120

Db 62 QGQDSITPAIDVTNLVVAVYAGDQSYFLRDPAGAEHLPTGTT--RSSLPFTGSYPL 119

QY 121 ERYAGHRDQIPGIGIOLQSVSALRYPGQSTPAQASITLILQMTSEKAEFPIIMRYRQ 180

Db 120 ERYAGHRDQIPGIGIDLIQSVLALRPQSGSTPAQASITLILQMTSEKAEFPIIMRYRQ 179

QY 181 DINSSESLPDMYMLLETRSGQSTQVQHSIDQVFNPFILISTGNFVTSNRSVIA 240

Db 180 YINSASLPDPMYMLLETRSGQSTQVQHSIDQVFNPFILISTGNFVTSNRSVIA 239

QY 241 SLAIIMLVCGERS 254

Db 240 SLAIIMLVCGERS 253

RESULT 14

AAV25971 ID AAV25971 standard; protein; 255 AA.

AAV25971;

18-OCT-1999 (first entry)

QY 1 YERLRVHTQTTGDEYFRFTLLRDVYSSGSFSNEIPALROSTIPVSDAKRFVVELTN 60
 DB 1 YERLRVHTQTTGDEYFRFTLLRDVYSSGSFSNEIPALROSTIPVSDAKRFVVELTN 60
 QY 61 QGQDSITPAIDVTNAYVAAYQADQSYFLDAPRAATHTFTTRDSSLPFGSYTL 120
 DB 61 QGQDSITPAIDVTNAYVAAYQADQSYFLDAPRAATHTFTTRDSSLPFGSYTL 118
 QY 121 ERYAGHRDQIPLGIEQLIOSVSAIRYPGSGSTRQAQSGILLIQMISEARFNPILMRQ 180
 DB 119 ERYAGHRDQIPLGIDQLIOSVTAIRPFGSGSTRQAQSGILLIQMISEARFNPILMRQ 178
 QY 181 DINGSESTPEDMVLEETSMGQOSTOVQSHTDGVNPFELAISTGNFVLISVRSVTA 240
 DB 179 YINSGASTPEDMVLEETSMGQOSTOVQSHTDGVNPFELAISTGNFVLISVRSVTA 238
 QY 241 SLAIMEFVCGRRS 254
 DB 239 SLAIMEFVCGRRS 252

RESULT 11

ID AAM10022 standard; Protein; 253 AA.
 XX AAM10022;

DT 18-DEC-1997 (first entry)
 DE Prepro mistletoe lectin A chain.

XX Mistletoe; lectin; cytotoxic; A chain; B chain; dimer.
 XX Viscum album.

XX EP/51221-A1.
 XX 02-JAN-1997.

XX 26-JUN-1995; 95EP-0105945.
 XX 26-JUN-1995; 95EP-0105945.

XX (MADU) MADUUS KOELEN AG.
 XX Baur A, Eck J, Lentzen H, Zinke H;

XX WPI; 1997-054678/06.
 XX N-PSDB; AAT70474.

XX Nucleic acid encoding pre-pro form of mistletoe lectin - for
 XX therapeutic or diagnostic use

XX Claim 12; Fig 4A; 30pp; German.
 XX Mistletoe lectin is a cytotoxic agent that has been used for tumour
 XX therapy. It can be used in immunotoxins and medicaments. Nucleic
 XX acid fragments can be used in diagnostic methods. Mistletoe lectin (

XX CC AAT70473) comprises an A chain (AAT70474) and a B chain (AAT70475).
 XX Sequence 253 AA;

XX Query Match 90.4%; Score 1174; DB 18; Length 253;
 XX Best Local Similarity 91.7%; Pred. No. 8, 1e-114;
 XX Matches 233; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 YERLRVHTQTTGDEYFRFTLLRDVYSSGSFSNEIPALROSTIPVSDAKRFVVELTN 60
 DB 2 YERLRVHTQTTGDEYFRFTLLRDVYSSGSFSNEIPALROSTIPVSDAKRFVVELTN 61
 QY 61 QGQDSITPAIDVTNAYVAAYQADQSYFLDAPRAATHTFTTRDSSLPFGSYTL 120
 DB 62 QGQDSITPAIDVTNAYVAAYQADQSYFLDAPRAATHTFTTRDSSLPFGSYTL 119

QY 121 ERYAGHRDQIPLGIEQLIOSVSAIRYPGSGSTRQAQSGILLIQMISEARFNPILMRQ 180
 DB 120 ERYAGHRDQIPLGIDQLIOSVTAIRPFGSGSTRQAQSGILLIQMISEARFNPILMRQ 179
 QY 181 DINGSESTPEDMVLEETSMGQOSTOVQSHTDGVNPFELAISTGNFVLISVRSVTA 240
 DB 180 YINSGASTPEDMVLEETSMGQOSTOVQSHTDGVNPFELAISTGNFVLISVRSVTA 239
 QY 241 SLAIMEFVCGRRS 254
 DB 240 SLAIMEFVCGRRS 253

RESULT 12

ID AAM90125 standard; Protein; 253 AA.
 XX AAM90125;

DT 20-MAR-2003 (updated)
 DT 30-APR-1999 (first entry)

XX Mistletoe ML A-chain protein.
 XX M; mistletoe; lectin; ML; A-chain; transgenic plant; glycosylation;
 XX dimer; immunotoxin; large-scale production; diagnosis; therapeutic;
 XX cancer.

XX Viscum album.
 XX EP884388-A1.

XX 16-DEC-1998.
 XX 26-JUN-1995; 98EP-0105660.

XX 26-JUN-1995; 95EP-0105945.
 XX 26-JUN-1995; 98EP-0105660.

XX (MADU) MADUUS KOELEN AG.
 XX Baur A, Eck J, Lentzen H, Zinke H;

XX WPI; 1993-026582/03.
 XX N-PSDB; AAT74180.

XX New transgenic plant expressing mistletoe lectin - useful for
 XX producing recombinant lectin in e.g. cancer diagnosis and therapy

XX Disclosure; Fig 4a; 30pp; German.
 XX This invention describes a novel transgenic plant transformed with a
 XX vector capable of encoding a mistletoe (Viscum album) lectin
 XX also describes a polypeptide produced by a plant where the polypeptide
 XX exhibits at least one enzymatic modification other than the glycosylation
 XX that occurs in Viscum album or the polypeptide is a fusion protein, a
 XX mistletoe lectin polypeptide dimer and an immunotoxin comprising the
 XX polypeptide or the polypeptide dimer. The plants are used for large-scale
 XX production of mistletoe lectin for diagnostic or therapeutic purposes
 XX (e.g. in cancer therapy). This sequence represents the mistletoe lectin
 XX A-chain which is contained in expression vector pTMAA.
 XX (Updated on 20-MAR-2003 to correct PF field.)

XX Query Match 90.4%; Score 1174; DB 20; Length 253;
 XX Best Local Similarity 91.7%; Pred. No. 8, 1e-114;
 XX Matches 233; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 YERLRVHTQTTGDEYFRFTLLRDVYSSGSFSNEIPALROSTIPVSDAKRFVVELTN 60
 DB 1 YERLRVHTQTTGDEYFRFTLLRDVYSSGSFSNEIPALROSTIPVSDAKRFVVELTN 60

ID AAY25982 standard; Protein: 532 AA.
 XX
 AC AAY25982;
 XX
 XX 18-OCT-1999 (first entry)
 XX
 DE Mistletoe lectin I (variant) protein fragment.
 XX
 KM Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
 KM ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KM cancer; cytotoxicity; antigen; isoform; lectin I.
 OS
 XX Viscum album.
 XX DRI9804210-A1.
 XX
 XX 12-AUG-1999.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 XX Morris P, Stiefel T, Voelter W, Walters P,
 XX WPI: 1999-44535/39.
 XX N-PSDB; AA209106.
 XX
 PT Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 PS Disclosure; Fig 4B; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (ALA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) stimulate immunity (I) and its
 CC fragments possess the ability to stimulate cell growth (particularly
 CC in lymphokine-producing macrophages) to treat uncontrolled cell growth (cancers)
 CC and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin I protein variant.
 XX
 XX Sequence 532 AA;
 SQ
 Query Match 91.1%; Score 1184; DB 20; Length 532;
 Best Local Similarity 92.2%; Pred. No. 2,2e-114;
 Matches 236; Conservative 6; Mismatches 12; Indels 2; Gaps 1;
 QY 1 YERLRLRVHQTGGYERFRLTLADYVSSGSPSEIPLLRSGTTPVSDAGRPVLVRLN 60
 DB 1 YERLRLRVHQTGGYERFRLTLADYVSSGSPSEIPLLRSGTTPVSDAGRPVLVRLN 60
 QY 61 QGQDSTIALDVTNAYVAVVAGQSGYFRLARPGATHLPTGTTNDGSPPTGSGYTL 120
 DB 61 QGQDSTIALDVTNAYVAVVAGQSGYFRLARPGATHLPTGTTNDGSPPTGSGYTL 120
 QY 121 ERYAGHRDPIELGIELTGGVAAKYGGSTPAQRARSLILLOMISAPARFPIIMARR 180
 DB 121 ERYAGHRDPIELGIELTGGVAAKYGGSTPAQRARSLILLOMISAPARFPIIMARR 180
 QY 119 ERYAGHRDPIELGIELTGGVAAKYGGSTPAQRARSLILLOMISAPARFPIIMARR 178
 DB 119 ERYAGHRDPIELGIELTGGVAAKYGGSTPAQRARSLILLOMISAPARFPIIMARR 178
 QY 181 DINGSESLPDMTLELETSTWQOQSTVOHSTGCVANNPRLATSGNEVTLNRYSLA 240
 DB 179 YINSGASFLPDVMELETSTWQOQSTVOHSTGCVANNPRLATSGNEVTLNRYSLA 238
 QY 241 STAINLFCGGRPSSS 256
 DB 241 STAINLFCGGRPSSS 256

DB 239 STAINLFCGGRPSSS 254
 RESULT 10
 ID AAM64661
 AC AAM64661 standard; Protein: 252 AA.
 XX
 AC AAM64661;
 XX
 XX 23-OCT-1998 (first entry)
 XX
 DE Mistletoe mMLA variant protein.
 XX
 KM Lectin A-chain; mistletoe; mMLA; fusion protein; effector; cytotoxic;
 KM intracellular; processing module; protease recognition; targeting module;
 KM internalisation; treatment; disorder; cell proliferation; activation;
 KM autoimmune disease; allergy; tumour; ricin; translocation; ss.
 OS
 XX Viscum album.
 XX
 XX Key Location/Qualifiers
 XX Protein 1..252 "partial"
 XX /note="partial"
 XX
 XX NC0829540-A2.
 XX
 XX 09-JUL-1998.
 XX
 XX 02-JAN-1998; 98WO-EP00009.
 XX
 XX 02-JAN-1997; 97EP-0100012.
 XX
 XX (BRAT-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.
 XX
 XX Beck U, Schmidt A, Zinke H,
 XX WPI: 1998-138122/33.
 XX N-PSDB; AAV51343.
 XX
 PT Nucleic acid encoding fusion protein containing mistletoe lectin A
 PT chain - useful for treatment of proliferative and autoimmune
 XX diseases, allergies and tumours
 XX
 PS Disclosure; Fig 11a'; 115pp; German.
 XX
 XX This sequence encodes a variant mistletoe lectin A-chain, mMLA. This
 CC sequence can be used in the construction of a fusion protein which
 CC comprises an effector module that is cytotoxic intracellularly, a
 CC processing module covalently bonded to the effector module and
 CC containing a protease recognition sequence, and a targeting module
 CC covalently bonded to the processing module, able to bind specifically to
 CC the surface of a cell so as to mediate internalisation of the fusion
 CC protein. Such a fusion protein can be used for treating disorders
 CC involving proliferation and/or elevated tumour antigen expression
 CC in autoimmune disease, allergy and tumours. The proteins can be administered
 CC e.g. by injection or topically, for example, by intravenous injection.
 CC at a dose of 1 mg/kg body weight, or daily, for example, at 1 pg to 500 ng/ml.
 CC cell. The processing module prevents extracellular dissociation, and
 CC fusion proteins based on mistletoe lectin A-chain are far more active
 CC than those based on ricin and do have the associated problems of
 CC non-specific toxicity. The protein may be expressed in a non-glycosylated
 CC form that does not bind to sugar receptors in the liver, and which has a
 CC long half-life in the blood. Where the mistletoe lectin B-chain is used,
 CC it actively assists in translocation of the M1 A-chain from the
 CC endoplasmic reticulum to the cytoplasm.
 XX
 XX Sequence 252 AA;
 SQ
 Query Match 90.4%; Score 1174; DB 19; Length 252;
 Best Local Similarity 91.7%; Pred. No. 8.1e-114;
 Matches 233; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

KM dimer; immunotoxin; large-scale production; diagnosis; therapeutic;
 cancer.
 XX
 XX Viscum album.
 XX
 XX EP884388-A1.
 XX
 XX 16-DEC-1998.
 XX
 XX 26-JUN-1995; 98EP-0105660.
 XX
 XX 26-JUN-1995; 95EP-0109949.
 XX
 XX 26-JUN-1995; 98EP-0105660.
 XX
 XX (MADU) MADRUS KOEHLIN AG.
 XX
 XX Baur A, Eck U, Lentzen H, Zinke H,
 XX
 XX WPI: 1999-026592/03.
 XX
 XX N-PSDB; AAV74182.
 XX
 XX New transgenic plant expressing mistletoe lectin - useful for
 PT producing recombinant lectin in e.g. cancer diagnosis and therapy
 XX
 XX
 XX Claim 1a: Fig 4c; 30pp; German.
 XX
 XX This invention describes a novel transgenic plant transformed with a
 CC vector capable of expressing a mistletoe lectin (ML) protein. The
 CC recombinant protein is a biologically active fragment. The specific
 CC also describes a polypeptide produced by a plant where the polypeptide
 CC exhibits at least one enzymatic modification other than the glycosylate
 CC that occurs in Viscum album or the polypeptide is a fusion protein, a
 CC mistletoe lectin polypeptide dimer and an immunotoxin comprising the
 CC production of mistletoe lectin dimer. The plants are used for large-scale
 CC production of mistletoe lectin for diagnostic or therapeutic purposes
 CC (e.g. in cancer therapy). This sequence represents the mistletoe lectin
 CC used in the method of the invention.
 CC (Updated on 20-MAR-2003 to correct PE field.)
 XX
 XX Sequence 564 AA;
 SO
 Query Match 91.5%; Score 1188; DB 20; Length 564;
 Best Local Similarity 92.6%; Pred No 9.3e-115;
 Matches 237; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 1 YERLRARVHTGTTGDEYFRFTLLADYVSSGSFSENEIPLRSGTTPVSDAQRFVLYELTN 60
 DB 34 YERLRARVHTGTTGDEYFRFTLLADYVSSGSFSENEIPLRSGTTPVSDAQRFVLYELTN 93
 QY 61 QGDSITLADITNAYVAVAGAGDSYFLADAPGAEHLFTGTRRSSLPFGSYTDL 120
 DB 94 QGDSITLADITNAYVAVAGAGDSYFLADAPGAEHLFTGTR--RSSLPFGSYTDL 151
 QY 121 ERYAGHRDIPLEGIDIGVSAALRYPGSGTRQAQSTILLIOMISAAARNPILMYRQ 180
 DB 152 ERYAGHRDIPLEGIDIGVSAALRYPGSGTRQAQSTILLIOMISAAARNPILMYRQ 211
 QY 181 DINSGEFLPDYWMLELETSWGQSTQVGHSTDCVFNPFRLAISTGNPVLTSVASYTA 240
 DB 212 YINSASFLPDYWMLELETSWGQSTQVGHSTDCVFNPFRLAISTGNPVLTSVADVYA 271
 QY 241 SLALMLFYGGERPSSS 256
 DB 272 SLALMLFYGGERPSSS 287

RESULT 8
 AAYZ5979
 ID AAYZ5979 standard; Protein; 531 AA.
 XX
 XX AAYZ5979;
 XX
 XX 18-OCT-1999 (first entry)

XX
 XX Mistletoe lectin I protein fragment.
 XX
 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MUA; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoforn; lectin I.
 XX
 XX Viscum album.
 XX
 XX DE19804210-A1.
 XX
 XX 12-AUG-1999.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIO8-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 XX Morris P, Stiefel T, Woelfel W, Woelfers P,
 XX
 XX WPI: 1999-445336/38.
 XX
 XX N-PSDB; AAZ09103.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 XX
 XX Claim 7: Fig 1b; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MUA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a mistletoe lectin I protein fragment.
 XX
 XX Sequence 531 AA;
 SO
 Query Match 91.1%; Score 1184; DB 20; Length 531;
 Best Local Similarity 92.2%; Pred. No. 2.2e-114;
 Matches 236; Conservative 6; Mismatches 12; Indels 2; Gaps 1;

QY 1 YERLRARVHTGTTGDEYFRFTLLADYVSSGSFSENEIPLRSGTTPVSDAQRFVLYELTN 60
 DB 1 YERLRARVHTGTTGDEYFRFTLLADYVSSGSFSENEIPLRSGTTPVSDAQRFVLYELTN 60
 QY 61 QGDSITLADITNAYVAVAGAGDSYFLADAPGAEHLFTGTRRSSLPFGSYTDL 120
 DB 61 QGDSITLADITNAYVAVAGAGDSYFLADAPGAEHLFTGTR--RSSLPFGSYTDL 118
 QY 121 ERYAGHRDIPLEGIDIGVSAALRYPGSGTRQAQSTILLIOMISAAARNPILMYRQ 180
 DB 119 ERYAGHRDIPLEGIDIGVSAALRYPGSGTRQAQSTILLIOMISAAARNPILMYRQ 178
 QY 181 DINSGEFLPDYWMLELETSWGQSTQVGHSTDCVFNPFRLAISTGNPVLTSVASYTA 240
 DB 179 YINSASFLPDYWMLELETSWGQSTQVGHSTDCVFNPFRLAISTGNPVLTSVADVYA 238
 QY 241 SLALMLFYGGERPSSS 256
 DB 239 SLALMLFYGGERPSSS 254

RESULT 9
 AAYZ5982

XX 03-FEB-1998; 98DB-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX MPI; 1999-445335/38.
 XX N-PSDB; AA209104.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 2b, 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The 286 subunit of
 CC of the mistletoe lectin binds to, and inactivates, the 286 subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of the mistletoe lectin A1 protein.
 XX
 SQ Sequence 254 AA;
 Query Match 92.7%; Score 1204; DB 20; Length 254;
 Best Local Similarity 93.0%; Pred. No. 6.1e-117;
 Matches 238; Conservative 7; Mismatches 9; Indels 2; Gaps 1;
 QY 1 YERLRARVHQTDEYPRFTLLADVYSSGSFSENEIPLRQSTIPVSDQRFLVVELTN 60
 DB 1 YERLRARVHQTDEYPRFTLLADVYSSGSFSENEIPLRQSTIPVSDQRFLVVELTN 60
 QY 61 QGDSITRAIDVTNAVVAQAGQSYFLRDPAGAEHLFTGTRDRSGLPFVGSYDL 120
 DB 61 QGDSITRAIDVTNAVVAQAGQSYFLRDPAGAEHLFTGTRDRSGLPFVGSYDL 120
 QY 61 QGDSITRAIDVTNAVVAQAGQSYFLRDPAGAEHLFTGTRDRSGLPFVGSYDL 118
 DB 61 QGDSITRAIDVTNAVVAQAGQSYFLRDPAGAEHLFTGTRDRSGLPFVGSYDL 118
 QY 121 ERYAGHRDQIPGLIGIQLQSVSALRYPGSGSTRAQASILLIOMISEAARFPIIMRYQ 180
 DB 121 ERYAGHRDQIPGLIGIQLQSVSALRYPGSGSTRAQASILLIOMISEAARFPIIMRYQ 180
 QY 119 ERYAGHRDQIPGLIGIQLQSVSALRYPGSGSTRAQASILLIOMISEAARFPIIMRYQ 178
 DB 119 ERYAGHRDQIPGLIGIQLQSVSALRYPGSGSTRAQASILLIOMISEAARFPIIMRYQ 178
 QY 181 DINGSEFLPDYVMELETSMQGSQTOYGHSTGVNRPFLAISTGNPVLLSNVASYA 240
 DB 181 DINGSEFLPDYVMELETSMQGSQTOYGHSTGVNRPFLAISTGNPVLLSNVASYA 240
 QY 179 YNSGASFLPDYVMELETSMQGSQTOYGHSTGVNRPFLAISTGNPVLLSNVASYA 238
 DB 179 YNSGASFLPDYVMELETSMQGSQTOYGHSTGVNRPFLAISTGNPVLLSNVASYA 238
 QY 241 SLATMLFVCGRRPSSS 256
 DB 241 SLATMLFVCGRRPSSS 254
 DB 239 SLATMLFVCGRRPSSS 254
 RESULT 4
 AA25983
 ID AA25983 standard; Protein; 254 AA.
 XX AA25983;
 XX
 XX 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin A1 (variant) protein fragment.
 XX
 XX Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
 XX ribosome 286 subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform; lectin A1.
 XX
 XX Viscum album.

PN DE19804210-A1.
 XX
 XX 12-AUG-1999.
 XX
 XX 03-FEB-1998; 98DB-1004210.
 XX
 XX 03-FEB-1998; 98DB-1004210.
 XX
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX MPI; 1999-445335/38.
 XX N-PSDB; AA209107.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 5b; 78pp; German.
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 286 subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin A1 protein variant.
 XX
 SQ Sequence 254 AA;
 Query Match 92.7%; Score 1204; DB 20; Length 254;
 Best Local Similarity 93.0%; Pred. No. 6.1e-117;
 Matches 238; Conservative 7; Mismatches 9; Indels 2; Gaps 1;
 QY 1 YERLRARVHQTDEYPRFTLLADVYSSGSFSENEIPLRQSTIPVSDQRFLVVELTN 60
 DB 1 YERLRARVHQTDEYPRFTLLADVYSSGSFSENEIPLRQSTIPVSDQRFLVVELTN 60
 QY 61 QGDSITRAIDVTNAVVAQAGQSYFLRDPAGAEHLFTGTRDRSGLPFVGSYDL 120
 DB 61 QGDSITRAIDVTNAVVAQAGQSYFLRDPAGAEHLFTGTRDRSGLPFVGSYDL 120
 QY 61 QGDSITRAIDVTNAVVAQAGQSYFLRDPAGAEHLFTGTRDRSGLPFVGSYDL 118
 DB 61 QGDSITRAIDVTNAVVAQAGQSYFLRDPAGAEHLFTGTRDRSGLPFVGSYDL 118
 QY 121 ERYAGHRDQIPGLIGIQLQSVSALRYPGSGSTRAQASILLIOMISEAARFPIIMRYQ 180
 DB 121 ERYAGHRDQIPGLIGIQLQSVSALRYPGSGSTRAQASILLIOMISEAARFPIIMRYQ 180
 QY 119 ERYAGHRDQIPGLIGIQLQSVSALRYPGSGSTRAQASILLIOMISEAARFPIIMRYQ 178
 DB 119 ERYAGHRDQIPGLIGIQLQSVSALRYPGSGSTRAQASILLIOMISEAARFPIIMRYQ 178
 QY 181 DINGSEFLPDYVMELETSMQGSQTOYGHSTGVNRPFLAISTGNPVLLSNVASYA 240
 DB 181 DINGSEFLPDYVMELETSMQGSQTOYGHSTGVNRPFLAISTGNPVLLSNVASYA 240
 QY 179 YNSGASFLPDYVMELETSMQGSQTOYGHSTGVNRPFLAISTGNPVLLSNVASYA 238
 DB 179 YNSGASFLPDYVMELETSMQGSQTOYGHSTGVNRPFLAISTGNPVLLSNVASYA 238
 QY 241 SLATMLFVCGRRPSSS 256
 DB 241 SLATMLFVCGRRPSSS 254
 DB 239 SLATMLFVCGRRPSSS 254
 RESULT 5
 AB279450
 ID AB279450 standard; Protein; 551 AA.
 XX AB279450;
 XX
 XX 08-JUL-2002 (first entry)
 XX
 XX Galactose-recognising mistletoe lectin.
 XX
 XX Mistletoe; galactose-recognising mistletoe lectin; MIII.

PI Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 8; Fig 3B; 78pp; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to, and activates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of the mistletoe lectin A2 protein.
 XX
 SQ Sequence 256 Aa;

Query Match 100.0%; Score 1299; DB 20; Length 256;
 Best Local Similarity 100.0%; Pred. No. 7,76-127;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YERLRVHTQTGDEYFRFTLLRDYVSSGSFSENIPLRQSTIPVSDAQRFVLYELTN 60
 Db 1 YERLRVHTQTGDEYFRFTLLRDYVSSGSFSENIPLRQSTIPVSDAQRFVLYELTN 60
 Oy 61 QGDSITPAIDVNAVVAQGDQSYFLDAPGAEHTLFTGTRRDSLPFGSYTDL 120
 Db 61 QGDSITPAIDVNAVVAQGDQSYFLDAPGAEHTLFTGTRRDSLPFGSYTDL 120
 Oy 121 ERYAGHDDIPIGIEQLIOSVSLAPYGSGTRQAASILLIOMISAPRNPILMKRYQ 180
 Db 121 ERYAGHDDIPIGIEQLIOSVSLAPYGSGTRQAASILLIOMISAPRNPILMKRYQ 180
 Oy 181 DINGGSEFLPDWMLLETSMGQSTOVQHSIDVNNPFLAISTGNVTLISNRSVYA 240
 Db 181 DINGGSEFLPDWMLLETSMGQSTOVQHSIDVNNPFLAISTGNVTLISNRSVYA 240
 Oy 241 SLAIPLFCGERPSS 256
 Db 241 SLAIPLFCGERPSS 256

RESULT 2
 AAY25984
 ID AAY25984 standard; Protein; 256 Aa.

XX AAY25984;

DT 18-OCT-1999 (first entry)

XX Mistletoe lectin A2 (variant) protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin A2.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

PF 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

PA (BIOOS-) BIOSYN ARZNEIMITTEL GMBH.

PI Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI: 1999-445335/38.
 DR N-PSDB; A4209108.
 XX
 CC Preparation of mistletoe lectins in heterologous systems,
 CC particularly for use as anticancer agents and immunostimulants
 XX
 XX Disclosure; Fig 6B; 78pp; German.

CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin A2 protein variant.

SQ Sequence 256 Aa;

Query Match 100.0%; Score 1299; DB 20; Length 256;
 Best Local Similarity 100.0%; Pred. No. 7,76-127;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YERLRVHTQTGDEYFRFTLLRDYVSSGSFSENIPLRQSTIPVSDAQRFVLYELTN 60
 Db 1 YERLRVHTQTGDEYFRFTLLRDYVSSGSFSENIPLRQSTIPVSDAQRFVLYELTN 60
 Oy 61 QGDSITPAIDVNAVVAQGDQSYFLDAPGAEHTLFTGTRRDSLPFGSYTDL 120
 Db 61 QGDSITPAIDVNAVVAQGDQSYFLDAPGAEHTLFTGTRRDSLPFGSYTDL 120
 Oy 121 ERYAGHDDIPIGIEQLIOSVSLAPYGSGTRQAASILLIOMISAPRNPILMKRYQ 180
 Db 121 ERYAGHDDIPIGIEQLIOSVSLAPYGSGTRQAASILLIOMISAPRNPILMKRYQ 180
 Oy 181 DINGGSEFLPDWMLLETSMGQSTOVQHSIDVNNPFLAISTGNVTLISNRSVYA 240
 Db 181 DINGGSEFLPDWMLLETSMGQSTOVQHSIDVNNPFLAISTGNVTLISNRSVYA 240
 Oy 241 SLAIPLFCGERPSS 256
 Db 241 SLAIPLFCGERPSS 256

RESULT 3
 AAY25980
 ID AAY25980 standard; Protein; 254 Aa.

XX AAY25980;

DT 18-OCT-1999 (first entry)

XX Mistletoe lectin A1 protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin A1.

XX Viscum album.

PN DE19804210-A1.

XX 12-AUG-1999.

PF 03-FEB-1998; 98DE-1004210.

Thu Dec 11 16:09:51 2003

us-09-601-667c-38.rag

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 25.2959 Seconds
(without alignments)
1606.345 Million cell updates/sec

Title: US-09-601-667C-38

Perfect score: 1299
Sequence: 1 YKRLRLVYHQTGDBYERF.....SVIASLALFVCGEPSSS 256

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 110763 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 110763

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: A_Geneseq_19jun03.*

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15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1299	100.0	256	AA25981	Mistletoe lectin A
2	1299	100.0	256	AA25984	Mistletoe lectin A
3	1204	92.7	254	AA25980	Mistletoe lectin A
4	1204	92.7	254	AA25983	Mistletoe lectin A
5	1202	92.5	551	ABR79450	Galactose-recognition
6	1188	91.5	564	AA110021	Prepro mistletoe I
7	1188	91.5	564	AAW90127	Mistletoe lectin P
8	1184	91.1	531	AA25979	Mistletoe lectin I
9	1184	91.1	532	AA25982	Mistletoe lectin I

10	1174	90.4	253	AA64661	Mistletoe rMLA var
11	1174	90.4	253	AA10022	Prepro mistletoe I
12	1174	90.4	253	AAW90125	Mistletoe Mt. A-cha
13	1171.5	90.2	255	AA25971	Mistletoe lectin A
14	1171.5	90.2	255	AA25974	Mistletoe lectin A
15	1171.5	90.2	253	AA25977	Mistletoe lectin A
16	1171.5	90.2	253	AA25979	Mistletoe lectin P
17	1171.5	90.2	533	AA25973	Mistletoe lectin P
18	1171.5	90.2	533	AA25976	Mistletoe lectin P
19	1170	90.1	253	AAW64659	Mistletoe rMLA pro
20	1142	87.9	254	AAW47090	A-chain isoform fo
21	1110	85.5	254	AAW47091	A-chain isoform fo
22	1039	80.0	256	AAW47092	A-chain isoform fo
23	650	50.0	174	AAW47097	Korean mistletoe I
24	474	35.5	251	AAW1287	Amino acid sequenc
25	466.5	35.9	250	AAW25137	Abstin A-A-chain xl
26	466.5	35.9	250	AAW21700	Recombinant abstin
27	466.5	35.9	252	AAW81376	Recombinant abstin
28	454	35.3	253	AAW81378	Recombinant abstin
29	452	34.8	253	AAW81378	Recombinant abstin
30	396	30.5	267	AAW37290	Ricin A chain (P1C1)
31	396	30.5	267	AAW37290	Ricin A chain (P1C1)
32	396	30.5	267	AAW37290	Ricin A chain (P1C1)
33	396	30.5	267	AAW37290	Ricin A chain (P1C1)
34	396	30.5	267	AAW37290	Ricin A chain (P1C1)
35	396	30.5	332	AAW70838	Sequence of Ricinu
36	396	30.5	332	AAW70838	Sequence of Ricinu
37	396	30.5	332	AAW70838	Sequence of Ricinu
38	396	30.5	332	AAW70838	Sequence of Ricinu
39	396	30.5	332	AAW70838	Sequence of Ricinu
40	396	30.5	332	AAW70838	Sequence of Ricinu
41	396	30.5	574	AAW70126	Sequence of Ricinu
42	396	30.5	574	AAW70126	Sequence of Ricinu
43	396	30.5	574	AAW70126	Sequence of Ricinu
44	396	30.5	574	AAW70126	Sequence of Ricinu
45	396	30.5	574	AAW70126	Sequence of Ricinu

ALIGNMENTS

RESULT 1	AA25981	AA25981
ID	AA25981	AA25981
AC	AA25981	AA25981
DT	18-OCT-1999	(first entry)
DE	Mistletoe lectin A2 protein fragment.	
KM	Mistletoe, lectin, antitumor; immunostimulant; A-chain; ML; immunity;	
KW	enzymic 268 substrate; non-cytotoxic; T-cell activation; immune response;	
KW	lymphokine-producing macrophages; uncontrolled cell growth; treatment;	
KW	cancer; cytotoxicity; antigen; isoform; lectin A2.	
OS	Vaccum album.	
XX	DE19804210-A1.	
XX	12-AUG-1999.	
XX	03-FEB-1998.	98DE-1004210.
XX	03-FEB-1998.	98DE-1004210.
XX	(BIOS-) BIOSYN ARZNEIMITTEL GMBH.	
XX	Morris P., Stiefel T., Woelker W., Woelker P.	
XX	WPI; 1999-445335/38.	
XX	N-PSDB; AA209105.	

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QY	9	THQTTGDEYFEFTLLADYVSSGSPNEIPILRO-STIPVSDAORFVVELTNOGDS-I	66
DB	40	TKRATYTSYTOFIELALQASGEFHGIDPVRERSTVP--DSKRFIVELSNWADSEV	97
QY	67	TAIDVTNAYVVAQAGDOSYELR-DAPRGATTH/LFTGTEDRSSLPFTGSYTDLERVAG	125
DB	98	TLAVDTNAYVVAFTGOSOFLEEDNDPALENLAPDT--KRYTFPSGSYTDLEGVAG	155
QY	126	HRDQPIGIEQLIOSVSNLRYG-GSTRQGRSIIILQWISBAAPNFIARQODIN	183
DB	156	ERKEHLDGMDPLENKLISNINNOGRALRSIIIVLQWYHAYRFRFIEYRGSIS	215
QY	184	SGESFLPDMNLELETSNQQOSTQVGHSTD-GVNNPFLAISTGNVYLSNVS--VIAS	241
DB	216	RAWFRPDPALENNNGALSNAVQCSNCGVFPSSVELNSISNRPYVGSVDRIYISG	275
QY	242	LATMLPVC--GESPSS	255
DB	276	LATMLFICRSTDRASS	291

Search completed: December 11, 2003, 14:01:05
CDB time : 20.732 secs

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DR PRINTS: F800396; SHHGAPRCIN.
DR SMART: SMO0488; RICIN. 2.
DR PROSITE: PS02031; RICIN_B_LECTIN. 2.
KM Hydrolase; Toxin.
FT NON TER
SQ SEQUENCE 549 AA: 60648 MW: 02607EB670CA44B0 CRO64;
Query Match 34.7%; Score 450.5; DB 10; Length 549;
Beech Local Similarity 45.38% (2); Mismatches 85; Indels 13; Gaps 10.
Matches 110; Conservative 42;
QY 5 THQDQDPEPTITLTPYSGSENFELPLAQ-STIPSGDQRYVRLVETQCOOS-1-66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 TKAQTKSYVQFLTALNQLAQAGSEPHGIPVMEKSTYF-DKSRFLIVELSMVAADSPV 65
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 TLAIDVTNAYVYVYVQAGSGSYLA-DAPQAGAEVHFLFTGTRRSGSLPFGYSYDLEFRAA 125
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 TLAVDVTNAYVYVYVYRTSGSEFLIEENDPDPALENLPDT-KRYTFPFGSSYTDLEGVAC 123
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Dd		124 ERREILLLOMPDEVALSALMISMLNOOHALASLIVVIMQVAARFEEYKRGSGIS 183
Cy	184	SOSEFLPDWNYLELTSGGOSTOVGHSTD-GYFNPNRLAISTGNPTLASNR-VTAS 241
Dd	184	RNFHFRPDMALIKRMSLSNNVOOSGVIFSHSLINKEPVAVSSVDRIASC 243
Cy	242	LAIHLFPVC--GEPPSS 255 :: :: :: ::
Dd	244	LAIHLFPCTSDTLASS 259 :: ::
RESULT 15		
O94BW5		
ID	PRELIMINARY:	PRT; 581 AA.
AC	O94BW5;	
DT	01-BEC-2001 (TEMBLel. 19, Created)	
DT	01-BEC-2001 (TEMBLel. 19, Last sequence update)	
DT	01-BEC-2001 (TEMBLel. 19, Last annotation update)	
DB	Type 2 ribosomal activating factor from cinnamon I precursor	
DB	(EC 3.2.2.22) (rRNA N-glycosidase)	
CS	Cinnamomum camphora (Camphor tree).	
CS	Cinnamomum camphora (Camphor tree).	
CS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	

RN [1] "SEQUENCE FROM N.A.
 RP Yang Q., Gong Z.Z., Liu M.Y. ;
 RA "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinnamomyn proteins and study of their expression
 RT patterns."
 RC Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC 1- CATALYTIC ACTIVITY: ENDORIBONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC 1- SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC EMBL: F00339P000725625.1; GI: 15674361.1
 DR Interpro: IPRO01574; RIP_1_lectin.
 DR Pfam: PF00652; Ricin I_lectin; 5.
 DR Pfam: PF00652; Ricin I_lectin; 5.
 DR PRINTS: PR003966; SHIGARICIN.
 DR SMART: SMO0458; RICIN; 2.
 DR PROSITE: PS02031; RICIN B LECTIN; 2.
 KW Hydrolase; signal; Toxin.
 FT SIGNAL
 FT CHAIN 1 581
 FT 33
 FT 32
 FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CINNAMOMYN I
 FT SEQUENCE 561 AA; 64215 MW; 65875595B3D196 CRC64;
 FT SQ
 Query Match 34.6%; Score 449.5; DB 10; Length 561;
 Query Identical Similarity 45.3%; E-Value No. = e-36;
 Matches 116; Conservative 41; Mismatches 86; Indels 13; Gaps 10.

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[illegible]

DT	01-VAR-203 (TREMblrel. 23, Last annotation update)	
DT	Type 2 ribosome-inactivating protein cinnaomom III precursor	
DT	(EC 3.2.2.22) (RNA N-glycosidase).	
OS	Cinnamomum camphora (Camphor tree).	
CS	Bakayarte, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;	
RT	Chlorophyta; Charophyta; Equisetum; Liliopsida; Magnoliopsida; Nymphaeales; Laurales; Lauraceae; Cinnamomum.	
NCBI	NCBI_TaxId=13429;	
PN	SEQUENCE FROM N.A.	
PN	Yang Q., Gong Z.Z., Liu W.Y.;	
RT	"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)	
RT	genes encoding cinnamomom proteins and study of their expression	
RT	patterns."	
RL	Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.	
CC	-1- CRYSTALLINE ACTIVITY OF ANTIHISTONIC OR OF THE N-GLYCOSIDIC BOND AT ONE	
CC	-1- SPECIFICALLY ADDRESSING THE PROBLEM OF THE 8S RIBOSOME INACTIVATING PROTEIN FAMILY.	
DR	EMBL: AY039803; AKS22460.1; -	
DR	InterPro: IPR000772; RICH_B_Lectin.	
DR	InterPro: IPR00572; RICH_B_Lectin; 6.	
DR	Pfam: PF00161; RIP; 1.	
DR	Pfam: PF00386; SHIGAICIN.	
DR	SMART: SM00458; RICH_N; 2.	
DR	PROSITE: PS00231; RICH_N_LECTIN; 2.	
FT	REGION: 1-32	
FT	STANDARD: 32	
FT	CHAIN	
FT	33	
FT	580	
FT	SEQUENCE	
FT	580 AA; 64421; Mw: 9401050.75; B558 CEC64;	
FT	Query Match	
FT	Best Local Similarity	
FT	Matches 117; Conservative 41; Mismatches 85; Indels 13; Gaps 10	
QY	9	
QY	40	
QY	98	
QY	126	
QY	156	
QY	184	
QY	216	
QY	242	
QY	276	
QY	304	
QY	332	
QY	360	
QY	388	
QY	416	
QY	444	
QY	472	
QY	500	
QY	528	
QY	556	
QY	584	
QY	612	
QY	640	
QY	668	
QY	696	
QY	724	
QY	752	
QY	780	
QY	808	
QY	836	
QY	864	
QY	892	
QY	920	
QY	948	
QY	976	
QY	1004	
QY	1032	
QY	1060	
QY	1088	
QY	1116	
QY	1144	
QY	1172	
QY	1200	
QY	1228	
QY	1256	
QY	1284	
QY	1312	
QY	1340	
QY	1368	
QY	1396	
QY	1424	
QY	1452	
QY	1480	
QY	1508	
QY	1536	
QY	1564	
QY	1592	
QY	1620	
QY	1648	
QY	1676	
QY	1704	
QY	1732	
QY	1760	
QY	1788	
QY	1816	
QY	1844	
QY	1872	
QY	1900	
QY	1928	
QY	1956	
QY	1984	
QY	2012	
QY	2040	
QY	2068	
QY	2096	
QY	2124	
QY	2152	
QY	2180	
QY	2208	
QY	2236	
QY	2264	
QY	2292	
QY	2320	
QY	2348	
QY	2376	
QY	2404	
QY	2432	
QY	2460	
QY	2488	
QY	2516	
QY	2544	
QY	2572	
QY	2600	
QY	2628	
QY	2656	
QY	2684	
QY	2712	
QY	2740	
QY	2768	
QY	2796	
QY	2824	
QY	2852	
QY	2880	
QY	2908	
QY	2936	
QY	2964	
QY	2992	
QY	3020	
QY	3048	
QY	3076	
QY	3104	
QY	3132	
QY	3160	
QY	3188	
QY	3216	
QY	32	

Dt	01-NOV-1998	(TRIMBLrel. 08, Last sequence update)
Dt	01-DEC-2001	(TRIMBLrel. 19, Last annotation update)
Dt	Abxin B	(RRNA N-glycosidase) (BC 3.2.2.22) [fragment]. RIP.
Gn	Abxus precatorius	(Indian licorice) (Crab's eye)
Oc	Abxus precatorius	(Crab's eye) (Crab's eye), Tracheophyta;
Oc	Sphenacantha	(Green sea slug) (Mollusca), Mollusca;
Oc	Sphenacantha	Mammillophyta, eudicotyledons; core eudicots; Rosidae;
Ox	eurosidis I	Fabaceae, Fabaceae; Papilionoideae; Aereae; Abxus. NCBI_TextID=3816;
Rn	[1]	
Rp	SEQUENCE FROM N.A.	
Rp	TISSUE=LEAF;	
Rc	MEDLINE=91201329; PubMed=2016300;	
Rc	Brensen G., Mathiesen A., Sundan A.;	
Rt	"Direct molecular cloning and expression of two distinct abxin A-	
Rt	Chains"; Chem. 266:6648-6652(1991).	
Cc	-1 FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN	
Cc	SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 6OS RIBOMMAL	
Cc	SUBUNITS BY REMOVING ALDEHYDE FROM POSITION 4,324 OF 26 S RRNA.	
Cc	ABXIN-A IS MORE TOXIC THAN RICIN.	
Cc	-1 FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT	
Cc	FACILITATES THE BINDING OF ABXIN TO THE CELL MEMBRANE THAT	
Cc	PREDICES ENDOCYTOSIS.	
Cc	-1 CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE	
Cc	TERMINUS OF AN N-GLYCAN.	
Cc	-1 SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.	
Cc	-1 DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN	
Cc	CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).	
Cc	-1 SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING	
Cc	PROTEINS. BELONGS TO TYPE 2 RIP.	
Dr	EMBL; X54872; CA38654.1; .	
Dr	HSSP; P1140; 1ABR.	
Dr	InterPro; IPR01574; RIP.	
Dr	Pfam; PF00161; RIP; A.RIPIN	
Dr	Rfam; RF00275; SHRNA_SICIN.	
Dr	Rfam; RF00275; SHRNA_SICIN. 1.	
Kw	Hydrolase, Glycosidase, Toxin, Repeat, Glycoprotein, Lectin,	
FT	CHAIN 1	
FT	NON TER	252
SO	SEQUENCE	253 AA; 28305 MW; BBFC846B9E92B5DE CMC64;
Query Match	35.6%; Score 462; DB 10; Length 252;	
Best Local Similarity	44.9%; Pred. No. 4.8e-36;	
Matches 10%	Conservative 36; Mismatches 96; Indels 6; Gaps 5	
Db	9 THGTCGGCCTTATTAAGYAGSGGSNSNEIFLPGSTPIPSDAQAPAVLTETOCQGSTA 68	
Db	10 TEGASGSKQPTLAIRRL-RKGHHDPVLAPDF-CYERNRRITVELSNSRSSTIEV 67	
Qy	69 AIDVNNVVAAOAGGQGYTFADAPAGAEHLFFGTGRDSSEPTGSDYLEEVAGH-R 127	
Qy	68 GIDVNNVVAAARGSQGYTFADAPASAYTLFGT--ORYSLRDQSVDGLEEMAHQR 125	
Db	126 FQSPGLIGTOLSVSAALPPGSTRQAORSLIILQMTSEAENPLMKRYKODINSGES 187	
Qy	126 FQSPGLIGTOLSVSAALPPGSTRQAORSLIILQMTSEAENPLMKRYKODINSGES 185	
Qy	188 FLDDPVYLLETLSNGGQGYTGSDGVANNPPG-TASTGNPYLTSANRVASVIAAIL 246	
Db	186 FQDDPMALSIENNKMILSRGVQESTVQDTPFNVLTERANNOPYVDSITHGVVALTML 245	
Qy	247 FVC 249	
Db	246 FVC 248	
RESULT 12		
Q94BM3	PRELIMINARY; PRT; 580 AA.	
Q94BM3		
Ac	Q94BM3	
Jt	01-DEC-2001	(TRIMBLrel. 19, Created)
Jt	01-DEC-2001	(TRIMBLrel. 19, Last sequence update)

DT	01-VAR-203 (TREMblrel. 23, Last annotation update)	
DT	Type 2 ribosome-inactivating protein cinnaomom III precursor	
DT	(EC 3.2.2.22) (RNA N-glycosidase).	
OS	Cinnamomum camphora (Camphor tree).	
CS	Bakayarte, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;	
RT	Chlorophyta; Charophyta; Equisetum; Liliopsida; Magnoliopsida; Nymphaeales; Laurales; Lauraceae; Cinnamomum.	
NCBI	NCBI_TaxId=13429;	
PN	SEQUENCE FROM N.A.	
PN	Yang Q., Gong Z.Z., Liu W.Y.;	
RT	"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)	
RT	genes encoding cinnamomom proteins and study of their expression	
RT	patterns."	
RL	Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.	
CC	-1- CRYSTALLINE ACTIVITY OF ANTIHISTONIC OR OF THE N-GLYCOSIDIC BOND AT ONE	
CC	SPECIFICALLY ADDRESSING THE PROBLEM OF THE 8S RIBOSOME INACTIVATING PROTEIN FAMILY.	
DR	EMBL: AY039803; AKS22460.1; -	
DR	InterPro: IPR000772; RICH_B_Lectin.	
DR	InterPro: IPR00572; RICH_B_Lectin; 6.	
DR	Pfam: PF00161; RIP; 1.	
DR	PRINTS: PR00386; SHIGACIN.	
DR	SMART: SM00458; RICH_N; 2.	
DR	PROSITE: PS00231; RICH_N_LECTIN; 2.	
FT	REGION: 1-32	
FT	STON1	
FT	CHAIN	
FT	33	
FT	580	
FT	SEQUENCE	
FT	580 AA; 64421; Mw; 9401050.75B58 CRC64;	
FT	Query Match	
FT	Best Local Similarity	
FT	Matches 117; Conservative 41; Mismatches 85; Indels 13; Gaps 10	
QY	9	
DB	40	
QY	67	
DB	98	
QY	126	
DB	156	
QY	184	
DB	216	
QY	242	
DB	276	
QY	291	
QY	325	
DB	355	
QY	385	
DB	415	
QY	445	
DB	475	
QY	505	
DB	535	
QY	565	
DB	595	
QY	625	
DB	655	
QY	685	
DB	715	
QY	745	
DB	775	
QY	805	
DB	835	
QY	865	
DB	895	
QY	925	
DB	955	
QY	985	
DB	1015	
QY	1045	
DB	1075	
QY	1105	
DB	1135	
QY	1165	
DB	1195	
QY	1225	
DB	1255	
QY	1285	
DB	1315	
QY	1345	
DB	1375	
QY	1405	
DB	1435	
QY	1465	
DB	1495	
QY	1525	
DB	1555	
QY	1585	
DB	1615	
QY	1645	
DB	1675	
QY	1705	
DB	1735	
QY	1765	
DB	1795	
QY	1825	
DB	1855	
QY	1885	
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QY	1945	
DB	1975	
QY	2005	
DB	2035	
QY	2065	
DB	2095	
QY	2125	
DB	2155	
QY	2185	
DB	2215	
QY	2245	
DB	2275	
QY	2305	
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DB	2395	
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QY	2965	
DB	2995	
QY	3025	
DB	3055	
QY	3085	
DB	3115	
QY	3145	
DB	3175	
QY	3205	
DB	3235	
QY	3265	
DB	3295	
QY	3325	
DB	3355	
QY	3385	
DB	3415	
QY	3445	
DB	3475	

QY 9 THQTTGDEYFFETTLADYSSSSPANEPLLRSGTTPVSDAQRFVLVETLNOQDQSTTA 68
DB 9 TEGATSSQYKQFTEALREK-REGALHIDIPVLPDPT-TLQERNRYITVELSNSTESIEV 66
QY 69 AIDVTNAYVVAQAGDSYFLRNDAPRGAEHLFTGTTDRSSLPFGSYTDLERYAGH-R 127
DB 67 GIDVTNAYVVAQAGDSYFLRNDAPRGAEHLFTGTTDRSSLPFGSYTDLERYAGH-R 124
QY 128 DOIPLGIEQLQSVSALRPGQSTPAQARSLILQMSBAARFNPILMRKODINSSES 187
DB 125 QOILPLGQLQTHGISFFRSGNDMEKARTLIVILQWVAALAFRIYSNRVYSIQGTA 184
QY 188 FLPPNMYALETSWQSQSTVQVHSTDGVNPNPRLAISTGNFTVLSNVS----- 237
DB 185 FQPDANMISTENNNDLSNRQVDSVQDTFPNQ-----VLTININEPVIYDLSLH 234
QY 238 -VITASLAIMLFCV 249
DB 235 PTVAVALMLFCV 247

RESULT 9

Q96237 PRELIMINARY; PRT; 251 AA.
ID Q96237
AC Q96237; (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
PCGNAC-1-E164/R167 protein (EC 3.2.2.22) (RNA N-glycosidase)
DE (Fragment).
CC Abrus precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OX NCBI_TaxId=3816;
RN 11
RS SEQUENCE FROM N.A.
RC TISSUE=Seed.
RX MEDLINE=94139756; PubMed=8307038;
RA Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
RT "Cloning and expression of three abrin A-chains and their mutants
derived by site-specific mutagenesis in Escherichia coli.",
RL Eur. J. Biochem. 219:83-87(1994).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR HSRP_P11140; IABR.
DR HSRP_P11140; IABR.
DR PFAM:PF00161; RIF.
DR PRINTS: PR00396; SHIGARICIN.
KW Hydrolase; Toxin.
FT NON_TER 1
FT NON_TER 251
SQ SEQUENCE 251 AA; 28055 MW; 6F6475CDEAFB79 CRC64;

Query Match

Best Local Similarity 43.1%; Score 473; DB 10; Length 251;
Matches 109; Conservative 37; Mismatches 81; Indels 26; Gaps 6;

QY 9 THQTTGDEYFFETTLADYSSSSPANEPLLRSGTTPVSDAQRFVLVETLNOQDQSTTA 68
DB 9 TEGATSSQYKQFTEALREK-REGALHIDIPVLPDPT-TLQERNRYITVELSNSTESIEV 66
QY 69 AIDVTNAYVVAQAGDSYFLRNDAPRGAEHLFTGTTDRSSLPFGSYTDLERYAGH-R 127
DB 67 GIDVTNAYVVAQAGDSYFLRNDAPRGAEHLFTGTTDRSSLPFGSYTDLERYAGH-R 124
QY 128 DOIPLGIEQLQSVSALRPGQSTPAQARSLILQMSBAARFNPILMRKODINSSES 187
DB 125 QOILPLGQLQTHGISFFRSGNDMEKARTLIVILQWVAALAFRIYSNRVYSIQGTA 184
QY 188 FLPPNMYALETSWQSQSTVQVHSTDGVNPNPRLAISTGNFTVLSNVS----- 237
DB 235 PTVAVALMLFCV 247

DB 185 FQPDANMISTENNNDLSNRQVDSVQDTFPNQ-----VLTININEPVIYDLSLH 234
QY 238 -VITASLAIMLFCV 249
DB 235 PTVAVALMLFCV 247

RESULT 10

Q96235 PRELIMINARY; PRT; 251 AA.
ID Q96235
AC Q96235;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
PCGNAC-1-E164/R167 (EC 3.2.2.22) (RNA N-glycosidase)
DE (Fragment).
CC Abrus precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OX NCBI_TaxId=3816;
RN 11
RS SEQUENCE FROM N.A.
RC TISSUE=Seed.
RX MEDLINE=94139756; PubMed=8307038;
RA Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
RT "Cloning and expression of three abrin A-chains and their mutants
derived by site-specific mutagenesis in Escherichia coli.",
RL Eur. J. Biochem. 219:83-87(1994).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR HSRP_P11140; IABR.
DR HSRP_P11140; IABR.
DR PFAM:PF00161; RIF.
DR PRINTS: PR00396; SHIGARICIN.
KW Hydrolase; Toxin.
FT NON_TER 1
FT NON_TER 251
SQ SEQUENCE 251 AA; 27997 MW; 3B60351839AEFBE7E CRC64;

Query Match

Best Local Similarity 42.7%; Score 467; DB 10; Length 251;
Matches 108; Conservative 37; Mismatches 82; Indels 26; Gaps 6;

QY 9 THQTTGDEYFFETTLADYSSSSPANEPLLRSGTTPVSDAQRFVLVETLNOQDQSTTA 68
DB 9 TEGATSSQYKQFTEALREK-REGALHIDIPVLPDPT-TLQERNRYITVELSNSTESIEV 66
QY 69 AIDVTNAYVVAQAGDSYFLRNDAPRGAEHLFTGTTDRSSLPFGSYTDLERYAGH-R 127
DB 67 GIDVTNAYVVAQAGDSYFLRNDAPRGAEHLFTGTTDRSSLPFGSYTDLERYAGH-R 124
QY 128 DOIPLGIEQLQSVSALRPGQSTPAQARSLILQMSBAARFNPILMRKODINSSES 187
DB 125 QOILPLGQLQTHGISFFRSGNDMEKARTLIVILQWVAALAFRIYSNRVYSIQGTA 184
QY 188 FLPPNMYALETSWQSQSTVQVHSTDGVNPNPRLAISTGNFTVLSNVS----- 237
DB 185 FQPDANMISTENNNDLSNRQVDSVQDTFPNQ-----VLTININEPVIYDLSLH 234
QY 238 -VITASLAIMLFCV 249
DB 235 PTVAVALMLFCV 247

RESULT 11
ID Q98760 PRELIMINARY; PRT; 255 AA.
AC Q98760;
DT 01-NOV-1998 (TREMBLrel. 08, Created)

RA Do M.-S., Song S.K.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL, AF508916; AM46934.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00275; SHIGARICIN.
 DR KX Glycosidase; Toxin.
 KY Hydrolase; Toxin.
 FT NON TER 251
 FT NON TER 251
 SQ SEQUENCE 251 AA; 28090 MW; A1177489012B989 CRC64;
 Query Match 79.1%; Score 1027; DB 10; Length 251;
 Best Local Similarity 84.1%; Pred. No. 2,7e-90;
 Matches 212; Conservative 9; Mismatches 25; Indels 6; Gaps 3;
 DB 1 YERLNLVHTQTDSEYFRFTLLADVVSSGSPSENEIFLRQSTIPVSDAOPVLVELTN 60
 QY 1 YERLNLVHTQTDSEYFRFTLLADVVSSGSPSENEIFLRQSTIPVSDAOPVLVELTN 60
 DB 1 YERLNLVHTQTDSEYFRFTLLADVVSSGSPSENEIFLRQSTIPVSDAOPVLVELTN 59
 QY 61 C---GGDSITAIIDVTAAVYVAGQSGSYFLADPQATPETHFTGTGTDSSIPRTGTY 117
 DB 60 QLGKWDSTIAIDVTNLVYVAYVAGQSGSYFLADPQATPETHFTGTGTDSSIPRTGTY 117
 QY 118 TDLERYAGRDQIFLGIEQLGVSAALRYPGSGSTRQAQSTILLIOMISEAARFETLMR 177
 DB 118 ADLERYAGRDQIFLGIEQLGVSAALRYPGSGSTRQAQSTILLIOMISEAARFETLMR 177
 QY 178 YRODINGSGSELPDQVTLMELETSNGQSGTQVQSHDTGVFNPPRLAISTGNFVTLGNRS 237
 DB 178 ARQYINSGVSLPDVTLMELETSNGQSGTQVQSHDTGVFNPPRLAISTGNFVTLGNRS 237
 QY 238 VTSALATMLPVC 249
 DB 238 VTSALATMLPVC 249
 QY 238 VTSALATMLPVC 249
 DB 238 VTSALATMLPVC 249
 RESULT 7
 Q38761 PRELIMINARY; PRT; 252 AA.
 AC Q38761; Q86234;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 02, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Ricin A-chain type 73 (EC 3.2.2.22) (RfNA N-glycosidase)
 DE (Fragment).
 GN RIP.
 OS Abrus precatorius (Indian licorice) (Crab's eye).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eutroside I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
 CX NCB1_TaxID:3816;
 RX 11-UNIQUE FROM N.A.
 RA TISSUE-Seed;
 RC TISSUE-Seed;
 RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 2-252 FROM N.A.
 RC TISSUE-Seed;
 RX MEDLINE=94139756; PubMed=8107038;
 RA Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
 RT Cloning and expression of three abrin A-chains and their mutants
 RT derived by site-specific mutagenesis in Escherichia coli.";
 RX 11-UNIQUE FROM N.A.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL, X54873; CA54855.1; -.
 DR EMBL, X76720; CA54138.1; -.
 DR HSSP; P11140; IABR.

DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00275; SHIGARICIN.
 DR PROSITE; PR00275; SHIGARICIN; 1.
 KY Glycosidase; Toxin.
 FT NON TER 252
 FT NON TER 252
 SQ SEQUENCE 252 AA; 28229 MW; 187B894E134EC5 CRC64;
 Query Match 37.0%; Score 480; DB 10; Length 252;
 Best Local Similarity 33.5%; Pred. No. 9e-30;
 Matches 110; Conservative 37; Mismatches 80; Indels 26; Gaps 6;
 DB 9 THQTGDYFRFTLLADVVSSGSPSENEIFLRQSTIPVSDAOPVLVELTNQGGDSTTA 68
 QY 9 THQTGDYFRFTLLADVVSSGSPSENEIFLRQSTIPVSDAOPVLVELTNQGGDSTTA 68
 DB 10 TQATSGSYQFETLERR-EGDLIHDPVLPDPT-TQERNRYITVELSNEDTSEIV 67
 QY 69 AIDVYAVYVAYVAGQSGSYFLADPQATPETHFTGTGTDSSIPRTGTYDLERYAGH-R 127
 DB 68 GIDVYAVYVAYVAGQSGSYFLADPQATPETHFTGTGTDSSIPRTGTYDLERYAGH-R 125
 QY 128 DQIFLGIEQLGVSAALRYPGSGSTRQAQSTILLIOMISEAARFETLMRQDINGSGS 187
 DB 126 QQLIDQQLTHGIFRSGDNDKAKKILVILQVADKRRYISMKRYVSLQVGR 185
 QY 188 FLPPMYVLELETSNGQSGTQVQSHDTGVFNPPRLAISTGNFVTLGNRS 237
 DB 186 FQPDAMTSLNNWMDNSGVQESVQDTFPCV-----VLTINIRNRPVYDLSH 235
 QY 238 -VTSALATMLPVC 249
 DB 236 FTVAVATMLPVC 248
 RESULT 8
 Q96236 PRELIMINARY; PRT; 251 AA.
 AC Q96236;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Abrin A chain (EC 3.2.2.22) (B164a) (rRNA N-glycosidase)
 DE (Fragment).
 GN PCDNAc-1-5164A.
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eutroside I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
 CX NCB1_TaxID:3816;
 RX 11-UNIQUE FROM N.A.
 RA TISSUE-Seed;
 RC TISSUE-Seed;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Seed;
 RX MEDLINE=94139756; PubMed=8107038;
 RA Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
 RT Cloning and expression of three abrin A-chains and their mutants
 RT derived by site-specific mutagenesis in Escherichia coli.";
 RX 11-UNIQUE FROM N.A.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL, X76721; CA54139.1; -.
 DR HSSP; P11140; IABR.
 RA InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00275; SHIGARICIN.
 KY Hydrolase; Toxin.
 FT NON TER 251
 FT NON TER 251
 SQ SEQUENCE 251 AA; 28040 MW; D57CB182E0ECC9 CRC64;
 Query Match 36.5%; Score 474; DB 10; Length 251;
 Best Local Similarity 43.1%; Pred. No. 3.4e-37;
 Matches 109; Conservative 37; Mismatches 81; Indels 26; Gaps 6;

DE Lectin chain A isoform 1 (EC 3.2.2.22) (tRNA N-glycosidase)
 DE (Fragment).
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 OC NCBI_TaxID=159976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21566752; PubMed=11710524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
 RT mistletoe (Viscum album coloratum).";
 RN [2]. Cells 12:215-220(2001).
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOTHEROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AF508914; AA046932.1; -
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR Hydrolase; Toxin.
 KM NON TER
 FM NON TER
 FT NON TER
 SQ SEQUENCE 254 AA; 28446 MW; 6DB5C313PAAPE20 CRC64;

Query Match 87.9%; Score 1142; DB 10; Length 254;
 Best Local Similarity 89.5%; Pred. No. 2.5e-101;
 Matches 229; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

QY 1 YERLRARVHTQGTGDEYFRTTLRLRDVSSGSPSNEIPLRQSTIVPSDAQRFVLELN 60
 DB 1 YERLRARVHTQGTGDEYFRTTLRLRDVSSGSPSNEIPLRQSTIVPSDAQRFVLELN 60
 QY 61 GGGSTLTAIDVTNAYVVAQAGQSYFLRPAQAEHLFTGTTDRSSLPPTGSYTDL 120
 DB 61 GGGSTLTAIDVTNAYVVAQAGQSYFLRPAQAEHLFTGTTDRSSLPPTGSYTDL 118
 QY 121 ERYAGRRQDPLGIGELIOVSALRYPGSGTRQAQSSILLIOWISAPARNPILMRRQ 180
 DB 119 ERYAGRRQDPLGIGELIOVSALRYPGSGTRQAQSSILLIOWISAPARNPILMRRQ 178
 QY 181 DINGSGSLPDMTLELETSWQSQSTOVQHSITDGVFNNPRLAISTGNFTLSNRSVIA 240
 DB 179 YISSGSLPDMTLELETSWQSQSTOVQHSITDGVFNNPRLAISTGNFTLSNRSVIA 238
 QY 241 SLATMFLVCGRRSSS 256
 DB 239 SLATMFLVCGRRSSS 254

RESULT 5
 QBLK05
 ID QBLK05 PRELIMINARY; PRT; 249 AA.
 AC QBLK05; (TEMPREL. 22, Created)
 DT 01-OCT-2002 (TEMPREL. 22, Last sequence update)
 DT 01-OCT-2002 (TEMPREL. 22, Last annotation update)
 DE Lectin chain A isoform 2 (EC 3.2.2.22) (tRNA N-glycosidase)
 DE (Fragment).
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 OC NCBI_TaxID=159976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,

RX MEDLINE=21566752; PubMed=11710524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
 RT mistletoe (Viscum album coloratum).";
 RN [2]. Cells 12:215-220(2001).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21566752; PubMed=11710524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOTHEROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AF508915; AA046933.1; -
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR Hydrolase; Toxin.
 KM NON TER
 FM NON TER
 FT NON TER
 SQ SEQUENCE 249 AA; 27821 MW; 3C5870F8338DBA5 CRC64;

Query Match 84.0%; Score 1091; DB 10; Length 249;
 Best Local Similarity 86.7%; Pred. No. 1.9e-96;
 Matches 216; Conservative 15; Mismatches 16; Indels 2; Gaps 1;

QY 61 GGGSTLTAIDVTNAYVVAQAGQSYFLRPAQAEHLFTGTTDRSSLPPTGSYTDL 120
 DB 61 GGGSTLTAIDVTNAYVVAQAGQSYFLRPAQAEHLFTGTTDRSSLPPTGSYTDL 118
 QY 121 ERYAGRRQDPLGIGELIOVSALRYPGSGTRQAQSSILLIOWISAPARNPILMRRQ 180
 DB 119 ERYAGRRQDPLGIGELIOVSALRYPGSGTRQAQSSILLIOWISAPARNPILMRRQ 178
 QY 181 DINGSGSLPDMTLELETSWQSQSTOVQHSITDGVFNNPRLAISTGNFTLSNRSVIA 240
 DB 179 YISSGSLPDMTLELETSWQSQSTOVQHSITDGVFNNPRLAISTGNFTLSNRSVIA 238
 QY 241 SLATMFLV 249
 DB 239 SLATMFLV 247

RESULT 6
 QBLK04
 ID QBLK04 PRELIMINARY; PRT; 251 AA.
 AC QBLK04; (TEMPREL. 22, Created)
 DT 01-OCT-2002 (TEMPREL. 22, Last sequence update)
 DT 01-OCT-2002 (TEMPREL. 22, Last annotation update)
 DE Lectin chain A isoform 3 (EC 3.2.2.22) (tRNA N-glycosidase)
 DE (Fragment).
 OS Viscum album subsp. coloratum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Viscaceae; Viscum.
 OC NCBI_TaxID=159976;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21566752; PubMed=11710524;
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
 RA Do M.-S., Song S.K.;
 RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
 RT mistletoe (Viscum album coloratum).";
 RN [2]. Cells 12:215-220(2001).
 RP SEQUENCE FROM N.A.
 RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,

QY 61 OGQDSTALADYTMVAVYVAGQDQSYVRLQAPGKATHTFPTGTTDRESSTPFGSYTDL 120
DB 61 EGQDSTALADYTMVAVYVAGQDQSYVRLQAPGKATHTFPTGTTDRESSTPFGSYTDL 118
QY 121 ERYAGHRDQIPGIGIOLQSVSLRYPGSGTAPQASILLIOMISAPARFPILMRYRQ 180
DB 119 ERYAGHRDQIPGIGIOLQSVSLRYPGSGTAPQASILLIOMISAPARFPILMRYRQ 178
QY 181 DINGSESLDPMWMLLETNSGQSTQYQCHSTQVFNPPRLAISTNNVTLANVSAYIA 240
DB 179 DINGSESLDPMWMLLETNSGQSTQYQCHSTQVFNPPRLAISTNNVTLANVSAYIA 236
QY 241 SLAINLFCVGERPSS 251
DB 239 SLAINLFCVGERPSS 249

RESULT 2
QWZ43 PRELIMINARY; PRT; 565 AA.
AC 08WZ43;
DT 01-MAR-2002 (Tremblrel, 20, Created)
DT 01-MAR-2002 (Tremblrel, 20, Last sequence update)
DT 01-OCT-2002 (Tremblrel, 22, Last annotation update)
DE VCA precursor (BC 3.2.2.22) (RNA N-glycosidase).
OS Viscum album subsp. coloratum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
NCBI_Taxid=159976;
RA SEQUENCE FROM N.A.
RA Park W.-B., Liu S.;
RT Cloning of Viscum album subsp. coloratum (Korean mistletoe).
RL Biochem. Biophys. Res. Commun. 0:0-0(2002).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DE EMBL; AF369961; AL040417.1;
DR INTERFAC; IR800072; Ricin_B_lectin.
DR Ffam; PRO0652; Ricin_B_lectin. 6.
DR PRINTS; PRO0396; SHICARICIN.
DR SMART; SMO0458; Ricin, 2.
DR PROSITE; PSS0231; Ricin_B_lectin; 2.
KW Hydrolyase; Signal; Toxin.
FT SIGNAL 22
FT CHAIN 233
FT STRAIN 233
SQ SEQUENCE 565 AA; 62401 MW; 591E399ED005F11 CRC64;

Query Match 91.5%; Score 1188; DB 10; Length 565;
Best Local Similarity 93.0%; Pred. No. 3.2e-105;
Matches 238; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

DB 272 SLAINLFCVGERPSS 287

RESULT 3
QWZ43 PRELIMINARY; PRT; 531 AA.
AC 08WZ43;
DT 01-MAR-2002 (Tremblrel, 21, Created)
DT 01-MAR-2002 (Tremblrel, 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)
DE Viscum album isoform 1 (BC 3.2.2.22) (RNA N-glycosidase)
OS Viscum album (European mistletoe).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Santalales; Viscaceae; Viscum.
NCBI_Taxid=3972;
RA SEQUENCE FROM N.A.
RA Paramastivum M., Misra V., Srivastava A., Singh T.P.;
RT Tissue-cultured.
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DE EMBL; AI061143; AL061006.1;
DR INTERFAC; IR800157; Ricin_B_lectin.
DR Ffam; PRO0652; Ricin_B_lectin. 6.
DR PRINTS; PRO0151; Ricin_B_lectin.
DR SMART; SMO0458; Ricin, 2.
DR PROSITE; PSS0231; Ricin_B_lectin; 2.
KW Hydrolyase; Toxin.
FT NON-TER 1
FT CHAIN 249
FT STRAIN 249
SQ SEQUENCE 531 AA; 58802 MW; 18244BEEF55422 CRC64;

Query Match 89.8%; Score 1166; DB 10; Length 531;
Best Local Similarity 90.6%; Pred. No. 3.8e-103;
Matches 232; Conservative 9; Mismatches 13; Indels 2; Gaps 1;

QY 1 YERLARVHTQTDDEYRFFILLDQVSSGSPFNEIPILRGSTIPVSDAQPFVLEVTN 60
DB 1 YERLARVHTQTDDEYRFFILLDQVSSGSPFNEIPILRGSTIPVSDAQPFVLEVTN 60
QY 61 OGQDSTALADYTMVAVYVAGQDQSYVRLQAPGKATHTFPTGTTDRESSTPFGSYTDL 120
DB 61 EGQDSTALADYTMVAVYVAGQDQSYVRLQAPGKATHTFPTGTTDRESSTPFGSYTDL 118
QY 121 ERYAGHRDQIPGIGIOLQSVSLRYPGSGTAPQASILLIOMISAPARFPILMRYRQ 180
DB 119 ERYAGHRDQIPGIGIOLQSVSLRYPGSGTAPQASILLIOMISAPARFPILMRYRQ 178
QY 181 DINGSESLDPMWMLLETNSGQSTQYQCHSTQVFNPPRLAISTNNVTLANVSAYIA 240
DB 179 DINGSESLDPMWMLLETNSGQSTQYQCHSTQVFNPPRLAISTNNVTLANVSAYIA 236
QY 241 SLAINLFCVGERPSS 251
DB 239 SLAINLFCVGERPSS 249

RESULT 4
QWZ43 PRELIMINARY; PRT; 254 AA.
AC 08WZ43;
DT 01-MAR-2002 (Tremblrel, 22, Created)
DT 01-OCT-2002 (Tremblrel, 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)

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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 19.7321 Seconds
(without a.i.environments)

3347.915 Million cell updates/sec

Title: US-09-601-667C-38

Sequence: 1 YERLRIRVTHQTGDEYFR.....SVIASLAIMFVCGERPSS 256

Scoring table: BLOSUM62

Gapor 10.0 , Gapext 0.5

searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

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Maximum DB seq length: 0
Minimum DB seq length: 20000000000

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Post-processing: Minimum March 0%

Maximum Match	10
1st time first	45

Database : CPTREMBL, 23.4

```
1: sp_archaea:*
```

```

3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mbc:*
8:  sp_organelle:*
9:  sp_plant:*
10: sp_virus:*
11: sp_vertebrate:*
12: sp_unclassified:*
13: sp_virus:*
14: sp_bacteria:*
15: sp_archaea:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Match	Length	DB	ID	Description
1	1196	92.1	249	10	08RXH7	08RXH7	Vascum albu
2	1189	91.5	551	10	08RW43	08RW43	Vascum albu
3	1166	89.8	535	10	08RXH6	08RXH6	Vascum albu
4	1142	87.9	524	10	08LKC6	08LKC6	Vascum albu
5	1051	84.0	529	10	08LKC5	08LKC5	Vascum albu
6	1034	82.1	521	10	08LKC4	08LKC4	Vascum albu
7	1080	87.1	521	10	08S216	08S216	Vascum albu
8	474	36.5	251	10	09A237	09A237	Vascum albu
9	473	36.4	251	10	09A235	09A235	Vascum albu
10	457	35.6	251	10	09A236	09A236	Vascum albu
11	462	35.6	282	10	03A760	03A760	Vascum albu
12	459.5	35.4	580	10	09ABW3	09ABW3	Vascum albu
13	453.5	34.7	580	10	09ABW4	09ABW4	Vascum albu
14	450.5	34.9	559	10	09FV22	09FV22	Vascum albu
15	448.5	34.6	551	10	09ABW5	09ABW5	Vascum albu
16	34.5	5.88	10	05076	05076	05076	Vascum albu

17	401	30.9	570	10	Q41338	Q4138 sambucus in
18	339	30.3	541	10	Q41174	ricinus com
19	392	30.2	570	10	Q22415	sambucus in
20	390	30.0	547	10	Q96659	Q9669 abrus prec
21	387.8	29.9	564	10	Q59152	Q5912 sambucus el
22	387.2	29.8	565	10	Q4071	sambucus in
23	384.9	29.6	565	10	Q4071	sambucus in
24	364	29.6	573	10	Q98268	Q9828 iis hollan
25	370.5	28.5	563	10	Q43367	Q4367 sambucus in
26	368	28.3	569	10	Q59553	sambucus in
27	368	28.3	569	10	Q4072	sambucus in
28	355.5	27.8	566	10	Q4072	sambucus in
29	354.5	27.4	604	10	Q96654	polygonatum
30	354	27.3	604	10	Q96654	polygonatum
31	353	27.1	604	10	Q81232	Q8122 sambucus in
32	350	26.9	604	10	Q81232	Q8122 sambucus in
33	330	25.4	289	10	Q94864	Q94864 trichosanthe
34	324	24.9	247	10	Q91823	Q91823 trichosanthe
35	324	24.9	270	10	Q91823	Q91823 trichosanthe
36	324	24.9	270	10	Q81267	Q81267 trichosanthe
37	324	24.9	289	10	Q41216	Q41216 trichosanthe
38	324	24.9	300	10	Q43367	Q43367 iis hollan
39	317.5	24.4	289	10	Q862029	Q862029 euphorbia s
40	317	24.4	299	10	Q862029	Q862029 euphorbia s
41	316	24.3	299	10	Q862029	Q862029 euphorbia s
42	312.6	24.2	277	10	Q862029	Q862029 euphorbia s
43	312	24.0	277	10	Q862029	Q862029 euphorbia s
44	312	24.0	286	10	Q96507	Q96507 gymnocista
45	312	24.0	286	10	Q96507	Q96507 gymnocista
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47	312	24.0	286	10	Q96507	Q96507 gymnocista
48	312	24.0	286	10	Q96507	Q96507 gymnocista
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54	312	24.0	286	10	Q96507	Q96507 gymnocista
55	312	24.0	286	10	Q96507	Q96507 gymnocista
56	312	24.0	286	10	Q96507	Q96507 gymnocista
57	312	24.0	286	10	Q96507	Q96507 gymnocista
58	312	24.0	286	10	Q96507	Q96507 gymnocista
59	312	24.0	286	10	Q96507	Q96507 gymnocista
60	312	24.0	286	10	Q96507	Q96507 gymnocista
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84	312	24.0	286	10	Q96507	Q96507 gymnocista
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87	312	24.0	286	10	Q96507	Q96507 gymnocista
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92	312	24.0	286	10	Q96507	Q96507 gymnocista
93	312	24.0	286	10	Q96507	Q96507 gymnocista
94	312	24.0	286	10	Q96507	Q96507 gymnocista
95	312	24.0	286	10	Q96507	Q96507 gymnocista
96	312	24.0	286	10	Q96507	Q96507 gymnocista
97	312	24.0	286	10	Q96507	Q96507 gymnocista
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99	312	24.0	286	10	Q96507	Q96507 gymnocista
100	312	24.0	286	10	Q96507	Q96507 gymnocista

ALIGNMENTS

[illegible]

RL Structure 2:7-16 (1994).
 RN X-RAY CRYSTALLOGRAPHY (2.16 ANGSTROMS).
 RX MEDLINE=94192822; PubMed=8143659;
 RA Hsueh J., Tickle I.J., Wood S.P.;
 RT "Crystal structure of momordin, a type I ribosome inactivating
 RT protein from the seeds of Momordica charantia.";
 RL FEBS Lett. 342:154-158 (1994).
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RP MEDLINE=9524435; PubMed=7676765;
 RA Huang Q., Lin S., Tang Y., Jin S., Wang Y.;
 RT "Studies on crystal structures active-centre geometry and
 RT dephosphorylating mechanism of two ribosome-inactivating proteins.";
 RL Biochem. J. 309:285-298 (1995).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC
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 CC
 DR EMBL; X57682; CAA04869.1; -
 DR PIR; S14273; RUPROG.
 DR PDB; 1A8H; 22-JUN-94.
 DR PDB; 1A8J; 22-JUN-94.
 DR PDB; 1A8C; 22-JUN-94.
 DR PDB; 1A8M; 31-MAY-94.
 DR PDB; 1A8G; 07-FEB-95.
 DR PDB; 1A8H; 07-FEB-95.
 DR PDB; 1A8I; 07-FEB-95.
 DR PDB; 1A8Q; 21-NOV-01.
 DR GlycoSuiteDB; E16094; -
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RPL16; RIBOSOMAL
 DR SMART; S000275; SHRNA_SICIN.
 DR PROSITE; PS00275; SHRNA_SICIN, 1.
 KW plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
 KW Glycoprotein; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 269
 FT PROPEP 270 286
 FT ACT SITE 183 183
 FT CARBOHYD 250 250
 FT STRAND 25 28
 FT HELIX 34 47
 FT STRAND 50 54
 FT TURN 55 56
 FT STRAND 57 60
 FT HELIX 66 69
 FT STRAND 70 76
 FT TURN 78 79
 FT STRAND 82 88
 FT TURN 89 92
 FT STRAND 93 99
 FT TURN 100 101
 FT STRAND 102 105
 FT HELIX 109 114
 FT TURN 115 117
 FT STRAND 120 121
 FT STRAND 124 127
 FT STRAND 134 134
 FT HELIX 141 144
 FT STRAND 150 150
 FT HELIX 152 162
 FT TURN 163 163
 RIBOSOME-INACTIVATING PROTEIN MOMORDIN I.
 MISSING IN MATURE PROTEIN.
 N-LINKED (GLCNAC...)
 /FTID-CAR_000082.

FT HELIX 167 186
 FT STRAND 187 187
 FT HELIX 188 195
 FT TURN 196 197
 FT STRAND 202 202
 FT HELIX 206 225
 FT TURN 226 230
 FT STRAND 231 238
 FT TURN 240 241
 FT STRAND 246 250
 FT TURN 251 252
 FT HELIX 254 258
 FT STRAND 259 259
 FT STRAND 260 260
 FT STRAND 263 263
 FT HELIX 266 268
 SQ SEQUENCE 286 AA; 31532 MW; E1B013ABEBC216CF CRC64;
 Query Match 22.1%; Score 286.5; DB 1; Length 286;
 Best Local Similarity 32.3%; From NCBI; 198-193;
 Matches 85; Conservative 44; Nonconservative 41; Indels 33; Gaps 9;
 14 GDEYR-----PILLRNVSSGSFSENPILRPGSTIPVSDAQRVYLVELTNOG 62
 23 GDVSRFLSGADREYGVETIKDLNNLPPREKVIPIILPS--VSGAQRVILMLHFNVD 79
 63 QDSITPAIDVTNNAVYVYQADQSYFLRD-ARQAVTHLFTGTRDSRLPPTGSYDLS 121
 80 GRTIVADVNTVINGTADITTSIFENRPAELASQVFRDNR-KITLPSNTERLQ 138
 122 RYAGE-DEQIPLEQLOSYSAIYVGSFPAQASITLITOMSSAARPIIWR-- 177
 139 IAAKPEKEKIFIGPAPLSAISTLH-YDSIAKAGALLVIGTTAAARFVIEQIOE 196
 178 --YQDINSSESLPEPMWLELETSWCOQSTQV--HSDGVNPPRLATSTQNPVLS 233
 197 RAYREYV-----PSLATISLENSWGLSKXOILAOQNGAIFRPIVLVWKNKQVIT 249
 234 NVESVYNSLAIKLFV 248
 250 NVTSKAVTSNIQILL 264

Search completed: December 11, 2003, 14:09:08
 Job time : 5.48263 secs

FT CONFLICT 152 152 A -> S (IN REF. 2).
 FT CONFLICT 174 174 C -> S (IN REF. 2).
 FT CONFLICT 245 245 N -> H (IN REF. 2).
 SQ SEQUENCE 294 AA; 32234 MW; DA4F8B7CE3290994 CRC64;

Query Match 23.0%; Score 298.5; DB 1; Length 294;
 Best Local Similarity 33.6%; Pred. No. 166-19;
 Matches 81; Conservative 45; Mismatches 100; Indels 15; Gaps 7;

13 TGEYEPFPTLRDVSQSGSFNEIPRLKOSTIPVSDQRFVLVETLNOGQDSITPAIDV 72
 29 TKKSYSPFTLRDLPQGVGQIPPLPST--AGSGWFFPFLTNDEFTVAVNV 85
 73 TNAVYVQMGDSYFLRDA-PRGAEHLFTGTDRSSLPFTGSDYLERVAG-GRDQIP 131
 86 TNAVYVQMGDSYFLRDA-PRGAEHLFTGTDRSSLPFTGSDYLERVAG-GRDQIP 143
 132 TNAVYVQMGDSYFLRDA-PRGAEHLFTGTDRSSLPFTGSDYLERVAG-GRDQIP 191
 144 TNAVYVQMGDSYFLRDA-PRGAEHLFTGTDRSSLPFTGSDYLERVAG-GRDQIP 246
 192 MWELETSWQSGSTVOV--HSTQGVNPPRLAISTGQVTLNVS--EQLIRISYKVPDLA 259
 200 QAVISLWMSLWGLSKQIQIARNTGQGFNPVLEYPDTPRESVYTSAGVYKNIKILL 259
 247 F 247
 260 Y 260

RESULT 14

RIP1_CDCFI STANDARD; PRT; 286 AA.

AC Q9FRX4; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
 DE EC 3.2.2.22
 OS Cucumis flaccidus
 CC Cucurbitales; Cucurbitaceae; Cucumis
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucotids I; Cucurbitales; Cucurbitaceae; Cucumis
 CX MCB1_Taxid=331071;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada T., Ohki S.T., Osaka T.;
 RA "Cloning and analysis of a cDNA coding a putative ribosome-
 RA inactivating protein from Cucumis flaccidus.";
 RA Plant Biotechnol 17:337-340(2000).
 RL -1- CATALYTIC ACTIVITY: Endoglycosylates the N-glycosidic bond at one
 CC -1- SPECIFIC ADENOSINE ON THE 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.

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DR EMBL; AB045560; BAB1977.1; -
 DR HSSP; P16094; IARC;
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIF1.
 DR PROSITE; PRO0336; STRAELCTIN.
 DR PROSITE; PS00275; SHIGA_RICH1.
 DR PlantDefens; Antiviral; Protein synthesis inhibitor; Hydrolase;
 KM Toxin; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 CHAIN 22 286 PUTATIVE RIBOSOME-INACTIVATING PROTEIN.

FT ACT SITE 185 185 BY SIMILARITY.
 FT CARBOHYD 103 103 N-LINKED (GLUCAC...) (POTENTIAL).
 FT CARBOHYD 110 110 N-LINKED (GLUCAC...) (POTENTIAL).
 FT CARBOHYD 252 252 N-LINKED (GLUCAC...) (POTENTIAL).
 SQ SEQUENCE 286 AA; 31771 MW; 4EPD4966B04D41 CRC64;

Query Match 22.4%; Score 290.5; DB 1; Length 286;
 Best Local Similarity 32.3%; Pred. No. 728-194;
 Matches 79; Conservative 49; Mismatches 94; Indels 15; Gaps 8;

17 YFSPFTLRDVSQSGSFNEIPRLKOSTIPVSDQRFVLVETLNOGQDSITPAIDV 76
 40 YFSPFTLRDVSQSGSFNEIPRLKOSTIPVSDQRFVLVETLNOGQDSITPAIDV 96
 77 VNAVQMGDSYFLRDA-PRGAEHLFTGTDRSSLPFTGSDYLERVAG-GRDQIP 134
 97 TNAVYVQMGDSYFLRDA-PRGAEHLFTGTDRSSLPFTGSDYLERVAG-GRDQIP 154
 135 EQLIRISYKVPDLA-209
 155 MALDQKISTLY--YDSNAPLAFVLCQTHAAKXKI--EQLIRISYKVPDLA 209
 194 MWELETSWQSGSTVOV--HSTQGVNPPRLAISTGQVTLNVS--EQLIRISYKVPDLA 248
 210 ARLSLEWMSLWGLSKQIQIARNTGQGFNPVLEYPDTPRESVYTSAGVYKNIKILL 266

RESULT 15

RIP1_MOMCH STANDARD; PRT; 286 AA.

AC P16094; P24697; 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1992 (Rel. 21, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribosome-inactivating protein precursor (rRNA N-glycosidase)
 DE EC 3.2.2.22 (Alpha-momochartin) (Alpha-MOMC).
 OS Momordica charantia (Bitter melon) (Balsam pear).
 CC Cucurbitales; Cucurbitaceae; Momordica
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophytes; Magnoliophyta; eudicotyledons; Rosidae;
 CC eucotids I; Cucurbitales; Cucurbitaceae; Momordica
 CX MCB1_Taxid=3673;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-91159486; PubMed=2001404;
 RA Ho W.K.K., Liu S.C., Shaw P.C., Young H.W., Ng T.B., Chan W.Y.;
 RA "Cloning of the cDNA of alpha-momochartin: a ribosome inactivating
 RA protein.";
 RA Biochem. Biophys. Acta 1088:311-314(1991).
 RL -1- CATALYTIC ACTIVITY: Endoglycosylates the N-glycosidic bond at one
 CC -1- SPECIFIC ADENOSINE ON THE 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.

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 CC or send an email to license@sib-sib.ch).

DR EMBL; AB045560; BAB1977.1; -
 DR HSSP; P16094; IARC;
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIF1.
 DR PROSITE; PRO0336; STRAELCTIN.
 DR PROSITE; PS00275; SHIGA_RICH1.
 DR PlantDefens; Antiviral; Protein synthesis inhibitor; Hydrolase;
 KM Toxin; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 CHAIN 22 286 PUTATIVE RIBOSOME-INACTIVATING PROTEIN.


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DT      01-DEC-1992 (Rel. 24, Created)
DT      01-DEC-1992 (Rel. 24, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DR      RIBOSOME-INACTIVATING PROTEIN ANNOTATION UPDATE
OC      Bacteria; Cyanobacteria; Eukaryota; Fungi; Archaea; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC      eumetazoa; Cnidaria; Mollusca; Chordata; Cephalopoda; Mammalia;
NCBI TaxId=3672;
RN      [SEQUENCE FROM N.A.]
RX      MEDLINE=93027170; PubMed=1408771;
RT      Orligao M., Better M.;
RL      Nucleic Acids Res. 20:4652-4662(1992).
CC      -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC      specific adenosine on the 28S rRNA.
CC      -1- TYPE I RIB SUBUNITARY
CC      --
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CC      modified and this statement is not removed, changed by and/or commented
CC      or send an email to license@db.sib.ch (see http://www.sib-swiss.ch/about/)
CC      --
DR      EMBL_212175; CAATG166.1; -.
DR      PIR: S25560; S25560.
DR      PDB: 1CF5; 07-JUN-99.
DR      InterPro:IPR001574; RTP.
DR      RefSeq:PF001574.1; RTP.
DR      PRINTS: P00136; SHUGARIN.
DR      PROSITE: PS00275; SHUG_RICHN. 1.
KW      Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
KW      3D-structure.
FT      SIGNAL        1    23
FT      CHAIN         24    285
FT      ACT_SITE     181    181
FT      SEQUENCE     286 AA; 92031 MW; 3B9FF1DEB325966 CCDC4;
Query Match          24.2%; Score 314; DB 1; Length 285;
Best Local Similarity 35.0%; Pred. No. 6.4e-21;
Matches   85; Conservancy 49; Mismatches 89; Indels 20; Gaps 9
OY      13 TACTTTCTTTLRDYVSSGSFSN--EPLFGSGTFPVDAGQRPVVLZVTMGQSDSTFA 69
OY      DB33 TACTTTCTTT---EDFAPILPSHKYDIPLGST---IDSKKFLDLDSYXAYELISHA 86
OY      DB70 IDVTAAVVAVYVAGQSYELTDAPGACATLTPTGTGRSDSLFPFGSYTLDERYAAGH--R 127
OY      DB87 IDVVVVVVVVVYVADVSYPFSSPEPAANILPKGR--KITLYPVGNENLQT-AAHKR 143
OY      OY128 DQLPGLGRIOLIOSVAARKPGSGTRDNASKILLIIONISEAPNPFLIMRHODINSSES 187
OY      DB144 ENIDGDLPALSAITTLTPYMAQSAPS--LVLIOTTHAKFKILERWAKV--AN 199
OY      OY188 FLDPMYMILETSNGQSGTV--GISTDVGVNNPRALISGNVFYLLSNRSVLAISALIM 245
OY      DB200 PKKNATIIISLENQNSALSKEQLELMQOGKGFRNPDLIKPFGQVRGYNTSDVYANKIK 259
OY      OY246 LSV 248
OY      DB260 LLL 262

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ID      R181 BRVYD1 STANDARD; FRT, 290 AA.
DR      P31851, 096819;
DT      01-OCT-1993 (Rel. 27, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DR      Rhodospirillum rubrum, last annotation update)
DR      Rhodospirillum rubrum, last annotation update)
DR      (EC 3.2.2.22) (ND1).
OS      Bryonia dioica (Red bryony).
OC      Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC      Spermatophyta; Magnoliopsida; eudicotyledons; core eudicot; Rosidae;
OC      eumecostis I; Cucurbitales; Cucurbitaceae; Bryonia.
DR      NCBI_TextID=95927;
DR      P1
DR      SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
DR      TISSUE=Leaf.
RC      MEDLINE=97228081; PubMed=9115985;
RA      GAWLIK S.L., NEUBAUER M., KLAET H.E., CHANG C.Y.Y., ELSAPPAH H.M.,
RA      SIEGALL C.B.;
RT      "Molecular, biological, and preliminary structural analysis of
RT      recombinant bryodin 1, a ribosome-inactivating protein from the plant
RT      Bryonia dioica."
RT      Biochemistry 36:1095-1103(1997).
RL      (2)
AP      SEQUENCE FROM N.A.
RA      Siegall C.B.;
RT      "Cloning and expression of a gene encoding bryodin 1 from Bryonia
RT      dioica."
RL      Patent number US5541110, 30-UTL-1996.
RL      P1
RL      SEQUENCE OF 24-66.
RL      TISSUE=seed.
RA      MEDLINE=89326691; PubMed=2753596;
RA      Matsuoka K., Lazear A.M., Barbieri L., Stille P., Sorita M.,
RA      Lapet D.;
RT      "N-terminal sequence of some ribosome-inactivating proteins."
RT      Int. J. Pept. Protein Res. 33:263-267(1989).
RL      P1
RL      SEQUENCE OF 24-43.
RL      TISSUE=Root.
RA      MEDLINE=9511812; PubMed=7849072;
RA      Siegall C.B., Gawlik S.L., Chase D., Wolfe E.A., Mixan B.,
RA      Manquardt H.;
RT      "Characterization of ribosome-inactivating proteins isolated from
RT      Bryonia dioica and their utility as carcinoma-reactive
RT      Histoconjugates."
RL      Bioconjug Chem. 5:423-429(1994).
RL      P1
RL      FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
CC      -1. PROTEIN SYNTHESIS IN ANIMAL CELLS.
CC      -1. CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one
CC      specific adenosine on the 28S rRNA.
CC      -1. PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THIS C-TERMINAL TO
CC      -1. PRODUCTION OF A SMALLER FORM THAT IS USEFUL AS IMMUNOPROTEIN FOR
CC      pharmacological applications as it has low toxicity in rats and
CC      mice but is potent once inside target cells.
CC      -1. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC      TYPE 1 RIP SUBFAMILY.
CC
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CC
CC      EMBL, J24020, -1, NCOT, UNANNOTATED, CDS.
CC      PIR, S16491, S16491.
CC      PIR, S16491, S16491.
CC      InterPro, IPR001574, RIP.
CC      Pfam, PF00161, RIP, 1.
CC      PRINTS, PR00396, SHIGALININ.
CC      PROSITE, PS00275, SHIGA ACIDIN, 1.

```

RESULT 12
RIP1_BRYDI

DR PRINTS; PRO0396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1

FT HELIX 109 114
 FT TURN 115 117
 FT TURN 118 121
 FT STRAND 122 124
 FT HELIX 134 141
 FT TURN 142 147
 FT HELIX 145 147
 FT STRAND 150 150
 FT HELIX 152 153
 FT TURN 154 155
 FT TURN 151 151
 FT TURN 151 151
 FT HELIX 182 186
 FT STRAND 187 187
 FT HELIX 188 195
 FT TURN 196 196
 FT STRAND 202 202
 FT HELIX 206 226
 FT TURN 227 230
 FT STRAND 231 239
 FT TURN 241 242
 FT STRAND 245 250
 FT TURN 251 252
 FT HELIX 254 258
 FT TURN 259 259
 FT STRAND 260 260
 FT STRAND 263 263
 FT TURN 266 269
 SQ SEQUENCE 289 AA; 31676 MW; 5CE09B630755B9 CRC64;

Query Match 25.3%; Score 329; DB 1; Length 289;
 Best Local Similarity 36.4%; Pred. No. 2, 9e-22;
 Matches 89; Conservative 52; Mismatches 84; Indels 18; Gaps 10;

QY 13 TGDFFRFTLLRDYVSGSFSNIEPLRQSTFVSDAQFVLEVLNQGDSITPAIDV 72
 DB 33 TSSYGVFISNLRALPNERKLYDIPILR-SLPGS--QVYALHINVADETSVAIDV 89
 QY 73 TNAYVVAQNGOSYFLRDA-PRGAETHLFTGTRDRSILPTSGYTDLEEVAG-RDQI 130
 DB 90 TNAYVVAQNGOSYFLRDA-PRGAETHLFTGTRDRSILPTSGYTDLEEVAG-RDQI 148
 QY 131 PLAGIQLGVSAALRYPGSSTRAPQASILLIOMISEAARNPILMKRQDINS--GESP 188
 DB 149 PLAGIQLGVSAALRYPGSSTRAPQASILLIOMISEAARNPILMKRQDINS--GESP 202
 QY 189 LPMVMELETSWQOOSTVOV--HSTGVFNNPRLAISTGFTLSNVS--VIASIAL 244
 DB 203 LPMVMELETSWQOOSTVOV--HSTGVFNNPRLAISTGFTLSNVS--VIASIAL 262
 QY 245 ME 246
 DB 263 LL 264

RESULT 10

RIPS TRIKI STANDARD; PRT; 289 AA.
 AC R24478;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein karasurin precursor (ZRNA
 DB N-glycosidase) (EC 3.2.2.22).
 OS Trichosanthes kirilowii (Mongolian snake-sourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Eudicotyledons; Eucommiales; Euphorbiaceae; Euphorbiaceae;
 OC Euphorbiaceae; Euphorbiaceae; Euphorbiaceae;
 NCBI_TaxId=3677;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Root culter;
 RX MEDLINE=97356562; PubMed=9212398;

RA Misukami H., Iida K., Kondo T., Ogihara Y.;
 FT "Cloning and bacterial expression of a gene encoding ribosome-
 FT inactivating protein, karasurin-A and karasurin-C, from Trichosanthes
 FT Biol. Pharm. Bull. 20:711-713 (1997).
 RN (21)
 RP SEQUENCE OF 24-270.
 XX MEDLINE=92005921; PubMed=1914000;
 RA Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
 FT "The complete amino acid sequence of an abortifacient protein,
 FT karasurin," Bull. 39:124-129 (1991).
 RN (21)
 RP FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC
 CC 60S RIBOSOMAL SUBUNIT.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.

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CC EMBL; AB000666; BAA21786.1; -
 DR F01; J05606; J05606.
 DR F01; J05606; J05606.
 DR F01; J05606; J05606.
 DR Interpro: IPR001574; RIP.
 DR Pfam: PF00161; RIP.
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 DR Plant defense; Antiviral; protein synthesis inhibitor; Hydrolase;
 FT Toxicity; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 270 KARASURIN-C.
 FT PROPEP 271 289 REMOVED IN NATURE FORM.
 FT ACT SITE 183 183 BY SIMILARITY.
 SQ SEQUENCE 289 AA; 31704 MW; 88D3E22428B7B2 CRC64;

Query Match 25.3%; Score 328; DB 1; Length 289;
 Best Local Similarity 37.2%; Pred. No. 3, 6e-22;
 Matches 90; Conservative 48; Mismatches 86; Indels 18; Gaps 10;

QY 13 TGDFFRFTLLRDYVSGSFSNIEPLRQSTFVSDAQFVLEVLNQGDSITPAIDV 72
 DB 33 TSSYGVFISNLRALPNERKLYDIPILR-SLPGS--QVYALHINVADETSVAIDV 89
 QY 73 TNAYVVAQNGOSYFLRDA-PRGAETHLFTGTRDRSILPTSGYTDLEEVAG-RDQI 130
 DB 90 TNAYVVAQNGOSYFLRDA-PRGAETHLFTGTRDRSILPTSGYTDLEEVAG-RDQI 148
 QY 131 PLAGIQLGVSAALRYPGSSTRAPQASILLIOMISEAARNPILMKRQDINS--GESP 188
 DB 149 PLAGIQLGVSAALRYPGSSTRAPQASILLIOMISEAARNPILMKRQDINS--GESP 202
 QY 189 LPMVMELETSWQOOSTVOV--HSTGVFNNPRLAISTGFTLSNVS--VIASIAL 244
 DB 203 LPMVMELETSWQOOSTVOV--HSTGVFNNPRLAISTGFTLSNVS--VIASIAL 262
 QY 245 ME 246
 DB 263 LL 264

RESULT 11

RIPS MOWBA STANDARD; PRT; 286 AA.
 ID R1P2 MOWBA
 AC P29336;

Best Local Similarity 38.4%; Pred. No. 1e-22;
Matches 94; Conservative 38; Mismatches 91; Indels 22; Gaps 11;
QY 13 TDEYFFFTLLRDVSSGS-FSENEIPRLROSTIPVSDAFVAVELINQOGSITAD 71
DB 32 TATYKTFIRLRTKLVGVGVYDIFLRAAAGA---RQVLTLINVSSTVALD 88
QY 72 YNNAYVAVAGCGSTFEPRAETHLETGTDRDSPTGSDTLEPVYK--RQ 129
DB 89 VNNYVAVYRAGNTAFVADSTREANNVLFAGINHR--LPYGVDELTAAGISREN 146
QY 130 IPAGIEQLIOVSAL--RYGSGSTRAQASILLIQWISAAAFNPIFRYQDINSDES 167
DB 147 IELGFSISIAIGMFRINQTSV---PAAIVITQVSEARKEIQVSE--NWGK 201
QY 188 FLFDYMLELSTWGGOSTVQ--HSDGVNPP--FLAISTGFYLSMVS-VIASL 242
DB 202 FKDPATLSIQWSSLSBQIQCTGCEFRVRLVSTPFPV--VNSVPVNGI 259
QY 243 AIMEF 247
DB 260 AILLY 264
RESULT 9
RIFT_TRIKI STANDARD; PRT; 289 AA.
ID P09989.1886 (Rel. 10 Created)
DC 01-NOV-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribosome-inactivating protein alpha-trichosanthin precursor
OS (rRNA N-glycosylase) (EC 3.2.2.22) (Alpha-TCG).
DB Trichosanthin Kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eucosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
CC NCBI_TaxID=3677;
RX 100% (100/100) (100/100) (100/100) (100/100) (100/100)
RP SEQUENCE FROM N.A.
RC STRAIN=Maximowicz;
RA MEDLINE=9113657; PubMed=199291;
RT "Cloning of trichosanthin cDNA and its expression in Escherichia
colli.";
RT Gene 97:267-272(1991).
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Plant Mol. Biol. 22:1181-1186 (1993).
-1- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN
PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN
SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS THROUGH THE CATALYTIC INACTIVATING PROTEIN
SUBUNIT. BY KNOCKING OUT THE CATALYTIC INACTIVATING PROTEIN
SUBUNIT IN A RIBOSOME-SPECIFIC LECTIN THAT FACILITATES THE
BINDING OF RIBOSOME TO THE CELL MEMBRANE THAT PRECEDES
ENDOCYTOSIS.
-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-1- SIMILARITY: Contains 2 ricin B-type lectin domains.

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DR EMBL, U41299; AAB39475.1; -
DR PIR, S37382; S37382.
DR InterPro, IPR000772; Ricin_B_lectin.
DR Pfam, PF00652; Ricin_B_lectin.6.
DR PRINTS, PR00366; SHIGARICIN.
DR SMART, SM00458; RICIN.2.
DR PROSITE, PS00275; SHIGA_RICIN.1.
DR PROSITE, PS50231; RICIN_B_LECTIN.2.
DR Plant defense; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;
KW Glycoprotein; Lectin; Signal.
FT SIGNAL 1 25
FT CHAIN 26 297 NIGRIN B A CHAIN.
FT DOMAIN 298 563 NIGRIN B B CHAIN.
FT DOMAIN 305 431 RICIN B-TYPE LECTIN 1.
FT REPEAT 432 452 RICIN B-TYPE LECTIN 2.
FT REPEAT 453 462 1 ALPHA.
FT REPEAT 463 482 1 ALPHA.
FT REPEAT 483 492 2 ALPHA.
FT REPEAT 493 502 2 ALPHA.
FT REPEAT 503 512 2 ALPHA.
FT REPEAT 513 522 2 ALPHA.
FT REPEAT 523 532 2 ALPHA.
FT ACT_SITE 533 537 K -> V (IN REP. 2).
FT CONFLICT 39 39
SQ SEQUENCE 563 AA; 62300 MW; F250CB2461BF14 CRC64;

Query Match 27.2%; Score 353; DB 1; Length 563;
Best Local Similarity 37.2%; Posed No. 5; 1e-24;
Matches 92; Conservative 50; Mismatches 87; Indels 18; Gaps 10;
QY 17 YRRTITLADVSSGSGS-REPLAOSTIPVDQRVAVLNGOQSITLADVYNA 75
DB 43 YRPLNLEKTVAGTGVVGVGPIARER-SVQVSRVAVLNVNGVITLADVYNA 101
QY 76 YVAVYQAGQGYFLDAPRGATHTLFTGTTRSSSLPTQSYTDLARVAG-HDQIPLGI 134
DB 102 YVAVFSGNANSTFFKLTREYQSKNLFVGL-KQNTLSTFQNTDMLNANTRISLIDG 159

135 ROLIGSVALRPGSTPRKQKESITLITOMTSEARPNILMRRODINGSGSFLPDMY 194
QY 160 SPLDVALISL-YHDSV--ARSLIVLQVSEARFRYICGEVRSLQQAQSTFPMALM 215
DB 195 LELSTSMQOQSTQVGHSTGVFNNPRLAISTGNF---VTLASVAV--IASLALMEPV 248
QY 216 LSNENWASMSLEIQAKNV--SPFQVQLNDYDTRFLVDFEELVYTGITALLFLR 273
DB 249 CGRRPS 255
QY 274 GSS-FSN 279

RESULT B
RIP2 BRVDI
ID RIP2 BRVDI STANDARD; PRT; 282 AA.
AC P98184; Q98800;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein Bryodin II precursor (RNA N-
glycosidase) (EC 3.2.2.22) (b22).
OS Bryonia dioica (Red Bryon) [Stratiotrypa; Embryophyta; Tracheophyta;
OC Eukaryota; Plantae; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosidia I; Cucurbitales; Cucurbitaceae; Bryonia.
OX NCBI_Taxid:3652;
RN [1]
RP SEQUENCE FROM N.A.
RA Siegal C.B., Gawlak S.L., Margardt H.;
RT "Bryodin 2, a ribosome-inactivating protein isolated from the plant
Bryonia dioica.";
RL Patent number US5597569, 28-JAN-1997.
RN (2)
RP SEQUENCE OF 22-42.
RA MEDLINE=95151812; PubMed=7849072;
RC MEDLINE=95151812; PubMed=7849072;
RA Siegal C.B., Gawlak S.L., Chace D., Wolff B.A., Mixan B.,
RT Margardt H.;
RT "Characterization of ribosome-inactivating proteins isolated from
Bryonia dioica and their utility as carcinoma-reactive
immunokonjugates.";
RL Bioconj. Chem. 5:423-429 (1994).
CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1. INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS (66 SIMILARITY)
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- TYPE 1 RIP SUBFAMILY.

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CC or send an email to license@sib-sib.ch).

DR EMBL, I14718; -; NOT_ANNOTATED_CDS.
DR HSRP, P09989; IMB1.
DR InterPro, IPR001574; RIP.
DR Pfam, PF00151; RIP.1.
DR PRINTS, PR00366; SHIGARICIN.
DR PROSITE, PS00275; SHIGA_RICIN.1.
DR Plant defense; Protein synthesis inhibitor; Hydrolyase; Toxin;
KW Multigene family; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 282 RIBOSOME-INACTIVATING PROTEIN BRVDIN II.
FT ACT_SITE 23 25 N-LINKED (GLCNAc...) (POTENTIAL).
FT CONFLICT 25 25
SQ SEQUENCE 282 AA; 30754 MW; C5B2BF8A73769C CRC64;

Query Match 25.7%; Score 334; DB 1; Length 282;

RX MEDLINE=96374422; PubMed=8780513; Monzingo A.F., Pascual J.M., Day P. J., Ernst S. R., Frankel A.E., Robertus J.D.
 RA Molina-Sytnich M.C., Robertus J.D.
 RT "Structure and activity of an active site substitution of ricin A chain."
 RL Biochemistry 35:11096-110103(1996).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RA Yan X., Hollis T., Sytnich M., Day P., Monzingo A.F., Milne G.W., Robertus J.D.
 RT "Structure-based identification of a ricin inhibitor."
 RL J. Mol. Biol. 366:1043-1049(1997).
 RN [14]
 RP MOTHUSINIS.
 RA Kohn J., Roberts J.
 RT "Analysis of several key active site residues of ricin A chain by mutagenesis and X-ray crystallography."
 RL Protein Eng. 5:775-779(1992).
 CC -1- FUNCTION: Ricin is highly toxic to animal cells and to a lesser extent to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal subunits. It acts as a glycosylase that removes a specific adenine residue from an exposed loop of 28S ribosomal RNA. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein synthesis. Phosphatidylcholine is hydrolyzed by the A chain per minute, thus inactivating them faster than the cell membrane new ones. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain. B chains are also responsible for cell agglutination (lectin activity). It binds to beta-D-galactopyranoside moieties.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -1- SUBUNIT: Disulfide-linked dimer of A and B chains.
 CC -1- DOMAIN: The B chain is composed of two domains, each domain contains two disulfide bridges and a beta sheet gamma.
 CC -1- PFM: THE MAJOR A-CHAIN IS GLYCOSYLATED AND IN POSITION 271 MINOR A-CHAIN IS GLYCOSYLATED ALSO; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION.
 CC -1- CAUTION: REF. 4 AND REF. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
 CC -1- DATABASE: NAME=Protein Spotlight;
 CC NAME=Issue 31 of February 2003;
 CC URL=<http://www.express.org/spotlight/articles/spot031.html>"
 CC ---
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL accession CC The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).
 CC CC
 DR EMBL, K03179, CA263939.1, -
 DR EMBL, X52908, CA37095.1, -
 DR EMBL, X02388, CA66230.1, -
 DR EMBL, A12892, CA601058.1, -
 DR PIR, A24041, RLCSO.
 DR PDB, 2A11, 31-JUN-94.
 DR PDB, 1APG, 31-JUN-94.
 DR PDB, 1FMP, 31-OCT-93.
 DR PDB, 1IES, 14-JUN-98.
 DR PDB, 1IFU, 14-JUN-98.
 DR PDB, 1ATC, 31-OCT-93.
 DR PDB, 1OBS, 16-JUN-97.
 DR PDB, 1OBT, 16-JUN-97.
 DR PDB, 1BR5, 02-SEP-98.

Query Match	Best Local Similarity	Score	Length	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414	DB 415	DB 416	DB
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FT DOMAIN 272 399 RICIN B-TYPE LECTIN 1.
FT REPEAT 402 526 RICIN B-TYPE LECTIN 2.
FT REPEAT 282 324 1-ALPHA.
FT REPEAT 325 365 1-BETA.
FT REPEAT 366 406 1-GAMMA.
FT REPEAT 407 447 2-GAMMA.
FT REPEAT 448 488 2-BETA.
FT REPEAT 489 527 2-GAMMA.
FT ACT SITE 163 163 BY SIMILARITY.
FT DISTALD 246 268 INTERCHAIN (BY SIMILARITY).
FT DISTALD 285 304 BY SIMILARITY.
FT DISTALD 328 345 BY SIMILARITY.
FT DISTALD 416 429 BY SIMILARITY.
FT MOD_RES 455 472 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLYCAN. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLYCAN. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLYCAN. . .) (POTENTIAL).
FT CONFLICT 282 282 N->D (IN REF. 2).
FT CONFLICT 291 291 D->N (IN REF. 2).
FT CONFLICT 350 351 AR->PQ (IN REF. 2).
FT CONFLICT 378 378 S->N (IN REF. 2).
FT CONFLICT 426 426 L->M (IN REF. 2).
FT CONFLICT 428 428 Y->D (IN REF. 2).
FT CONFLICT 431 431 N->S (IN REF. 2).
FT CONFLICT 434 434 R->S (IN REF. 2).
FT CONFLICT 435 435 N->S (IN REF. 2).
FT CONFLICT 436 436 H->G (IN REF. 2).
FT CONFLICT 502 502 E->Q (IN REF. 2).
FT CONFLICT 509 509 E->Q (IN REF. 2).
FT CONFLICT 513 513 H->W (IN REF. 2).
FT CONFLICT 516 516 H->T (IN REF. 2).
SQ SEQUENCE 527 AA; 5914 MW; 3253A490CE9494A CRC64;

Query Match 32.6%; Score 423.5; DB 1; Length 527;
Best Local Similarity 42.4%; Pred. No. 2.1e-30;
Matches 103; Conservative 40; Mismatches 93; Indels 7; Gaps 6;

OY 9 THQTCDYFRITLIDYVSSSSBSNFIPLROSTIPVSDAQRVYELTNGQSDITR 68
DB 9 TEGATSGYKQFIENLQRI-IGDLHGIIVLPDPT-TLOERKRIVSELSNSTSLIA 66
OY 69 AIDVNAVYVAVQAGDSYFPRDPRGAEHLEFVETTRDSILPFTGSDYDLEVAGH-R 127
DB 67 GIDVSNAVYVAVRAGNSYFPRDPRGAEHLEFVETTRDSILPFTGSDYDLEVAGH-R 124
OY 128 DOIPIGIBOLIOSVAKRYPGSTRAQASIIILQITSEASRPNIMFYKQDINSGES 187
DB 125 QQLPDELQPLRAHLSFQ-SGDDQELRTLVIIQWSEASRPNISYVGVSRINVA 183
OY 188 ELPMWMLFESWQSGTQVCKSTDTGYVNFPL-AISTGAEVTLNVAASYSLALNE 246
DB 184 FQPDAMISLENNONISGSGVQSDVDFNMYLSEVNGPVIYDLSLQGVAYALNL 243
OY 247 FVC 249
DB 244 FVC 246

RESUME
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CC	-1	DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC	-1	CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC	-1	SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
CC	-1	INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.
CC	-1	SIMILARITY: Contains 2 rich B-type lectin domain.
CC		
CC		This Swiss-PROT entry is copyrighted. It is produced through a collaboration
CC		between the Swiss Institute for Bioinformatics and the EMBL Data Bank.
CC		use by non-profit institutions as long as its context is in no way
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (See http://www.isb-sib.ch/announcement
CC		or send an email to license@isb-sib.ch).
CC		
DR	EMBL: X55667; CAA39202.1; -	
DR	PIR: S16022; S16022.	
DR	HSSP: P11410; 1MR.	
DR	InterPro: IPR00574; RIP.	
DR	Pfam: PF00652; Rictin_B_lectin, 6.	
DR	Pfam: PFO0161; RIP_I_lectin, 6.	
DR	PRINTS: PRO0396; SHGALICIN.	
DR	SMART: SMO0458; RICTIN, 2.	
DR	PROSITE: PS00231; RICTIN B LECTIN, 2.	
DR	PROSITE: PS00275; SHIGA_RICTIN, 1.	
KW	Plant defense; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;	
KW	Glycoprotein; Lectin; Signal; Pyruvate carboxylic acid.	
KW	CHAIN 1 1 284	
FT	CHAIN 1 1 284	
FT	PEPTIDE 286 285	
FT	CHAIN 286 285	
FT	DOMAIN 307 434	
FT	DOMAIN 437 561	
FT	REPEAT 317 359	
FT	REPEAT 360 400	
FT	REPEAT 403 435	
FT	REPEAT 448 483	
FT	REPEAT 483 526	
FT	REPEAT 526 561	
FT	ACT SITE 158 158	
FT	DISULFID 281 303	
FT	DISULFID 320 339	
FT	DISULFID 363 380	
FT	DISULFID 451 464	
FT	DISULFID 490 507	
FT	MOD_RES 35 35	
FT	CARDOND 234 234	
FT	CARDOND 325 325	
FT	CARDOND 435 435	
FT	CARDOND 435 435	
FT	SEQUENCE 562 AA; 62817 MW; 1PFOABCTD7B56278 CMC64;	
QY	Query Match 34.5%; Score 448; DB 1; Length 562;	
QY	Best Local Similarity 44.4%; Pred. No. 1.5e-32;	
QY	Matches 108; Conservative 36; Mismatches 93; Indels 6; Gaps 5	
Db	9 THOYTGDERFRTILDVYSSGSFSEIFLLRSTIIPYSDAQRFLVETLWQSDSITA 68	
Db	43 TBAISGSIQKILRNRQLTGLINDVLEDPRTVYERKRTVILNLSIRSESLIV 100	
QY	69 AIDYNNVYVAQAGOSQIFLRAPRAGAEHFLFGTRSSRSIPFGSYGSDLEAYGH- 8 127	
Db	101 GIDVNNVYVAVRAGSQSIFLRAPASASTYLEFET-GRSIRPQSGYDDEMAHQR 168	
QY	128 DOIPLGRIOLISVSLARPQSGTAQASRIILIIQWISKAPFNPIMVYKQINSGES 167	
Db	158 BESIISGQRLTATSLRSGASDEKRLTILVILQWESKAPKIRISLVIRGTH 218	
QY	168 PLDMYVLETFSGVQSGSDVDF-NRPVRLASTANVLTISVYASVSLATE 246	
Db	219 FQDDPAULSLKNDMLISGQVQSGVDFNPFNVRLISLIRQPVVDSLSHFVAVIALML 278	
QY	247 FVC 249	

D6

279 FVC 281

	RESULT_4
RN	TARS_ABRP
RC	NAMES_ABRP STANDARD; RRT; 527 AA.
AC	Oae0677; Atg174;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Abrin-B precursor [contains: Abrin-A B chain (rRNA N-glycosidase)] [EC 3.2.2.2]; Abrin-B B chain].
OS	Abrus precatorius (Indian locoweed) ('Crab's eye').
CX	Spermatophyte Magnoliopsida; Ericaceales; Rubiales; Rubiaceae; Papilionoideae; Abresee; Abrus. eucosids I Fabales; Fabaceae,
CC	[NCBI_TextID=3916;]]]
XN	_
RN	SEQUENCE FROM N.A.
RX	MEDLINE=g312796; PubMed=8423113;
RX	Hung C.-H., Lee M.-C.; Lee T.C., Lin J.-Y.; primary structure of three distinct isoforms determined by cDNA sequencing. Comp Biochem Physiol Part D Mol Biol. 2003 Feb 26;1(193).
RL	J MOL. BIOL. 225:263-267(1993). [2]
RP	SEQUENCE OF 260-527.
RC	TISSUE:Sseed;
RK	MEDLINE=g3169023; PubMed=7763422;
RA	Kimura M., Sumitawa T., Funatsu G.; The complete amino acid sequences of the B-chains of abrin-a and abin-b, toxic proteins from the seeds of Abrus precatorious.'; Biochim Biophys Acta. 1993 May 18;1159(1):1-7.
EL	-I- SIMILARITY: THE N-TERMINAL SECTION BELONGS TO THE RIBOSOME-SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. ABRIN-A IS MORE TOXIC THAN RICIN.
CC	-I- FUNCTION: THIS B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
CC	-I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific asparagine on the B-chain RNA. A AND B CHAINS.
CC	-I- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC	-I- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.
CC	-I- SIMILARITY: Contains 2 riclin B-type lectin domains.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at DESY Hamburg. The content herein may be used without restriction provided it is acknowledged its source and no way can be modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isdb-sib.ch/announce/) or send an email to licenses@isdb-sib.ch).
CC	-- -- -- -- --
DR	BMRB; P08345; AAA33625.1 ;
DR	FIR; S34430; S32430.
DR	PDB; 1PTO; 1PTO; 1PTO; Ricin_B_lecAin.
DR	Interpro; IPRO01574; RIP.
DR	Pfam; PF00562; Ricin_B_lecain; 6.
DR	Pfam; Pf00161; RiP; 1.
DR	PRINTS; PR00396; SHIGARIQIN.
DR	SMART; SMO0458; Ricin_2
DR	PROSITE; PS00731; RICIN_B_LECTIN; 2.
DR	PROSITE; PS00731; SHIGA_RICLIN; 1.
NR	GlycoSite; GlycoSite; Hydroxylation synthesis inhibitor; Toxin; Repeat; glycoprotein; Lectin; 250
FM	CHAIN LINKER PEPTIDE; ABRIN-B A CHAIN
FT	CHAIN LINKER PEPTIDE; ABRIN-B B CHAIN

FT TURN 10 11
 FT HELIX 14 28
 FT STRAND 34 32
 FT TURN 32 32
 FT STRAND 36 38
 FT TURN 42 43
 FT HELIX 47 49
 FT STRAND 51 57
 FT STRAND 63 69
 FT TURN 70 72
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Query Match 37.0% Score 480; DB 1; Length 528.
 Best local similarity 47.9% Free Mismatches 30; Indels 26; Gaps 6;
 Matches 110; Conservative 37; Mismatches 30; Indels 26; Gaps 6;

Qy 9 TQQTGDEYFPFTILRDYSSGSFSEIPLRQSTIPVSDAQREVAVLIMQOQSITA 68
 Db 9 TEGATOSQKQFIEALRERL-RGLIHIDIPVLPDP-FLQERNRYITVELNSPDSIEV 66
 Qy 69 AIDYNAVYVAYQADQSYETLADAPRGATTHLPFTGTTRDSRSLPTGSYTDLERYAGH-R 127
 Db 67 GIDVNAVYVAYRAGQSTFLADAPSSADSLPFGT--DQHSIPYGTGDLERMAHQR 124
 Qy 128 DQIPFIBOLQSYVALYFGSSTRQASLILQIMISAAAPPLIMRQDINSSES 187
 Db 125 QQFPEIQ/LHGISFPGSGDNEKAKTILVILQVAAERAPFYSNRVARSIGCTA 184
 Qy 188 FLPDVYMLELSTSGQSTQVGHSTQGVNPNPFLAISTGVLSVNS----- 237
 Db 185 FQPDAMISLNNNDLRSRGVGSYQDTPPQ-----VITLHNPVYVDSISH 234
 Qy 238 -VIASLAIMLFC 249
 Db 235 PTVAVLALMLFC 247

RESULT 3
 ID ABRIC ABRPR STANDARD; FRT; 562 AA.
 AC P28590;
 DT 01-DEC-1992 (Rel. 24, Created)
 DE 01-DEC-1992 (Rel. 24, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ABRIC-9 precursor (containing: ABRIC-6 & ABRIC-7) (RNA N-glycosidase)
 OS ABRIC-9 (28590) (28590) (28590) (28590) (28590) (28590) (28590) (28590)
 OS ABRIC-9 (28590) (28590) (28590) (28590) (28590) (28590) (28590) (28590)
 CC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 CC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicotyledons: Rosidae;
 CC eucotyledons I; Fabales; Fabaceae; Papilionoideae; Abraceae; Abrus.
 NCBI TaxID=3816;
 RN [1]
 SM SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RC MEDLINE=9126697; PubMed=2050149;
 RA Wood K.A., Lord C.M., Wawrzyniak E.J., Patrak M.;
 FT "Peptide:in: genomic cloning, characterization and the expression of
 the A-chain in Escherichia coli.";
 FT "FUNCTION: THE A-CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. THE
 B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
 BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
 CC -1- CATALYTIC ACTIVITY: Endo-N-glycosidase of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.

F:70,158,161/Active site: Tyr, Glu, Arg #status predicted
F:155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 23.8%; Score 309.5; DB 2; Length 245;
Best Local Similarity 34.8%; Pred. No. 1.9e-20;
Matches 84; Conservative 42; Mismatches 100; Indels 15; Gaps 7;

QY 13 TGDYFRFTLLADYVSSGSSNSNIPILRGSTIFVSDAQRFVLVEITNGQDSTTAIDV 72
DB 10 IKSYSSTPQLNDALPTGTVYGLHLSPT---ASGSKRFRKMLNHYNDVTVYADV 66
QY 73 TNAYVVAACAGGQGYFLRDAFGAETHLFTGTRDSRLPTGQSYDLERYAG-HRQIP 131
DB 67 TNYIVNVRADAVSFEDPTAEPKLIFFAGKTVK--LPGSNVDKLGQSVGKQRMIR 124
QY 133 LGTEQLIOSVALRYPGSGSTRAQASLILIQMISEARFNPIIRYRQDINSSEFLPD 191
DB 125 LGIPALSAITMNY--YDQSTPAALVLIQSTAEKARYKIEQVSHIS--NRYEN 180
QY 192 MWLELETWGGQSTQVQ--HSTDQFNNFRLAISTG--FTLSNVSYSIAIIML 246
DB 181 QAVISLKKWALSKQIQANRKGQCPENPVELYNPDTRRSYHRSAGVKNITML 240
QY 247 F 247
DB 241 Y 241

Search completed: December 11, 2003, 13:55:47
Job time : 8.95754 secs

OY 13 TGDYFRFTLLRDVYSSGSFSN--EIPLLRSTIPVSDAQRFLVETLNGQDSTAAIDV 72
DB 10 TSSGIVFISNRKALPERKLYDILR-STLRGS--QRYALHILNVADETISVAIDV 66
OY 73 TNAYVAVQAGDQSYFLRDA-FRGAFTLFTGTRBSSLPFGSYTDLRYAAGH-RDOI 130
DB 67 TNYVWGRAGDTSIFPNSASAEAKVYKDAK-KVTLFYSNTERLOIAKIKRNI 125
OY 131 PLGIEQLQSVASALRYPGSGTFAQAASILLIQMISAPAREPILMYRRODINS--GSEF 188
DB 126 PLGIPALDSAITLFTYNNASASA--LWVLIQSTSSAAKXFI---EQGIKRYDKTF 179
OY 189 LPMVWLELFTSMQGSQTVQ--HSTDGVPNNPFLAISTGNFYLISVNS--VIALAI 244
DB 180 LPSALISLNSMSLSKQIQIASTNQCETFPVLINQORVITVDAVTSNIAL 239
OY 245 ML 246
DB 240 LL 241

RESULT 13

UC5606
Karasurin C - Trichosanthes kirilowii var. japonica
N/Contains: Karasurin A
C/Species: Trichosanthes kirilowii var. japonica
C/Date: 25-Feb-1997 #sequence_revision 23-Sep-1997 #text_change 19-Jul-2002
C/Accession: J05032
R/Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.
Biol. Pharm. Bull. 20, 711-713, 1997
A/Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating prote
A/Reference number: J05606; MUID:97356562; PMID:9212998
A/Accession: J05606
A/Molecule type: DNA
A/Residues: 1-289 <M12>
A/Cross-references: DBJ:AB00666; NID:92329830; PIND:BA21786.1; PID:92329831
R/Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19, 1465-1489, 1996
A/Title: Isolation and characterization of a cDNA encoding a ribosome-inactivating protein from Karasurin-B and Ka
A/Reference number: J05032; MUID:97108849; PMID:8951163
A/Accession: J05033
A/Status: preliminary
A/Molecule type: protein
A/Residues: 22-270 <KON>
C/Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F/22-270/Product: Karasurin C #status predicted <MKG>
F/24-270/Product: Karasurin A #status predicted <MKG>
F/27-266/Domain: rRNA N-glycosidase homology <RNG>

Query Match

Best Local Similarity 37.2%; Score 328; DB 2; Length 289;
Matches 90; Conservative 48; Mismatches 86; Indels 16; Gaps 10;

OY 13 TGDYFRFTLLRDVYSSGSFSN--EIPLLRSTIPVSDAQRFLVETLNGQDSTAAIDV 72
DB 33 TSSGIVFISNRKALPERKLYDILR-STLRGS--QRYALHILNVADETISVAIDV 89
OY 73 TNAYVAVQAGDQSYFLRDA-FRGAFTLFTGTRBSSLPFGSYTDLRYAAGH-RDOI 130
DB 90 TNYVWGRAGDTSIFPNSASAEAKVYKDAK-KVTLFYSNTERLOIAKIKRNI 148
OY 131 PLGIEQLQSVASALRYPGSGTFAQAASILLIQMISAPAREPILMYRRODINS--GSEF 188
DB 149 PLGIPALDSAITLFTYNNASASA--LWVLIQSTSSAAKXFI---EQGIKRYDKTF 202
OY 189 LPMVWLELFTSMQGSQTVQ--HSTDGVPNNPFLAISTGNFYLISVNS--VIALAI 244
DB 203 LPSALISLNSMSLSKQIQIASTNQCETFPVLINQORVITVDAVTSNIAL 262
OY 245 ML 246

DB 263 LL 264

RESULT 14

UC5606
rRNA N-glycosidase (EC 3.2.2.22) momordin II - balsam apple
C/Species: Trichosanthes anguina (snake gourd)
C/Date: 15-Aug-1996 #sequence_revision 24-Oct-1997 #text_change 05-Dec-1997
C/Accession: J25560
R/Ortigao, M.; Better, M.
Nucleic Acids Res. 20, 4662, 1992
A/Title: Momordin II, a ribosome inactivating protein from Momordica balsamina, is hom
A/Reference number: J25560; MUID:93021710; PMID:1408771
A/Accession: J25560
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-286 <KON>
A/Cross-references: DBJ:U012175; NID:919525; PIND:CA78166.1; PID:919526
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C/Keywords: Glycosidase; hydrolase
F/27-264/Domain: rRNA N-glycosidase homology <RNG>

Query Match

Best Local Similarity 24.2%; Score 314; DB 2; Length 286;
Matches 85; Conservative 49; Mismatches 89; Indels 20; Gaps 9;

OY 13 TGDYFRFTLLRDVYSSGSFSN--EIPLLRSTIPVSDAQRFLVETLNGQDSTAA 69
DB 33 TKTITFT--EDFKALTFPSKHTVILALYST--LSSKRFLLDDISVAYETISA 86
OY 70 IDNVAVVAVQAGDQSYFLRDAFRGAFTLFTGTRBSSLPFGSYTDLRYAAGH--R 127
DB 87 IDNVAVVAVRTRDVSYPFKESPFAKVVILFQTR-KITPLGYENLQ7-AAHTR 143
OY 128 DQPLGIEQLQSVASALRYPGSGTFAQAASILLIQMISAPAREPILMYRRODINS 187
DB 144 ENIDGLPLSSAITLFTYNNQSPSA--LWVLIQSTSSAAKXFI--ATN 199
OY 189 LPMVWLELFTSMQGSQTVQ--HSTDGVPNNPFLAISTGNFYLISVNS--VIALAI 245
DB 200 LPSALISLNSMSLSKQIQIASTNQCETFPVLINQORVITVDAVTSNIAL 259
OY 246 LFV 248
DB 260 LL 262

RESULT 15

UC8440
rRNA N-glycosidase (EC 3.2.2.22) trichogangulina - snake gourd
C/Species: Trichosanthes anguina (snake gourd)
C/Date: 15-Aug-1996 #sequence_revision 24-Oct-1997 #text_change 05-Dec-1997
C/Accession: J25560
R/Chow, L.P.; Kame, N.; Kan, G.T.; Ueno, Y.; Tsugita, A.
Biomol. Sci. 3, 178-186, 1996
A/Title: Amino acid sequence of trichogangulina, a ribosomal-inactivating protein from
A/Reference number: J08440
A/Accession: J08440
A/Molecule type: protein
A/Residues: 1-132, 'S', 134-245 <CHO1>
A/Experimental source: seed
A/Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Tak
A/Accession: J08440
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-50, 'V', 52-245 <CHO2>
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C/Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed
F/4-242/Domain: rRNA N-glycosidase homology <RNG>
F/51-201/Binding site: carbohydrate (asn) (covalent) #status experimental

A:Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'E', 405, 527, 'E', 529-564, 'W', 566, 'H', 567-570, 'LI', 573-574, 'F', 'PUN>
A:Note: this paper, one of a series, summarizes the experimental details for the determi
R:Ready, M.P.; Kim, Y.; Robertus, J.D.
Protein 10, 270-278, 1991
A:Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism c
A:Accession: A24261, A24210
A:Contents: annotation active site
R:Rutemeyer, E.; Robertus, J.D.
Protein 10, 260-269, 1991
A:Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A:Reference number: A48239; PMID:91352005; PMID:1881882
A:Contents: annotation; X-ray crystallography, 2.5 angstroms
R:Katzin, B.J.; Collins, E.J.; Robertus, J.D.
Protein 10, 251-259, 1991
A:Title: Structure of ricin A-chain at 2.5 angstroms.
A:Reference number: A48239; PMID:91352004; PMID:1881881
A:Contents: annotation; X-ray crystallography, 2.5 angstroms
C:Comment: The functional mechanism of ricin is the inhibition of the 60S ribosomal sub
C:Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal sub
C:Comment: This protein is cytotoxic and very poisonous to animals.
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
C:Superfamily: ricin; RNA N-glycosidase homology
F/1-35/Domain: signal sequence #status predicted <SIG>
F/36-302/Product: ricin D chain A #status experimental <ACH>
F/46-293/Domain: RNA N-glycosidase homology <RNG>
F/315-576/Product: ricin D chain B #status experimental <BCB>
F/325-329/Domain: 417-485, 462-497, 501-540, 543-576/Region: 40-Residue repeats
F/315-576/Region: 417-485, 462-497, 501-540, 543-576/Region: 40-Residue repeats
F/115-158/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/115-158/Binding site: carbohydrate (Glu, Tyr, Glu, Asn) #status predicted
F/212/Active site: Arg #status experimental
F/215/Active site: Arg #status predicted
F/294-318/334-353, 377-394, 465-478, 504-521/Disulfide bonds: #status experimental
F/336, 349, 360/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status experimental
F/358, 569/Binding site: N-acetylglucosamine (Asp, Asn) #status experimental
Query Match 30.5%; Score 396; DB 1; Length 576;
Best Local Similarity 40.2%; Pred. No. 9, 8e-28;
Matches 103; Conservative 45; Mismatches 96; Indels 12; Gaps 8;
9 THQTGDEYFPTILADYVSSGS-FSNEPPL-RSGTIPVSDQRFVLELNOGQDSI 66
48 TAAQVGSYTNFIRAVGRHTTGADVREHFPILPRVGLPIN-QRFILVLSNHAELSV 105
67 TAAIDVTNAVYVAVOAGQSYFLR-DAPRGAR-THLFTGTRRSSTLFTGSYDLEKY 123
106 TLADVTNAVYVAVOAGQSYFLR-DAPRGAR-THLFTGTRRSSTLFTGSYDLEKY 123
124 AGR-RDQIFGIRBOLIOSVALRY--FGSSTRAQANSTLILOMISAAKRNPILMRYR 179
165 AGNKRKRIELGNGPLERIALSALYVSTGQCPILASFWICLQMSAAKFOYIEBMR 224
180 QDINGSSEFLPMWVLELFTSMGQSGTOVGHSTGVNPRILASTGNVTLNSVASYA 239
225 TRIVYRRSADPDSVITLNSMGRSLTIQESNQCAPASPIQGRNNGSKFYVDVSLII 284
240 ASLAIWLFVCGEPPSS 255
285 PRLIMVYRCAPPPSS 300
RESULT 9
agglutinin precursor - castor bean
N:Contents: RNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C>Date: 31-Dec-1993 #sequence _revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: A24261, A24210
R:Robertus, J.D.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
J:BioL. Chem. 260, 15682-15686, 1985
A:Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
A:Reference number: A24261; PMID:85059449; PMID:2999130

A:Accession: A24261
A:Molecule type: mRNA
A:Residues: 1-564 <RNB>
A:Cross-references: GB:MI2089; NID:9169700; PIRN:AAA3869.1; PIR:G169701
R:Markl, T.; Yoshioke, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A:Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglu
A:Accession: A24210 A24210
A:Molecule type: protein
A:Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553
C:Comment: This protein has strong agglutinating activity and weak cytotoxicity compar
C:Superfamily: ricin; RNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F/25-230/Product: signal sequence #status predicted <SIG>
F/25-230/Product: agglutinin chain A #status predicted <ACH>
F/25-281/Domain: RNA N-glycosidase homology <RNG>
F/315-576/Product: agglutinin chain B #status experimental <BCB>
F/315-576/Region: 417-485, 462-497, 501-540, 543-576/Region: 40-Residue repeats
F/315-576/Region: 417-485, 462-497, 501-540, 543-576/Region: 40-Residue repeats
F/104-147/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/104-147/Binding site: carbohydrate (Glu, Tyr, Glu, Asn) #status predicted
F/200, 203/Active site: Glu, Arg #status predicted
F/282-306, 322-341, 365-382, 453-465, 492-509/Disulfide bonds: #status predicted
F/324, 337, 348/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status predicted
F/397, 437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/336, 557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
Query Match 30.2%; Score 392.5; DB 1; Length 564;
Best Local Similarity 39.2%; Pred. No. 2e-27100; Indels 11; Gaps 7;
Matches 100; Conservative 44; Mismatches 100; Indels 11; Gaps 7;
9 THQTGDEYFPTILADYVSSGS-FSNEPPL-RSGTIPVSDQRFVLELNOGQDSI 66
37 TAAQVGSYTNFIRAVGRHTTGADVREHFPILPRVGLPIN-QRFILVLSNHAELSV 94
67 TAAIDVTNAVYVAVOAGQSYFLR-DAPRGAR-THLFTGTRRSSTLFTGSYDLEKY 123
95 TLADVTNAVYVAVOAGQSYFLR-DAPRGAR-THLFTGTRRSSTLFTGSYDLEKY 123
124 AGR-RDQIFGIRBOLIOSVALRY--FGSSTRAQANSTLILOMISAAKRNPILMRYR 180
165 AGNKRKRIELGNGPLERIALSALYVSTGQCPILASFWICLQMSAAKFOYIEBMR 213
181 DINGSSEFLPMWVLELFTSMGQSGTOVGHSTGVNPRILASTGNVTLNSVASYA 240
214 RIVYRRSADPDSVITLNSMGRSLTIQESNQCAPASPIQGRNNGSKFYVDVSLII 273
241 ASLAIWLFVCGEPPSS 255
274 PRLIMVYRCAPPPSS 288
RESULT 10
karsanin-B - Trichosanthes kirilowii var. japonica
C:Species: Trichosanthes kirilowii var. japonica
C>Date: 27-Feb-1997 #sequence _revision 27-Feb-1997 #text_change 23-May-1997
C:Accession: U05032
R:Kondo, T.; Mizukami, H.; Takeda, T.; Ogiwara, Y.
BioL. Pharm. Bull. 19, 1485-1489, 1996
A:Title: Amino acid sequences and ribosome-inactivating activities of karsanin-B and
A:Reference number: U05032; PMID:97108848; PMID:8951169
A:Accession: U05032
A:Status: preliminary
A:Keywords: type I ricin
C:Comment: This protein belongs to type I ribosomal-inactivating proteins which catal
C:Superfamily: ricin; RNA N-glycosidase homology
F/4-243/Domain: RNA N-glycosidase homology <RNG>
Query Match 25.4%; Score 330; DB 2; Length 247;
Best Local Similarity 37.2%; Pred. No. 2.7e-72;
Matches 90; Conservative 48; Mismatches 86; Indels 18; Gaps 10;

Db 125 ECISLGQALFHAISFASGASNDSEKXETLVLIIOMASBNARYETNSRVGSIKCTA 184
 QY 188 FLPMYVLELTSWGQOSTVOYHSTDCVNRNPFEL-AISTGNFVTLNSVSVIASLAIATL 246
 Db 185 FOEPDPAULSLNNWMDLNSRGVGSVQDTPFNPAVTLNRVQNPVIVDSLTHGSAVALATL 244
 QY 247 FVC 249
 Db 245 FVC 247

RESULT 4

S32431
 abrin-d precursor - Indian licorice (fragment)
 N/contains: rRNA N-glycosidase (EC 3.2.2.22)
 C/species: Abrus precatorius (Indian licorice)
 C/date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
 R/accession: S32431, S34408
 R/mol: Biol 229, 263-267 1993
 J Mol Biol 229, 263-267 1993
 A/title: Primary structure of three distinct isobritins determined by cDNA sequencing.
 A/reference number: S32429; PMID:93132798; PMID:842333
 A/accession: S32431
 A/molecule type: mRNA
 A/residues: 1-528 <HND>
 A/cross-references: GB:M98346
 R/hung, C.; Lee, M.; Lee, T.; Lin, J.
 submitted to the EMBL Data Library, March 1993
 A/reference number: S34408
 A/molecule type: mRNA
 A/residues: 1-169 'C', 171-320 'U', 322-628 <HD>
 A/cross-references: GB:M98346
 C/comment: Abirin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.
 C/superfamily: ricin; rRNA N-glycosidase homology
 C/keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F
 F/1-251/Product: abrin-d chain A #status predicted <RCH>
 F/1-246/Domains: rRNA N-glycosidase homology <RNG>
 F/261-328/Product: abrin-d chain B #status predicted <RCH>
 F/261-328/Domains: rRNA N-glycosidase homology <RNG>
 F/1/Modified site: pyrolydione 49,153,371; 42,483,538/Region: 40-residue repeats
 F/74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F/164,167/Active site: Glu, Arg #status predicted
 F/200,253,361,401,402/Binding site: carboxylate (Asp) (covalent) #status predicted
 F/247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
 F/288,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F/500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 34.5%; Score 448; DB 2; Length 528;
 Best Local Similarity 44.4%; Pred. No. 1.7e-32;

Matches 108; Conservative 36; Mismatches 93; Indels 6; Gaps 5;

QY 9 THCTGDEYRFTLLADPVSSGSFNSLPLKQSTTVSDAQSPVAVELTNGQDSTRA 68
 Db 9 TEGATSSYKQFTEALRQRL-TGGLIHDPVLPDPT-TVEERKRITVLSNSRSESLV 66
 QY 69 AIDVTNAVVAAYQAGQSYFLADARGGTEHLFTGTRRGRASLPTGSGYTLDERYAGH-R 127
 Db 67 GIDVTNAVVAAYRAGQSYFLADARGGTEHLFTGTRRGRASLPTGSGYTLDERYAGH-R 124
 QY 128 DOIPIGIEGLQISVALRYFGSSTPAQARSILLIOMISBAAPNPILMARVODINSSES 187
 Db 128 DOIPIGIEGLQISVALRYFGSSTPAQARSILLIOMISBAAPNPILMARVODINSSES 187
 QY 125 EELISGQALFHAISFASGASNDSEKXETLVLIIOMASBNARYETNSRVGSIKCTA 184
 Db 125 EELISGQALFHAISFASGASNDSEKXETLVLIIOMASBNARYETNSRVGSIKCTA 184
 QY 188 FLPMYVLELTSWGQOSTVOYHSTDCVNRNPFEL-AISTGNFVTLNSVSVIASLAIATL 246
 Db 188 FOEPDPAULSLNNWMDLNSRGVGSVQDTPFNPAVTLNRVQNPVIVDSLTHGSAVALATL 244
 QY 247 FVC 249
 Db 245 FVC 247

RESULT 5

S16022
 abrin-c precursor - Indian licorice
 N/contains: rRNA N-glycosidase (EC 3.2.2.22)
 C/species: Abrus precatorius (Indian licorice)
 C/date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
 R/accession: S16022, S16023
 R/mol: Biochem 198, 723-732, 1991
 Eur J Biochem 198, 723-732, 1991
 A/title: Preproabrin: genomic cloning, characterization and the expression of the A-chain
 A/reference number: S16022; PMID:9166997; PMID:2050149
 A/accession: S16022
 A/status: preliminary
 A/molecule type: DNA
 A/residues: 1-562 <MOD>
 A/cross-references: EMBL:X55667; NID:G16084; PIDN:CA939202.1; PID:G16085
 C/comment: Abirin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.
 C/superfamily: ricin; rRNA N-glycosidase homology
 C/keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid
 F/41-280/Product: abrin-c chain A #status predicted <RCH>
 F/295-562/Product: abrin-c chain B #status predicted <RCH>
 F/317-359,360-400,403-441,448-483,487-526,529-562/Region: 40-residue repeats
 F/35/Modified site: pyrolydione carboxylic acid (Gln) (in mature form) #status predicted
 F/108,147,229,230/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F/198,201/Active site: Glu, Arg #status predicted
 F/234,287,335,435,435,435/Binding site: carboxylate (Asn) (covalent) #status predicted
 F/252-303,320-359,369-380,431-464,480-507/Disulfide bonds: #status predicted
 F/531,555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 34.5%; Score 448; DB 2; Length 562;
 Best Local Similarity 44.4%; Pred. No. 1.9e-32;

Matches 108; Conservative 36; Mismatches 93; Indels 6; Gaps 5;

QY 9 THCTGDEYRFTLLADPVSSGSFNSLPLKQSTTVSDAQSPVAVELTNGQDSTRA 68
 Db 9 TEGATSSYKQFTEALRQRL-TGGLIHDPVLPDPT-TVEERKRITVLSNSRSESLV 100
 QY 69 AIDVTNAVVAAYQAGQSYFLADARGGTEHLFTGTRRGRASLPTGSGYTLDERYAGH-R 127
 Db 67 GIDVTNAVVAAYRAGQSYFLADARGGTEHLFTGTRRGRASLPTGSGYTLDERYAGH-R 124
 QY 128 DOIPIGIEGLQISVALRYFGSSTPAQARSILLIOMISBAAPNPILMARVODINSSES 187
 Db 128 DOIPIGIEGLQISVALRYFGSSTPAQARSILLIOMISBAAPNPILMARVODINSSES 187
 QY 125 EELISGQALFHAISFASGASNDSEKXETLVLIIOMASBNARYETNSRVGSIKCTA 218
 Db 125 EELISGQALFHAISFASGASNDSEKXETLVLIIOMASBNARYETNSRVGSIKCTA 218
 QY 188 FLPMYVLELTSWGQOSTVOYHSTDCVNRNPFEL-AISTGNFVTLNSVSVIASLAIATL 246
 Db 188 FOEPDPAULSLNNWMDLNSRGVGSVQDTPFNPAVTLNRVQNPVIVDSLTHGSAVALATL 278
 QY 247 FVC 249
 Db 279 FVC 281

RESULT 6

S32430
 abrin-b precursor - Indian licorice (fragment)
 N/contains: rRNA N-glycosidase (EC 3.2.2.22)
 C/species: Abrus precatorius (Indian licorice)
 C/date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
 R/accession: S32430, S34408
 R/mol: Biol 229, 263-267 1993
 J Mol Biol 229, 263-267 1993
 A/title: Primary structure of three distinct isobritins determined by cDNA sequencing.
 A/reference number: S32429; PMID:93132798; PMID:842333
 A/accession: S32430
 A/molecule type: mRNA
 A/residues: 1-527 <HND>
 A/cross-references: GB:M98345; NID:G166296; PIDN:AAA36255.1; PID:G166297

A:Accession: S32429
 A:Status: nucleic acid sequence not shown
 A:Residues: 178
 A:Residues: 178
 A:Cross-references: GB:M8344; NID:9166294; PTDN:AAA3624.1; PID:9166295
 A:Note: the coding region for the sequence shown is preceded by an ATG codon
 A:Note: residues 1-8 were derived from the synthesized primer
 R:Punatsu, G.; Taguchi, Y.; Kamemoto, M.; Yanaka, M.
 A:Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from
 A:Reference number: J0202
 A:Accession: J0202
 A:Molecule type: protein
 A:Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 R:Evensen, G.; Mathiesen, A.; Sundan, A.
 A:Title: Direct molecular cloning and expression of two distinct abrin A-chains.
 A:Reference number: A39761; MIMD:91201329; PMID:2016300
 A:Accession: A39761
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 78, '2-251, <EVZ>
 A:Cross-references: GB:M8344
 A:Note: residues 1-8 were derived from the synthesized primer
 R:Punatsu, G.; Taguchi, Y.; Kamemoto, M.; Yanaka, M.
 A:Title: The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic
 A:Reference number: J01398; MIMD:91201329; PMID:7763422
 A:Contents: seeds
 A:Accession: J01398
 A:Molecule type: protein
 A:Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>
 A:Experimental source: seed
 R:Evensen, G.; Mathiesen, A.; Sundan, A.
 A:Title: The complete primary structure of abrin-a, B chain.
 A:Description: Direct molecular cloning of two distinct abrin A-chains.
 A:Accession: S14471
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 78, '2-251, <EVZ>
 A:Cross-references: EMBL:X54873; NID:9166294; PTDN:CAA3655.1; PID:9166295
 R:Chen, Y.L.; Chow, L.P.; Tsugita, A.; Lin, C.Y.
 A:Title: The complete primary structure of abrin-a, B chain.
 A:Reference number: S24133; MIMD:92371656; PMID:1505674
 A:Accession: S24133
 A:Molecule type: protein
 A:Residues: 262-257, 'Y', 259-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 <CHE>
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 R:Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
 A:Title: Probing the domain structure of abrin-a by tryptic digestion.
 A:Reference number: S74110; MIMD:97008945; PMID:8856055
 A:Accession: S74110
 A:Molecule type: protein
 A:Residues: 89-108, 154-172 <LIN>
 A:Experimental source: seed
 A:Accession: S74110
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 262-276, 'X', 278-280, 329-348, 369-388, 399-418 <LIN>
 A:Experimental source: seed
 A:Comment: Abtin-a is more toxic than rich. The toxin consists of an A chain, which has
 C:superfamily: ricin, rRNA N-glycosidase homology
 C:Keywords: duplication; glycoprotein; glycosidase; hydrolyase; lectin; pyroglycamic acid
 F:1-251/Protein: abrin-a chain A #status experimental <KIM>
 F:7-246/Domain: rRNA N-glycosidase homology experimental <KIM>
 F:261-326/Protein: abrin-a chain B #status experimental <KIM>
 F:327-407/Domain: rRNA N-glycosidase homology experimental <KIM>
 F:2/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:164,167/Active site: Glu, Arg #status predicted

F:247-269, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted
 F:288, 312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F:361, 401/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:500, 521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 Query Match 37.08; Score 460; DB 1; Length 528;
 Best Local Similarity 33.58; Evalue 2.2e-35;
 Matches 110; Conservative 37; Mismatches 80; Indels 26; Gaps 6;
 QY 9 THGTTGDEYRFTLLRDVSSGSPENETPLRQETIPVSDAQRFLVETLNGQDSITL 68
 DB 9 TGAATGQSYQFTALRRLRGLHIDIVLPDPT-TLQERNRYITVELSDTESIEV 66
 QY 69 AIDVTAAVVAQAGDSYFLRDPAPGAETHLFTGTRRSALPFGSYDLERYAHR-R 127
 DB 67 GIDVTAAVVAQAGDSYFLRDPAPGAETHLFTGTRRSALPFGSYDLERYAHR-R 124
 QY 128 DQITPLGDLQSGALRRFGSTRKORRSTILMOKISAPAPNITLMRRQDINSGES 187
 DB 125 QDITPLGDLQSGALRRFGSTRKORRSTILMOKISAPAPNITLMRRQDINSGES 184
 QY 188 ELPPMTATLEPTSGQDSYQVGHSTGCVFNNPRLATSGNFVTLNPNVS----- 237
 DB 185 POPDAMTSLNNMNLRSQVGVOCDFPVO-----VTLNTRNRPVYDLSLH 234
 QY 238 -VTSALATMFPVC 249
 DB 235 PTVAVALMLFVC 247
 RESULT 3
 C39761 (clone 7.2) precursor - Indian joricice (fragment)
 N:Contig: rRNA N-glycosidase (EC 3.2.2.22)
 C:Species: Abiru precatocius (Indian joricice)
 C:Date: 21-Feb-1992 #sequence revision 31-Dec-1993 #text change 20-Aug-1993
 C:Accession: C39761; S14471
 J:Evensen, G.; Mathiesen, A.; Sundan, A.
 A:Title: Direct molecular cloning and expression of two distinct abrin A-chains.
 A:Reference number: A39761; MIMD:91201329; PMID:2016300
 A:Accession: C39761
 A:Molecule type: DNA
 A:Residues: 78, '2-251, <EVZ>
 A:Cross-references: EMBL:X54873; NID:9166294; PTDN:CAA3655.1; PID:9166295
 R:Evensen, G.; Mathiesen, A.; Sundan, A.
 A:Title: The complete primary structure of abrin-a, B chain.
 A:Description: Direct molecular cloning of two distinct abrin A-chains.
 A:Reference number: S14471
 A:Accession: S14471
 A:Molecule type: protein
 A:Residues: 89-108, 154-172 <LIN>
 A:Experimental source: seed
 A:Accession: S74110
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 262-276, 'X', 278-280, 329-348, 369-388, 399-418 <LIN>
 A:Experimental source: seed
 A:Comment: Abtin-a is more toxic than rich. The toxin consists of an A chain, which has
 C:superfamily: ricin, rRNA N-glycosidase homology
 C:Keywords: duplication; glycoprotein; glycosidase; hydrolyase; lectin; toxin
 F:1-251/Protein: abrin-a chain A #status experimental <KIM>
 F:7-246/Domain: rRNA N-glycosidase homology experimental <KIM>
 F:261-326/Protein: abrin-a chain B #status experimental <KIM>
 F:327-407/Domain: rRNA N-glycosidase homology experimental <KIM>
 F:2/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:164,167/Active site: Glu, Arg #status predicted
 Query Match 35.64; Score 462; DB 2; Length 251;
 Best Local Similarity 44.94; Evalue 3.2e-34;
 Matches 109; Conservative 36; Mismatches 92; Indels 6; Gaps 5;
 QY 9 THGTTGDEYRFTLLRDVSSGSPENETPLRQETIPVSDAQRFLVETLNGQDSITL 68
 DB 9 TGAATGQSYQFTALRRLRGLHIDIVLPDPT-TLQERNRYITVELSDTESIEV 66
 QY 69 AIDVTAAVVAQAGDSYFLRDPAPGAETHLFTGTRRSALPFGSYDLERYAHR-R 127
 DB 67 GIDVTAAVVAQAGDSYFLRDPAPGAETHLFTGTRRSALPFGSYDLERYAHR-R 124
 QY 128 DQITPLGDLQSGALRRFGSTRKORRSTILMOKISAPAPNITLMRRQDINSGES 187
 DB 125 QDITPLGDLQSGALRRFGSTRKORRSTILMOKISAPAPNITLMRRQDINSGES 184
 QY 188 ELPPMTATLEPTSGQDSYQVGHSTGCVFNNPRLATSGNFVTLNPNVS----- 237
 DB 185 POPDAMTSLNNMNLRSQVGVOCDFPVO-----VTLNTRNRPVYDLSLH 234
 QY 238 -VTSALATMFPVC 249
 DB 235 PTVAVALMLFVC 247

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us-09-601-667c-11.ra1

Page 8

Query Match 8.7%; Score 122.5; DB 2; Length 492;
Best Local Similarity 32.4%; Pred. No. 0.00021;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;
QY 22 VYRDDPFDENQOLMESKNNNDNQATIKDQTIKNSG-CITTYGTAKYTMFD 80
DB 379 IDVKNATADGQVQVLDCHGS--NQWYTSAGCFRIENKCLDAGSGMNAVQIYS 436
QY 81 CHTAVREKATYQIMWNGTIIIPRSNVLAASSGIKSTITVQ 122
DB 437 CWGQANOK--WELRDGIIYVQSGICLDVGGGTNGRIQ 476

Search completed: December 11, 2003, 14:11:36
JOB time : 10.1403 secs

Thu Dec 11 16:09:47 2003

us-09-601-667c-11.ra1

Page 7

Oy 7 ASEP-----TVAIGRNKRVYDDDFHDSNQIOLMPKSNNDPVQMTIKRD 55
Db 354 SSSPPXXXXXADGQIKGVG-SRCLDVPDASISDGLQMDCHSGT--NQMAATDA 410
Oy 56 GTIRSNQ-SCLTGYGTAGVYVMI FDCNTAVREATTIQTIMQNTIINRSNLVLA--SS 112
Db 411 GELRYVGDCLDPAAGTSNGSKVQIYSCMGDNGK--RLNSDGVYGVQSLCLDAVNG 468
Oy 113 GIKGTTLVQTLDTYLGQGW 132
Db 469 TANGTLIOLYTCSNGSNRW 488

RESULT 14
US-09-770-621-8

Sequence 8, Application US/09770621
US-09-770-621-8
GENERAL INFORMATION:
Applicant: M nyl, Atja
Applicant: Vehmaaper, Jari
Applicant: Fagerstr m, Richard
Applicant: Lantto, Raija
Applicant: Palohelmo, Marja
Applicant: Suominen, Piirko
Applicant: Lahtinen, Taina
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDNESS: No. 6506593 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-09-770-621-8

Query Match 8.7%; Score 122.5; DB 4; Length 491;
Best Local Similarity 28.6%; Pred.No.0.00021;
Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;
Oy 7 ASEP-----TVAIGRNKRVYDDDFHDSNQIOLMPKSNNDPVQMTIKRD 55
Db 354 SSSPPXXXXXADGQIKGVG-SRCLDVPDASISDGLQMDCHSGT--NQMAATDA 410
Oy 56 GTIRSNQ-SCLTGYGTAGVYVMI FDCNTAVREATTIQTIMQNTIINRSNLVLA--SS 112
Db 411 GELRYVGDCLDPAAGTSNGSKVQIYSCMGDNGK--RLNSDGVYGVQSLCLDAVNG 468
Oy 113 GIKGTTLVQTLDTYLGQGW 132
Db 469 TANGTLIOLYTCSNGSNRW 488

RESULT 15
US-08-468-812-4

Sequence 4, Application US/09468812
US-08-468-812-4
GENERAL INFORMATION:
Patent No. 5938836
Applicant: Vehmaaper, Jari
Applicant: M nyl, Atja
Applicant: Fagerstr m, Richard
Applicant: Lantto, Raija
Applicant: Palohelmo, Marja
Applicant: Suominen, Piirko
Applicant: Lahtinen, Taina
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-812-4

Thu Dec 11 16:09:47 2003

us-09-601-667c-11.rat

Page 6

DB 379 IDVPKNTADGTQVYKDCSSG--NOQVTTSSGSEFIFKNCICLDAGSSNGAVVQIS 436
QY 81 CNTAVRENTIWOIMNGTINPNSLVLAASSGINKETTLVQ 122
DB 437 CWGANCK--WELRADGTIVGVSGICLDVAGGTSNGETILQ 476

RESULT 12
US-08-468-812-8
Sequence 8, Application US/08468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vahmanper, Jari
APPLICANT: M nyl, Arja
APPLICANT: Pagarstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lantinen, Tarja
APPLICANT: Kistio, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION/DOCKET NUMBER: 35,086
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2640
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDNESS: not relevant
MOLECULAR TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-08-468-812-8

Query Match 8.7%; Score 122.5; DB 2; Length 491;
Best Local Similarity 28.6%; Pred. No. 0.00021;
Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;

DB 7 ASEP-----TWRIYGRNQMVDVDDDFHDGQIQWPSKSNDDPQWLTIKRD 55
354 SSEPXXXXXXADGGQIKVIG-SRGLDVPDASTSDTOLJMDCHSCT--NOQMAATDA 410

QY 56 GTIRANG-SCLTGYGYAGVYVWIFDCNRAVENTIWOIMNGTINPNSLVLA--SS 112
DB 411 GELRYVDPKCLDAGTSGNSKVOIYSCGSDNCK--WELNSDSYGVSGICLDVANG 468
QY 113 GIKGTTLVQTLIDVTLGQGM 132
DB 469 TANGTLQTLTCSGNGNM 488

RESULT 13
US-08-590-563-8
Sequence 8, Application US/08590563
Patent No. 6300114
GENERAL INFORMATION:
APPLICANT: Vahmanper, Jari
APPLICANT: M nyl, Arja
APPLICANT: Pagarstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lantinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION/DOCKET NUMBER: 35,086
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2640
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDNESS: not relevant
MOLECULAR TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-08-590-563-8

Query Match 8.7%; Score 122.5; DB 4; Length 491;
Best Local Similarity 28.6%; Pred. No. 0.00021;
Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;

Db 379 IDVENNTADGTVOYLIDCHSSG--NQOMTYTSSGGERIFGKMLDAGSSNCAVVOYIS 436
Qy 81 CNTAVREATITWQITINRSNTVLAASGIGKTTITVQ 122
Db 437 CNGANOK--WEIRADGITIVGSGCLDAVGGGTGNGTRLD 476

RESULT 10
US-08-590-563-5
Sequence 5, Application US/08590563
Patent No. 6300114
GENERAL INFORMATION:
APPLICANT: M. Kivela, Arja
APPLICANT: Vennamper, Jari
APPLICANT: Fagerstedt, Richard
APPLICANT: Lantto, Ralfja
APPLICANT: Palohimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and secretion of proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JUN-1996
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STANDARDNESS: not relevant
MOLECULE TYPE: peptide
TOPOLOGY: linear
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-08-590-563-5

Query Match 8.7%; Score 122.5; DB 4; Length 480;
Best Local Similarity 32.4%; Pred. No. 0.0002;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;
Qy 22 VDVARDDFHGNQIQLPKSKNDNPQMLTKRKDTIRNSGS-CLTYGYTAAGVYVIMFD 80

Db 379 IDVENNTADGTVOYLIDCHSSG--NQOMTYTSSGGERIFGKMLDAGSSNCAVVOYIS 436
Qy 81 CNTAVREATITWQITINRSNTVLAASGIGKTTITVQ 122
Db 437 CNGANOK--WEIRADGITIVGSGCLDAVGGGTGNGTRLD 476

RESULT 11
US-09-770-621-5
Sequence 5, Application US/09770621
Patent No. 6506593
GENERAL INFORMATION:
APPLICANT: M. Kivela, Arja
APPLICANT: Vennamper, Jari
APPLICANT: Fagerstedt, Richard
APPLICANT: Lantto, Ralfja
APPLICANT: Palohimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and secretion of proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STANDARDNESS: No. 6506593 Relevant
MOLECULE TYPE: peptide
TOPOLOGY: linear
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-09-770-621-5

Query Match 8.7%; Score 122.5; DB 4; Length 480;
Best Local Similarity 32.4%; Pred. No. 0.0002;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;
Qy 22 VDVARDDFHGNQIQLPKSKNDNPQMLTKRKDTIRNSGS-CLTYGYTAAGVYVIMFD 80

Thu Dec 11 16:09:47 2003

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Page 4

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; APPLICANT: Halkier, Torben
; APPLICANT: Hedegaard, Lisbeth
; TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
; FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159.106
; EARLIER FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1996-08-23
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1997-04-14
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-15

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Query Match
Best Local Similarity 9.6%; Score 136; DB 3; Length 132;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;

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OY 18 NGNRVYVDDDDPHDNGNOIQLPKSKNDPNQMTIRKDGITRSNGSCLTYY--GYTAGY 75
DB 14 NGMCVDPWADPFTGNPVQVITGSGN--AAQWTFRSGDTPVRLAKGLVDRDSTTRGA 71
OY 76 VMIPDCTAVREATIWOIW--DNGT--INPRSNLYLAASSGI--KQTLTVQGLDPTL 128
DB 72 VQWWTGN-----GTGAKRKAYDAGSKALRNPQSGCLDHTGAPLRDQRLQWTWNGTT 126
OY 129 GQGM 132
DB 127 AQGM 130

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RESULT 8
US-09-159-106-11
; Sequence 11, Application US/09159106
; Patent No. 6284509
; GENERAL INFORMATION:
; APPLICANT: Dietter, Ivan
; APPLICANT: Hedegaard, Lisbeth
; TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
; FILE REFERENCE: 4693.204-US
; CURRENT APPLICATION NUMBER: US/09/159.106
; EARLIER FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: 0427/96
; EARLIER FILING DATE: 1996-12-04
; EARLIER APPLICATION NUMBER: 0885/96
; EARLIER FILING DATE: 1998-08-23
; EARLIER APPLICATION NUMBER: PCT/DK97/00160
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11

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Query Match
Best Local Similarity 9.6%; Score 136; DB 3; Length 435;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;
OY 18 NGNRVYVDDDDPHDNGNOIQLPKSKNDPNQMTIRKDGITRSNGSCLTYY--GYTAGY 75
DB 317 NGMCVDPWADPFTGNPVQVITGSGN--AAQWTFRSGDTPVRLAKGLVDRDSTTRGA 374

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OY 76 VMIPDCTAVREATIWOIW--DNGT--INPRSNLYLAASSGI--KQTLTVQGLDPTL 128
DB 14 NGMCVDPWADPFTGNPVQVITGSGN--AAQWTFRSGDTPVRLAKGLVDRDSTTRGA 71
OY 129 GQGM 132
DB 430 AQGM 433

```

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RESULT 9
US-08-468-812-5
; Sequence 5, Application US/08468812
; Patent No. 5935836
; GENERAL INFORMATION:
; APPLICANT: Vermaander, Jari
; APPLICANT: M neyl, Arja
; APPLICANT: Fagerberg, Richard
; APPLICANT: Pajolahti, Risto
; APPLICANT: Pajolahti, Maria
; APPLICANT: Suominen, Marko
; APPLICANT: Lahtinen, Tarja
; APPLICANT: Kristo, Paula
; TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.812
; FILING DATE: 06-08-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332.412
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 08/282.001
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BEGLISBY, Jarry J.
; RESIDENTIAL OR COMMERCIAL NUMBER: 31.086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2640
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FUNCTION: unknown
; POSTTRANSLSIONAL MODIFICATION:
; CHARACTERISTICS/REMARKS:
; SOURCE: GENBANK/SEQUENT: AM50
US-08-468-812-5

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Query Match
Best Local Similarity 8.7%; Score 122.5; DB 2; Length 480;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;
OY 22 VVVRDDDDPHDNGNOIQLPKSKNDPNQMTIRKDGITRSNGS--CLTGYTAGYVWTFD 80

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Page 3

QY 5 CSASEPTVAIVGRNMGKRVDDDFHDNQIOLMPKSNNDPNQIWKIKEDGTIRNSGC 64
DB 282 CMDEPTVAIVGRNMGKRVDDDFHDNQIOLMPKSNNDPNQIWKIKEDGTIRNSGC 341
QY 65 LITVGTAGVYVIMFPCNTARENTIWOIINGTIIIPRSNTIILASSGICITITLQTL 124
DB 342 LITKSSPRQCVIYVNCSTATVQATRMQITKMTIIPRSQIILASSGICITITLQTL 401
QY 125 DYLGGQMLAGNDTAREVTIYGFEDLCMESNGSVVETCDSSQKQKALYDGSIR 184
DB 402 IYVAGQMLPTNNTOPEFTIYVGLYGMCLQANSKQVLEDC-TSEKAEQMALYDGSIR 460
QY 185 PRONODCLTSGRDSVSTVINIVSCGASGQWVFTNEGAILMLKSLMDVYQAQPKI 244
DB 461 PRONODCLTIDNANIKQIVKILSCGPASGQWVFTNEGAILMLKSLMDVYQAQPKI 520
QY 245 RRIIYVATKGRKQWMLPVP 264
DB 521 KQIIVHPFRNINQIWLPLF 540

RESULT 5

US-08-485-286-77
Sequence 77, Application US/08485286
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESS: ANDREA T. BORKUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485/286
FILING DATE: 4/3
SUBSTANTIAL INVENTION: 435
PRIORITY INFORMATION:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORKUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acids
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-485-286-77

Query Match 54.3%; Score 77.5; DB 1; Length 540;
Best Local Similarity 55.8%; Pred. No. 26-73;
Matches 145; Conservative 42; Mismatches 72; Indels 1; Gaps 1;

QY 5 CSASEPTVAIVGRNMGKRVDDDFHDNQIOLMPKSNNDPNQIWKIKEDGTIRNSGC 64
DB 282 CMDEPTVAIVGRNMGKRVDDDFHDNQIOLMPKSNNDPNQIWKIKEDGTIRNSGC 341
QY 65 LITVGTAGVYVIMFPCNTARENTIWOIINGTIIIPRSNTIILASSGICITITLQTL 124
DB 342 LITKSSPRQCVIYVNCSTATVQATRMQITKMTIIPRSQIILASSGICITITLQTL 401
QY 125 DYLGGQMLAGNDTAREVTIYGFEDLCMESNGSVVETCDSSQKQKALYDGSIR 184
DB 402 IYVAGQMLPTNNTOPEFTIYVGLYGMCLQANSKQVLEDC-TSEKAEQMALYDGSIR 460
QY 185 PRONODCLTSGRDSVSTVINIVSCGASGQWVFTNEGAILMLKSLMDVYQAQPKI 244
DB 461 PRONODCLTIDNANIKQIVKILSCGPASGQWVFTNEGAILMLKSLMDVYQAQPKI 520
QY 245 RRIIYVATKGRKQWMLPVP 264
DB 521 KQIIVHPFRNINQIWLPLF 540

RESULT 6

US-09-512-342-14
Sequence 14, Application US/09512342
Patent No. 638068
GENERAL INFORMATION:
APPLICANT: SATOH, SHIGERU
TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT
TITLE OF INVENTION: INTERCELLULAR FLUID
FILE REFERENCE: 081356/0142
CURRENT APPLICATION NUMBER: US/09/512/342
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 14
LENGTH: 293
TYPE: PRT
ORGANISM: Cucumis sativus
US-09-512-342-14

Query Match 13.1%; Score 185.5; DB 4; Length 293;
Best Local Similarity 27.4%; Pred. No. 2-2e-11;
Matches 66; Conservative 35; Mismatches 101; Indels 39; Gaps 10;

QY 14 IYVGRNMGKRVDDDFHDNQIOLMPKSNNDPNQIWKIKEDGTIRNSGC 59
DB 41 IYVGRNMGKRVDDDFHDNQIOLMPKSNNDPNQIWKIKEDGTIRNSGC 89
QY 60 SNSSGCLT--YGTAGVYVIMFPCNTARENTIWOIINGTIIIPRSNTIILASSGIC 116
DB 90 SNSSGCLT--YGTAGVYVIMFPCNTARENTIWOIINGTIIIPRSNTIILASSGIC 145
QY 117 TLTVGQMLAGNDTAREVTIYGFEDLCMESNGSVVETCDSSQKQKALYDGSIR 174
DB 146 TLTVGQMLAGNDTAREVTIYGFEDLCMESNGSVVETCDSSQKQKALYDGSIR 202
QY 175 WLYVAGSIRPKQNDCLTSGRDSVSTVINIVSCGASGQWVFTNEGAILMLKSLM 234
DB 203 WLYVAGSIRPKQNDCLTSGRDSVSTVINIVSCGASGQWVFTNEGAILMLKSLM 260
QY 235 V 235
DB 261 V 261

RESULT 7

US-09-159-106-15
Sequence 15, Application US/09159106
Patent No. 6284509
GENERAL INFORMATION:
APPLICANT: Ferret, Pau
APPLICANT: Diets, Ivan

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Page 2

```
RESULT 2
US-08-776-059-33
Sequence 33, Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
TYPE: PRT
ORGANISM: Viscum album

Query Match
US-08-776-059-33
Best Local Similarity 93.1%; Score 1318.5; DB 3; Length 264;
Matches 248; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 1 DVTGASBPYVAVGNKGVVDDDDPDGNOIQMFSSKSNDDPQMLTKKDDGTS 60
DB 2 DVTGASBPYVAVGNKGVVDDDDPDGNOIQMFSSKSNDDPQMLTKKDDGTS 61
QY 61 NSCLTYGTAGYVMIEDCNVAREXTIWMQNGTINPESNVLAASSGKGTLL 120
DB 62 NSCLTYGTAGYVMIEDCNVAREXTIWMQNGTINPESNVLAASSGKGTLL 121
QY 121 VQTLDTLGGMLAGNDTAPREVTIYGFRLCSNCSGVSWEVTCSSQKQGMALYD 180
DB 122 VQTLDTLGGMLAGNDTAPREVTIYGFRLCSNCSGVSWEVTCSSQKQGMALYD 180
QY 181 GSIRPKQNDCLTSGRDSVTVIVSCSGASGSGQWVFTNEGALINLKNLMDVVAQA 240
DB 181 GSIRPKQNDCLTSGRDSVTVIVSCSGASGSGQWVFTNEGALINLKNLMDVVAQA 240
QY 241 NPKLRRIIIPATGKPMQMLPV 263
DB 241 NPKLRRIIIPATGKPMQMLPV 263

RESULT 3
US-08-776-059-35
Sequence 35, Application US/08776059B
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: BAUR, Axel
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
TYPE: PRT
ORGANISM: Viscum album
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US-08-776-059-35
Query Match
US-08-776-059-35
Best Local Similarity 93.1%; Score 1318.5; DB 3; Length 564;
Matches 248; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 1 DVTGASBPYVAVGNKGVVDDDDPDGNOIQMFSSKSNDDPQMLTKKDDGTS 60
DB 2 DVTGASBPYVAVGNKGVVDDDDPDGNOIQMFSSKSNDDPQMLTKKDDGTS 61
QY 61 NSCLTYGTAGYVMIEDCNVAREXTIWMQNGTINPESNVLAASSGKGTLL 120
DB 62 NSCLTYGTAGYVMIEDCNVAREXTIWMQNGTINPESNVLAASSGKGTLL 121
QY 121 VQTLDTLGGMLAGNDTAPREVTIYGFRLCSNCSGVSWEVTCSSQKQGMALYD 180
DB 122 VQTLDTLGGMLAGNDTAPREVTIYGFRLCSNCSGVSWEVTCSSQKQGMALYD 180
QY 181 GSIRPKQNDCLTSGRDSVTVIVSCSGASGSGQWVFTNEGALINLKNLMDVVAQA 240
DB 181 GSIRPKQNDCLTSGRDSVTVIVSCSGASGSGQWVFTNEGALINLKNLMDVVAQA 240
QY 241 NPKLRRIIIPATGKPMQMLPV 263
DB 241 NPKLRRIIIPATGKPMQMLPV 263

RESULT 4
US-08-776-761A-77
Sequence 77, Application US/08776761A
Patent No. 5633984
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE E
TITLE OF INVENTION: INHIBITORS OF INACTIVATING PROTEINS, INACTIVE
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESS: ANDREA T. BORUCKI
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/776, 761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: (317) 337-4848
FAX: (317) 337-4848
INSTRUMENT CHARACTERISTICS: 77;
LENGTH: 540 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match
US-08-776-761A-77
Best Local Similarity 54.8%; Score 777.5; DB 1; Length 540;
Matches 145; Conservative 42; Mismatches 72; Indels 1; Gaps 1;
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Thu Dec 11 16:09:47 2003

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Page 6

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDNESS: No. US20010024815A1 Relevant
MOLECULE TYPE: linear
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-09-770-621-8

Query Match: 8.7%; Score 122.5; DB 9; Length 491;
Best Local Similarity: 28.6%; Pred. No. 0.00075;
Matches: 40; Conservative: 20; Mismatches: 61; Indels: 19; Gaps: 6;

QY 7 ASEP-----TVRIYGNMNVYVDDDFDQNGOIQMPSSNNDPNQLTKED 55
DB 354 SSEPXXXXXXXXXADGQIRKVG-SRCLDVPASSTDSGTCLMDCHST--NCOMALTA 410
QY 56 CTRISNG-SCITTYGTHGIVYMIFPCNTNREACTIQIMDGIINPRSNVLA--SS 112
DB 411 GELRYVGKCKLDAAGTSMGSKVQYSCVGGDNOK--WRINSDGSVVGSGCLDAVNG 468
QY 113 GIKGTTLVVOTLDYTLGQGW 132
DB 469 TANGTLDIOLYTCNSGNSQRM 488

US-09-770-621-4
Sequence 4: Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M acyl, Arja
APPLICANT: Vermaasmp, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Maria
APPLICANT: Suominen, Eiriko
APPLICANT: Suominen, Raija
INVENTOR: Suominen, Raija
TITLE: Identification and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & POX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIA: 178; floppy disk
SOFTWARE: Patent Invention System, Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
US-09-770-621-4

Query Match: 8.7%; Score 122.5; DB 9; Length 492;
Best Local Similarity: 32.4%; Pred. No. 0.00076;
Matches: 33; Conservative: 16; Mismatches: 48; Indels: 5; Gaps: 3;

QY 22 VPRDDDFDQNGOIQMPSSNNDPNQLTKED 122
DB 379 IDVPRGNTDGVQVQYCHSS--NQVTTSSGEFRIFENKCLDAGSSNGAVVQIYS 436
QY 81 CNTAVPRAITWQIDNGITINPSRVLVLAASGIKGTTLVQ 122
DB 437 CWCANOK--WELRADGITVVGSGCLDAVGGTNGTFLQ 476

Search completed: December 11, 2003, 14:48:51
Job time: 18.0129 secs

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Page 5

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/ GENERAL INFORMATION:
/ APPLICANT: OMOGA, SATOSHI
/ APPLICANT: OMOGA, SATOSHI
/ APPLICANT: ISHIKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HATTORI, MASAHISA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCES: 249-262
/ CURRENT APPLICATION NUMBER: US/10/156,761
/ PRIORITY DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: JP 2001-204089
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ. ID NOS.: 15109
/ SEQ. ID NO. 10246
/ LENGTH: 647
/ TYPE: PRT
/ ORGANISM: Streptomyces avermectilis
/ US-10-156-761-10246

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Query Match      8.5%; Score 126; DB 15; Length 647;
Best Local Similarity 26.3%; Pred. No. 0.00048;
Matches 45; Conservative 20; Mismatches 60; Indels 46; Gaps 8;

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Qy      9  EPTVRLVGRNRGVYVDDDFHGNQIQWPKSKNDPVCLMTIKDGTISNSCT--T 66
Db      520 DGTGSPVGLAKGLDVAASSANGTAVOLY--DCNGSTKQWTVVADSVQAKKLDVT 577
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy      67  TTYGTVGVYVMTFCQNTAVREATTQIWDNGTIIIPRSLVLAASSGKNTTLVQTLDY 126
Db      578 SASITADGAKIQLDYDN---GTPAQKRSYN-----ASTGVVYVMTADKCLDV 620
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy      127  TLGGWGLAGNTAPREVTIIGFDLCJMESHSYVWETCISSQKQKRAL 177
Db      621 T-----GNSR-----NRRQIWSCTGAAQ--KML 646

```

RESULT 13

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US-09-770-621-5
/ Sequence 5, Application US/0970621
/ Patent No. US20010024815A1
/ GENERAL INFORMATION:
/ APPLICANT: M nyl, Arja
/ APPLICANT: Velmamper, Jari
/ APPLICANT: Fagerster m, Richard
/ APPLICANT: Rantto, Raija
/ APPLICANT: Rantto, Raija
/ APPLICANT: Suominen, Pirkko
/ APPLICANT: Lahtinen, Taina
/ TITLE OF INVENTION: Production and Secretion of Proteins of
/ NUMBER OF SEQUENCES: 39
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
/ STREET: 1100 New York Ave., N.W. Suite 600
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/770,621
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/590,563
/ FILING DATE:

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/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/332,412
/ FILING DATE: 31-OCT-1994
/ CLASSIFICATION:
/ APPLICATION DATA:
/ APPLICATION NUMBER: US 08/282,001
/ FILING DATE: 29-JUL-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2500
/ TELEFAX: 202-371-2540
/ INFORMATION CONTAINED HEREIN IS UNCLASSIFIED
/ LENGTH: 480 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: No. US20010024815A1 Relevant
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ POSITION IN GENOME:
/ CHROMOSOME/SEGMENT: AM50
/ US-09-770-621-5

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Query Match      9.7%; Score 122.5; DB 9; Length 480;
Best Local Similarity 32.4%; Pred. No. 0.00073;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;

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Qy      22  VVRRDDFHGNQIQWPKSKNDPVCLMTIKDGTIRKSGS-CITTYGTVGVYVMTFC 80
Db      379 IIVPRGKTGDTQVQVLYDCHSGS--NQMTYSSGFIFGRKCLDAGSSNGAVQIYS 436
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy      81  CNTAVREATTQIWDNGTIIIPRSLVLAASSGKNTTLVQ 122
Db      437 CWGANQR--WEIRADGTIVQSGICLDLAVAGTGNGTQLQ 476

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RESULT 14

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US-09-770-621-8
/ Sequence 8, Application US/0970621
/ Patent No. US20010024815A1
/ GENERAL INFORMATION:
/ APPLICANT: M nyl, Arja
/ APPLICANT: Velmamper, Jari
/ APPLICANT: Fagerster m, Richard
/ APPLICANT: Rantto, Raija
/ APPLICANT: Rantto, Raija
/ APPLICANT: Suominen, Pirkko
/ APPLICANT: Lahtinen, Taina
/ TITLE OF INVENTION: Production and Secretion of Proteins of
/ NUMBER OF SEQUENCES: 39
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
/ STREET: 1100 New York Ave., N.W. Suite 600
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/770,621
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/590,563
/ FILING DATE:

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Page 4

;; PRIOR APPLICATION NUMBER: JP 2001-272697
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ ID NOS: 15109
;; SEQ ID NO 8170
;; LENGTH: 536
;; TYPE: PRT
;; ORGANISM: Streptomyces avermectilis
us-10-156-761-8170

Query Match 9.5%; Score 134; DB 15; Length 536;
Best Local Similarity 30.1%; Pred. No. 5.6e-05;
Matches 40; Conservative 18; Mismatches 59; Indels 16; Gaps 6;

QY 14 IVGNRGR-VDPDDEHGRQIQLPSPKSNNDPQWLTIKROGTRISNG--SCLTTY-- 68
DB 409 LVGASNECLDYNNGTAFGRKLEIWDG--GGANQVYITTAAGSLRVGGTCLDANDN 465
QY 69 GYTAGVYVMTEDCTAVREATIQTQINDGTTINPSSNLVLT-----AASSGKGTTLTVQ 122
DB 466 GTTSGTKVQLYTCNGANQK--WSINPENGVTGTSGLDVTGSDQNSVNGTALIEIM 523
QY 123 TLDYTLGGWLAG 135
DB 524 TONGANQQRRLD 536

RESULT 9

US-10-137-077-18
;; Sequence 18, Application US/10137077
;; Publication No. US20030092109A1
;; GENERAL INFORMATION:
;; APPLICANT: Goldstein, Irwin J.
;; APPLICANT: Mincer, Harry C.
;; APPLICANT: Mincer, Robert C.
;; TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin
;; FILE REFERENCE: US-071924
;; CURRENT APPLICATION NUMBER: US/10/137,077
;; CURRENT FILING DATE: 2002-05-02
;; PRIOR APPLICATION NUMBER: 60/288,596
;; PRIOR FILING DATE: 2001-05-03
;; PRIOR APPLICATION NUMBER: 60/354,322
;; PRIOR FILING DATE: 2002-02-04
;; NUMBER OF SEQ ID NOS: 32
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 18
;; SEQ ID NO 48
;; TYPE: PRT
;; ORGANISM: Ricinus communis
US-10-137-077-18

Query Match 9.0%; Score 127; DB 15; Length 41;
Best Local Similarity 53.7%; Pred. No. 8.6e-06;
Matches 22; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 224 GATLNKSNLMVDVQAQNPFLKRIITTPATGKNGMPLPYF 264
DB 1 GATLNKSNLMVDVQAQNPFLKRIITTPATGKNGMPLPYF 41

RESULT 10

US-09-973-457-5
;; Sequence 5, Application US/09973457
;; Patent No. US20020164746A1
;; GENERAL INFORMATION:
;; APPLICANT: Kapeller-Liberman, Rosana
;; TITLE OF INVENTION: 4,7,8,9 NOVEL HUMAN GLYCOSYLTRANSFERASE
;; TITLE OF INVENTION: AND USE THEREOF
;; FILE REFERENCE: 10448-099001
;; CURRENT APPLICATION NUMBER: US/09/973,457
;; PRIOR FILING DATE: 2001-10-09
;; PRIOR APPLICATION NUMBER: 60/228,849
;; PRIOR FILING DATE: 2000-10-06
;; NUMBER OF SEQ ID NOS: 6

;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5
;; LENGTH: 135
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match 9.0%; Score 127; DB 10; Length 135;
Best Local Similarity 25.7%; Pred. No. 4.4e-05;
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;

QY 14 IVGNRGRVDP--RDDPHGRQIQLPSPKSNNDPQWLTI---KRDGTRISNGS-CLTT 67
DB 7 IGVNVTGLDYNNGTSKSDGNPQWLMDHGG--NQLMELTVESGALINSGLITLV 64
QY 68 YGTAGVYVMTEDCTAVR--EATIQINDGTTINPSSNLVLAASSGKGTTLTVQ 125
DB 65 NG-----TVTISGDTTKRNGNQRHFWKDTIRNR--SKKKGYDSG----- 106
QY 126 YTLGGWLAGNDTAPRVTIYGRFLDQNE--SNGSVYVETCSSQKQKRN 175
DB 107 -----LCDVQDNKVTQLMTGNSDAPNOKN 132

RESULT 11

US-10-074-527-6
;; Sequence 6, Application US/10074527
;; Publication No. US2002014246A1
;; GENERAL INFORMATION:
;; APPLICANT: Olanet, Peter J.
;; APPLICANT: Mincer, Harry C.
;; APPLICANT: Mincer, Robert E.
;; TITLE OF INVENTION: 33945, A Human Glycosyltransferase and
;; TITLE OF INVENTION: Uses Therefor
;; FILE REFERENCE: MP12001-018P(KCP1M)
;; CURRENT APPLICATION NUMBER: US/10/074,527
;; CURRENT FILING DATE: 2002-02-12
;; PRIOR APPLICATION NUMBER: 60/269202
;; PRIOR FILING DATE: 2000-02-15
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6
;; LENGTH: 135
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: consensus
US-10-074-527-6

Query Match 9.0%; Score 127; DB 14; Length 135;
Best Local Similarity 25.7%; Pred. No. 4.4e-05;
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;

QY 14 IVGNRGRVDP--RDDPHGRQIQLPSPKSNNDPQWLTI---KRDGTRISNGS-CLTT 67
DB 7 IGVNVTGLDYNNGTSKSDGNPQWLMDHGG--NQLMELTVESGALINSGLITLV 64
QY 68 YGTAGVYVMTEDCTAVR--EATIQINDGTTINPSSNLVLAASSGKGTTLTVQ 125
DB 65 NG-----TVTISGDTTKRNGNQRHFWKDTIRNR--SKKKGYDSG----- 106
QY 126 YTLGGWLAGNDTAPRVTIYGRFLDQNE--SNGSVYVETCSSQKQKRN 175
DB 107 -----LCDVQDNKVTQLMTGNSDAPNOKN 132

RESULT 12

US-10-156-761-10246
;; Sequence 10246, Application US/10156761
;; Publication No. US20030119018A1

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QY 121 VOTLDYTLGGWLAGNDTAPREVITYGPRDLCSNCSGQWVETCDSSQKQKQKALYGD 180
DB 121 VOTLDYTLGGWLAGNDTAPREVITYGPRDLCSNCSGQWVETCDSSQKQKQKALYGD 179
QY 181 GSIRPRONODQCLTSGRDSVSTVINIVCSGASGSGQWVETCDSSQKQKQKALYGD 240
DB 180 GSIRPRONODQCLTSGRDSVSTVINIVCSGASGSGQWVETCDSSQKQKQKALYGD 239
QY 241 NPKLRRIITYPATKPKQWMLPV 263
DB 240 NPKLRRIITYPATKPKQWMLPV 262

RESULT 2

US-09-347-064-4

/ Sequence 4, Application US/09347064A
/ Patent No. US20020045208A1
/ GENERAL INFORMATION:
/ APPLICANT: Beck, Jürgen
/ APPLICANT: Schmidt, Arno
/ APPLICANT: Zimmer, Holger
/ TITLE OF INVENTION: Ribosome-inactivating Protein Based on
/ TITLE OF INVENTION: album
/ TITLE OF INVENTION: album
/ FILE REFERENCE: 09282-5
/ CURRENT APPLICATION NUMBER: US/09/347,064A
/ EARLIER FILING DATE: 1999-07-02
/ EARLIER APPLICATION NUMBER: PCT/EP98/00009
/ EARLIER FILING DATE: 1998-01-02
/ EARLIER APPLICATION NUMBER: EP 97 10 0012.0
/ EARLIER FILING DATE: 1997-01-02
/ NUMBER OF SEQ ID NOS: 38
/ SEQ ID NO 1: Patent in Ver. 2.1
/ LENGTH: 267
/ TYPE: PRP
/ ORGANISM: Viscum album
US-09-347-064-4

Query Match

Best Local Similarity 93.1%; Score 1318.5; DB 9; Length 267;
Matches 248; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 1 DDTGASSEPTVIVGNKGRVDDDFHNOICLMSKNDNDQTLTIRGRTIS 60
DB 1 DDTGASSEPTVIVGNKGRVDDDFHNOICLMSKNDNDQTLTIRGRTIS 60
QY 61 NSGCLTGYTAGYVWIPCKITVBEATIMQWNGTINPRSNIVLAASGIGTTLT 120
DB 61 NSGCLTGYTAGYVWIPCKITVBEATIMQWNGTINPRSNIVLAASGIGTTLT 120
QY 121 VOTLDYTLGGWLAGNDTAPREVITYGPRDLCSNCSGQWVETCDSSQKQKQKALYGD 180
DB 121 VOTLDYTLGGWLAGNDTAPREVITYGPRDLCSNCSGQWVETCDSSQKQKQKALYGD 179
QY 181 GSIRPRONODQCLTSGRDSVSTVINIVCSGASGSGQWVETCDSSQKQKQKALYGD 240
DB 180 GSIRPRONODQCLTSGRDSVSTVINIVCSGASGSGQWVETCDSSQKQKQKALYGD 239
QY 241 NPKLRRIITYPATKPKQWMLPV 263
DB 240 NPKLRRIITYPATKPKQWMLPV 262

RESULT 3

US-10-083-336A-1

/ Sequence 3, Application US/10083336A
/ Patent No. US2003018165M1
/ GENERAL INFORMATION:
/ APPLICANT: Olson, Mark A
/ APPLICANT: Millard, Charles B
/ APPLICANT: Byrne, Michael P
/ APPLICANT: Mannemacher, Robert W

/ TITLE OF INVENTION: Racin Vaccine and Methods of Making and Using Thereof
/ FILE REFERENCE: P6745200 (R1D 01-58)
/ CURRENT APPLICATION NUMBER: US/10/083,336A
/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patent in Ver. 2.1
/ SEQ ID NO 1: 576
/ TYPE: PRP
/ ORGANISM: Rattus communis
US-10-083-336A-1

Query Match

Best Local Similarity 63.7%; Score 901.5; DB 12; Length 576;
Matches 165; Conservative 34; Mismatches 60; Indels 1; Gaps 1;

QY 5 GSASSEPTVIVGNKGRVDDDFHNOICLMSKNDNDQTLTIRGRTIS 64
DB 318 GSASSEPTVIVGNKGRVDDDFHNOICLMSKNDNDQTLTIRGRTIS 63
QY 65 LTTGAGYVWIPCKITVBEATIMQWNGTINPRSNIVLAASGIGTTLT 124
DB 378 LTTGAGYVWIPCKITVBEATIMQWNGTINPRSNIVLAASGIGTTLT 123
QY 125 DDTGASSEPTVIVGNKGRVDDDFHNOICLMSKNDNDQTLTIRGRTIS 184
DB 438 DDTGASSEPTVIVGNKGRVDDDFHNOICLMSKNDNDQTLTIRGRTIS 183
QY 145 PRONODQCLTSGRDSVSTVINIVCSGASGSGQWVETCDSSQKQKQKALYGD 244
DB 457 PRONODQCLTSGRDSVSTVINIVCSGASGSGQWVETCDSSQKQKQKALYGD 243
QY 245 RRIITYPATKPKQWMLPV 264
DB 557 RRIITYPATKPKQWMLPV 263

RESULT 4

US-10-137-077-17

/ Sequence 17, Application US/10137077
/ Patent No. US2003092109M1
/ GENERAL INFORMATION:
/ APPLICANT: Gotsch, Irwin J.
/ APPLICANT: Kruess, Robert P.
/ TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin
/ FILE REFERENCE: US-07124
/ CURRENT APPLICATION NUMBER: US/10/137,077
/ EARLIER FILING DATE: 2002-05-02
/ EARLIER APPLICATION NUMBER: 60/288,596
/ EARLIER FILING DATE: 2001-05-03
/ EARLIER APPLICATION NUMBER: 60/354,322
/ EARLIER FILING DATE: 2002-02-04
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 17
/ LENGTH: 44
/ TYPE: PRP
/ ORGANISM: Rattus communis
US-10-137-077-17

Query Match

Best Local Similarity 13.1%; Score 186; DB 15; Length 44;
Matches 34; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 12 VRIYRGKNDYVDDDFHNOICLMSKNDNDQTLTIRGRTIS 55
DB 1 VRIYRGKNDYVDDDFHNOICLMSKNDNDQTLTIRGRTIS 54

RESULT 5

US-10-074-527-5

/ Sequence 5, Application US/10074527

XX Sequence 264 AA;
 SQ Query Match 93.5%; Score 1324.5; DB 20; Length 264;
 Best Local Similarity 94.7%; Pred. No. 2,3e-119;
 Matches 249; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DDTCSASEPTVAVGRNGKRVVDDEPHDQNOIQLPFSKSNBDPQMLTKKIDGTRIS 60
 DB 1 DDTCSASEPTVAVGRNGKRVVDDEPHDQNOIQLPFSKSNBDPQMLTKKIDGTRIS 60
 QY 61 NSGCLTGYGTAAGVYVWIFPCNTAREATITQIMDNGTIIINRSNLVLAASGIGKTLT 120
 DB 61 NSGCLTGYGTAAGVYVWIFPCNTAREATITQIMDNGTIIINRSNLVLAASGIGKTLT 120
 QY 121 VQTLDTYLLGQGLAGNDTAPREVITVIGPRDLCMSNGSGVWETCVSSQONQ-RMALYGD 180
 DB 121 VQTLDTYLLGQGLAGNDTAPREVITVIGPRDLCMSNGSGVWETCVSSQONQ-RMALYGD 179
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWFTFEGALINLKNSLMWVDAQ 240
 DB 180 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWFTFEGALINLKNSLMWVDAQ 239
 QY 241 NPKLRRIITVATGKRNQMLPV 263
 DB 240 NPKLRRIITVATGKRNQMLPV 262

RESULT 13
 AAY25979
 ID AAY25979 standard; Protein; 531 AA.
 XX AAY25979;
 AC 18-OCT-1999 (first entry)
 XX DT Mistletoe lectin I protein fragment.
 XX DE Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 XX KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin I.
 XX OS Viscum album.
 XX PN DE19804210-A1.
 XX PD 12-AUG-1999.
 XX PR 03-FEB-1998; 98DE-1004210.
 XX PR 03-FEB-1998; 98DE-1004210.
 XX PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX PI Morris P, Stiefel T, Voelter W, Welters P.
 XX DR MPI, 1999-445335/38.
 XX DR N-PSDB; AA209103.
 XX PT Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Claim 7; Fig 1B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate human T-lymphocytes
 CC fragments and used to increase the strength of the
 CC immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a mistletoe lectin I protein fragment.

SQ Sequence 531 AA;
 Query Match 93.5%; Score 1324.5; DB 20; Length 531;
 Best Local Similarity 94.7%; Pred. No. 6,2e-119;
 Matches 249; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

QY 1 DDTCSASEPTVAVGRNGKRVVDDEPHDQNOIQLPFSKSNBDPQMLTKKIDGTRIS 60
 DB 269 DDTCSASEPTVAVGRNGKRVVDDEPHDQNOIQLPFSKSNBDPQMLTKKIDGTRIS 328
 QY 61 NSGCLTGYGTAAGVYVWIFPCNTAREATITQIMDNGTIIINRSNLVLAASGIGKTLT 120
 DB 329 NSGCLTGYGTAAGVYVWIFPCNTAREATITQIMDNGTIIINRSNLVLAASGIGKTLT 368
 QY 121 VQTLDTYLLGQGLAGNDTAPREVITVIGPRDLCMSNGSGVWETCVSSQONQ-RMALYGD 180
 DB 369 VQTLDTYLLGQGLAGNDTAPREVITVIGPRDLCMSNGSGVWETCVSSQONQ-RMALYGD 447
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWFTFEGALINLKNSLMWVDAQ 240
 DB 448 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQWFTFEGALINLKNSLMWVDAQ 507

RESULT 14
 AAY25982
 ID AAY25982 standard; Protein; 532 AA.
 XX AAY25982;
 AC 18-OCT-1999 (first entry)
 XX DT Mistletoe lectin I (variant) protein fragment.
 XX DE Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 XX KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin I.
 XX OS Viscum album.
 XX PN DE19804210-A1.
 XX PD 12-AUG-1999.
 XX PR 03-FEB-1998; 98DE-1004210.
 XX PR 03-FEB-1998; 98DE-1004210.
 XX PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX PI Morris P, Stiefel T, Voelter W, Welters P.
 XX DR MPI, 1999-445335/38.
 XX DR N-PSDB; AA209106.
 XX PT Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 4B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of

QY 61 NSGCLTYGYTAGYVWIMFDCTAVREATTWQIMDNGTIINPRSNLWLAASSGIKGTTLT 120
 DB 61 NSGCLTYGYTAGYVWIMFDCTAVREATTWQIMDNGTIINPRSNLWLAASSGIKGTTLT 120
 QY 121 VQTLDTYTLGGCMLAGNDTAPRETTIYGFRLCHESNGSGVWETCTDSQCKRAIYGD 180
 DB 121 VQTLDTYTLGGCMLAGNDTAPRETTIYGFRLCHESNGSGVWETCTDSQCKRAIYGD 180
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQRFVFNKALINLKSGIMVQVQA 240
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQRFVFNKALINLKSGIMVQVQA 240
 QY 241 NPKLRRIITTPATKRNQMLPVF 264
 DB 241 NPKLRRIITTPATKRNQMLPVF 264

RESULT 11

ID AAY25985 standard; Protein; 263 AA.

XX AAY25985;

XX 18-OCT-1999 (first entry)

XX Mistletoe lectin B protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

KM ribozyme 288 subunit; non-cytotoxic; T-cell activation; immune response;

KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;

KX cancer; cytotoxicity; antigen; isoform; lectin B.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelter W, Welters P;

XX WPI; 1999-445335/38.

XX N-PSDB; AA209109.

XX Preparation of mistletoe lectins in heterologous systems,

XX particularly for use as anticancer agents and immunostimulants

XX Claim 9; Fig 7B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response. Particularly, the method allows production of the
 CC (tumour-associated bacterial or viral) recombinant antigen isoforms
 CC of mistletoe lectin, and its individual chains. Recombinant products are
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B protein.

XX Sequence 263 AA;

XX Query Match 93.5%; Score 1324.5; DB 20; Length 263;
 XX Best Local Similarity 94.7%; Pred. No. 2,3e-119.

Matches 249; Conservative 3; Mismatches 10; Indels 1; Gaps 1;
 QY 1 DVTCSASEPTVRLVGRNGKRVDRDDDPHQDQQLWPKSKNDPROLWTRKDGRTS 60
 DB 1 DVTCSASEPTVRLVGRNGKRVDRDDDPHQDQQLWPKSKNDPROLWTRKDGRTS 60
 QY 61 NSGCLTYGYTAGYVWIMFDCTAVREATTWQIMDNGTIINPRSNLWLAASSGIKGTTLT 120
 DB 61 NSGCLTYGYTAGYVWIMFDCTAVREATTWQIMDNGTIINPRSNLWLAASSGIKGTTLT 120
 QY 121 VQTLDTYTLGGCMLAGNDTAPRETTIYGFRLCHESNGSGVWETCTDSQCKRAIYGD 180
 DB 121 VQTLDTYTLGGCMLAGNDTAPRETTIYGFRLCHESNGSGVWETCTDSQCKRAIYGD 180
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQRFVFNKALINLKSGIMVQVQA 240
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQRFVFNKALINLKSGIMVQVQA 240
 QY 241 NPKLRRIITTPATKRNQMLPVF 263
 DB 241 NPKLRRIITTPATKRNQMLPVF 262

RESULT 12

ID AAY25991 standard; Protein; 264 AA.

XX AAY25991;

XX 18-OCT-1999 (first entry)

XX Mistletoe lectin B variant protein fragment.

KM Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

KW ribozyme 288 subunit; non-cytotoxic; T-cell activation; immune response;

KX lymphokine-producing macrophages; uncontrolled cell growth; treatment;

XX cancer; cytotoxicity; antigen; isoform; lectin B.

XX Viscum album.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P, Stiefel T, Voelter W, Welters P;

XX WPI; 1999-445335/38.

XX N-PSDB; AA209115.

XX Preparation of mistletoe lectins in heterologous systems,

XX particularly for use as anticancer agents and immunostimulants

XX Disclosure; Fig 13B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MIA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response. Particularly, the method allows production of the
 CC (tumour-associated bacterial or viral) recombinant antigen isoforms
 CC of mistletoe lectin, and its individual chains. Recombinant products are
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B protein.

Db 181 GSIRPRKQNDQCLTSGRDSVSTVINIVSCGASGSGRWVETNEBAILNKSGPAMVDVQA 240
 QY 241 NPKLRRIIIVPATGKPNQMWLPVF 264
 Db 241 NPKLRRIIIVPATGKPNQMWLPVF 264

RESULT 9

ID AAY25987 standard; Protein; 264 AA.
 XX AAY25987;

18-OCT-1999 (first entry)

Mistletoe lectin B2 protein fragment.

Mistletoe lectin; antitumour; immunostimulant; A-chain; MAb; immunity;
 ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 cancer; cytotoxicity; antigen; isoform; lectin B2.

Viscum album.

DE19804210-A1.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

03-FEB-1998; 98DE-1004210.

(BIOS-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelter W, Walters P;

WPI; 1999-44535/38.

N-PDB; AA209111.

Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants

Claim 9; Fig 9B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments
 which have antitumour and immunostimulatory activity. The A-chain (MA) of
 the mistletoe lectin binds to, and inactivates, the 28S subunit of
 ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 lymphokine-producing macrophages, so stimulate immunity. (I) and its
 fragments are used to treat uncontrolled cell growth (particularly
 cancers) and if they lack cytotoxicity, to increase the strength of the
 immune response, particularly to a co-administered antigen
 (tumour-associated, bacterial or viral). The method allows production of
 recombinant products of (I) and its fragments, and on a large scale, and
 on a large scale, at any time of the year. Recombinant products are
 free from toxins present in natural mistletoe extracts. This sequence
 represents a fragment of a mistletoe lectin B2 protein.

Sequence 264 AA;

Query Match 96.3%; Score 1364; DB 20; Length 264;
 Best Local Similarity 96.6%; Pred. No. 3,6e-123;

Matches 255; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DDTGASAPPTVIRVGRNKNVDVDDPHDQIOCLWPSKSNDDPNQWIKKIDCTIFS 60
 Db 1 DDTGASAPPTVIRVGRNKNVDVDDPHDQIOCLWPSKSNDDPNQWIKKIDCTIFS 60
 QY 61 NSCLTYGTAGYVWIFDCNVAVEATIMQWNGTINPRSNVLAASGIGTTLT 120
 Db 61 NSCLTYGTAGYVWIFDCNVAVEATIMQWNGTINPRSNVLAASGIGTTLT 120

QY 121 VQTLDTYTLGGQMLAGNDPAFEVITVGFPRDLCEWSNGSGVWETCDSSQKQKQKALYCD 180
 Db 121 VQTLDTYTLGGQMLAGNDPAFEVITVGFPRDLCEWSNGSGVWETCDSSQKQKQKALYCD 180
 QY 181 GSIRPRKQNDQCLTSGRDSVSTVINIVSCGASGSGRWVETNEBAILNKSGPAMVDVQA 240
 Db 181 GSIRPRKQNDQCLTSGRDSVSTVINIVSCGASGSGRWVETNEBAILNKSGPAMVDVQA 240
 QY 241 NPKLRRIIIVPATGKPNQMWLPVF 264
 Db 241 NPKLRRIIIVPATGKPNQMWLPVF 264

RESULT 10

ID AAY25993 standard; Protein; 265 AA.
 XX AAY25993;

18-OCT-1999 (first entry)

Mistletoe lectin B2 variant protein fragment.

Mistletoe lectin; antitumour; immunostimulant; A-chain; MAb; immunity;
 ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 cancer; cytotoxicity; antigen; isoform; lectin B2.

Viscum album.

DE19804210-A1.

12-AUG-1999.

03-FEB-1998; 98DE-1004210.

03-FEB-1998; 98DE-1004210.

(BIOS-) BIOSYN ARZNEIMITTEL GMBH.

Morris P, Stiefel T, Voelter W, Walters P;

WPI; 1999-44535/38.

N-PDB; AA209111.

Preparation of mistletoe lectins in heterologous systems,
 particularly for use as anticancer agents and immunostimulants

Disclosure; Fig 15B; 78pp; German.

This invention describes a novel mistletoe lectin (I) and its fragments
 which have antitumour and immunostimulatory activity. The A-chain (MA) of
 the mistletoe lectin binds to, and inactivates, the 28S subunit of
 ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
 fragments are used to treat uncontrolled cell growth (particularly
 cancers) and if they lack cytotoxicity, to increase the strength of the
 immune response, particularly to a co-administered antigen
 (tumour-associated, bacterial or viral). The method allows production of
 recombinant products of (I) and its fragments, and on a large scale, and
 on a large scale, at any time of the year. Recombinant products are
 free from toxins present in natural mistletoe extracts. This sequence
 represents a fragment of a variant mistletoe lectin B2 protein.

Sequence 265 AA;

Query Match 96.3%; Score 1364; DB 20; Length 265;
 Best Local Similarity 96.6%; Pred. No. 3,6e-123;

Matches 255; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DDTGASAPPTVIRVGRNKNVDVDDPHDQIOCLWPSKSNDDPNQWIKKIDCTIFS 60
 Db 1 DDTGASAPPTVIRVGRNKNVDVDDPHDQIOCLWPSKSNDDPNQWIKKIDCTIFS 60

ID AAY25989 standard; Protein; 264 AA.
 XX
 AC AAY25989;
 XX
 DT 18-OCT-1999 (first entry)
 XX
 DE Mistletoe lectin B4 protein fragment.
 XX
 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
 XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform; lectin B4.
 XX
 XX Viscum album.
 XX
 XX DE19804210-A1.
 XX
 XX 12-NOV-1999.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 XX Morris P, Siefel T, Voelter W, Welters P;
 XX WPI: 1999-445335/38.
 XX N-PSDB; AA209113.
 XX
 PT Preparation of mistletoe lectin in heterologous systems,
 particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 9; Fig 11B; 78pg; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MHA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly of the
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumor-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B4 protein.
 XX
 XX Sequence 264 AA;
 SQ
 Query Match 98.24; Score 1390; DB 20; Length 264;
 Best Local Similarity 98.14; Pred. No. 1,1e-125;
 Matches 259; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVTTCGASEPTVRIYGRNGMNVYRDDPFDNDNOIQUMPSKSNNDPQLMTIKKDGITRS 60
 DB 1 DVTTCGASEPTVRIYGRNGMNVYRDDPFDNDNOIQUMPSKSNNDPQLMTIKKDGITRS 60
 QY 61 NGSCITTYGTAGYVWIFDNCNVAERATVWQIMDNGTIIIPSSNVLVAASGKIGTTLT 120
 DB 61 NGSCITTYGTAGYVWIFDNCNVAERATVWQIMDNGTIIIPSSNVLVAASGKIGTTLT 120
 QY 121 VQTLIDYTLGGMLAGNTAPREVTIYGRDLCHESNGSVWETCDSSQNGKMAIYGD 180
 DB 121 VQTLIDYTLGGMLAGNTAPREVTIYGRDLCHESNGSVWETCDSSQNGKMAIYGD 180
 QY 122 VQTLIDYTLGGMLAGNTAPREVTIYGRDLCHESNGSVWETCDSSQNGKMAIYGD 180
 DB 122 VQTLIDYTLGGMLAGNTAPREVTIYGRDLCHESNGSVWETCDSSQNGKMAIYGD 180
 QY 181 GSIRPKQNGQCLTSGRDSVTVIINISCGASGSGRWFTNBSGAILMLNLSLWVDAQ 240
 DB 181 GSIRPKQNGQCLTSGRDSVTVIINISCGASGSGRWFTNBSGAILMLNLSLWVDAQ 240
 QY 241 NPKLRITITIPATGKPNQMWLPVF 264
 DB 241 NPKLRITITIPATGKPNQMWLPVF 264

ID AAY25995 standard; Protein; 265 AA.
 XX
 AC AAY25995;
 XX
 DT 18-OCT-1999 (first entry)
 XX
 DE Mistletoe lectin B4 variant protein fragment.
 XX
 XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
 XX ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 XX cancer; cytotoxicity; antigen; isoform; lectin B4.
 XX
 XX Viscum album.
 XX
 XX DE19804210-A1.
 XX
 XX 12-NOV-1999.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 XX Morris P, Siefel T, Voelter W, Welters P;
 XX WPI: 1999-445335/38.
 XX N-PSDB; AA209119.
 XX
 PT Preparation of mistletoe lectin in heterologous systems,
 particularly for use as anticancer agents and immunostimulants
 XX
 XX Disclosure; Fig 17B; 78pg; German.
 XX
 CC This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumor and immunostimulatory activity. The A-chain (MHA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly of the
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumor-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B4 protein.
 XX
 XX Sequence 265 AA;
 SQ
 Query Match 98.24; Score 1390; DB 20; Length 265;
 Best Local Similarity 98.14; Pred. No. 1,1e-125;
 Matches 259; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVTTCGASEPTVRIYGRNGMNVYRDDPFDNDNOIQUMPSKSNNDPQLMTIKKDGITRS 60
 DB 1 DVTTCGASEPTVRIYGRNGMNVYRDDPFDNDNOIQUMPSKSNNDPQLMTIKKDGITRS 60
 QY 61 NGSCITTYGTAGYVWIFDNCNVAERATVWQIMDNGTIIIPSSNVLVAASGKIGTTLT 120
 DB 61 NGSCITTYGTAGYVWIFDNCNVAERATVWQIMDNGTIIIPSSNVLVAASGKIGTTLT 120
 QY 121 VQTLIDYTLGGMLAGNTAPREVTIYGRDLCHESNGSVWETCDSSQNGKMAIYGD 180
 DB 121 VQTLIDYTLGGMLAGNTAPREVTIYGRDLCHESNGSVWETCDSSQNGKMAIYGD 180
 QY 122 VQTLIDYTLGGMLAGNTAPREVTIYGRDLCHESNGSVWETCDSSQNGKMAIYGD 180
 DB 122 VQTLIDYTLGGMLAGNTAPREVTIYGRDLCHESNGSVWETCDSSQNGKMAIYGD 180
 QY 181 GSIRPKQNGQCLTSGRDSVTVIINISCGASGSGRWFTNBSGAILMLNLSLWVDAQ 240
 DB 181 GSIRPKQNGQCLTSGRDSVTVIINISCGASGSGRWFTNBSGAILMLNLSLWVDAQ 240

KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 cancer; cytotoxicity; antigen; isoform; lectin B3.
 XX Vascum album.
 OS DE19804210-A1.
 XX
 XX
 XX
 XX 12-AUG-1999.
 XX
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIO-S) BIOSYN ARZNEIMITTEL GMBH.
 XX
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI: 1999-44535/38.
 XX N-PSDB; AA209112.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX
 XX Claim 9; Fig 10B; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to, and inactivates, the A subunit of
 CC ribosomes. Non-cytotoxic forms of A stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC lymphoma) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B3 protein.
 XX
 XX Sequence 264 AA:
 SQ
 Query Match 98.7%; Score 1397; DB 20; Length 264;
 Seq. Ident. Similarity 98.5%; Pred. No. 2,4e-126;
 Matches 260; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVTYCSASEPTVRIYVGNMGAVRDVDDPDGQNIQLWPKSKNDPNQWLTTRKDFTRIS 60
 DB 1 DVTYCSASEPTVRIYVGNMGAVRDVDDPDGQNIQLWPKSKNDPNQWLTTRKDFTRIS 60
 QY 61 NSGCLTFTYGTAGVYVMEFCQNTNREATINQIMDNGTINRSNVLAAASGIKETLT 120
 DB 61 NSGCLTFTYGTAGVYVMEFCQNTNREATINQIMDNGTINRSNVLAAASGIKETLT 120
 QY 121 VQTLDTLGGWLAGNDTAPREVITYGFRLDQMSNGSVWATCDSSQNGKMALYGD 180
 DB 121 VQTLDTLGGWLAGNDTAPREVITYGFRLDQMSNGSVWATCDSSQNGKMALYGD 180
 QY 181 GSIRPKQNDQCLTSGRDSVSTVINVSQSGASGQWFTNKGALINLKNLWTVYQA 240
 DB 181 GSIRPKQNDQCLTSGRDSVSTVINVSQSGASGQWFTNKGALINLKNLWTVYQA 240
 QY 241 NPKLRRIITTPATGKNQWMLPVF 264
 DB 241 NPKLRRIITTPATGKNQWMLPVF 264

RESULT 6
 AAY25994
 ID AAY25994 standard; Protein; 265 AA.
 XX
 AC AAY25994;
 XX
 DT 18-OCT-1999 (first entry)

XX Mistletoe lectin B3 variant protein fragment.
 DE
 XX
 XX Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B3.
 XX Vascum album.
 OS DE19804210-A1.
 XX
 XX
 XX
 XX 12-AUG-1999.
 XX
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 XX (BIO-S) BIOSYN ARZNEIMITTEL GMBH.
 XX
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI: 1999-44535/38.
 XX N-PSDB; AA209118.
 XX
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX
 XX Disclosure; Fig 16B; 78pp; German.
 XX
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to, and inactivates, the A subunit of
 CC ribosomes. Non-cytotoxic forms of A stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC lymphoma) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B3 protein.
 XX
 XX Sequence 265 AA:
 SQ
 Query Match 98.7%; Score 1397; DB 20; Length 265;
 Seq. Ident. Similarity 98.5%; Pred. No. 2,4e-126;
 Matches 260; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVTYCSASEPTVRIYVGNMGAVRDVDDPDGQNIQLWPKSKNDPNQWLTTRKDFTRIS 60
 DB 1 DVTYCSASEPTVRIYVGNMGAVRDVDDPDGQNIQLWPKSKNDPNQWLTTRKDFTRIS 60
 QY 61 NSGCLTFTYGTAGVYVMEFCQNTNREATINQIMDNGTINRSNVLAAASGIKETLT 120
 DB 61 NSGCLTFTYGTAGVYVMEFCQNTNREATINQIMDNGTINRSNVLAAASGIKETLT 120
 QY 121 VQTLDTLGGWLAGNDTAPREVITYGFRLDQMSNGSVWATCDSSQNGKMALYGD 180
 DB 121 VQTLDTLGGWLAGNDTAPREVITYGFRLDQMSNGSVWATCDSSQNGKMALYGD 180
 QY 181 GSIRPKQNDQCLTSGRDSVSTVINVSQSGASGQWFTNKGALINLKNLWTVYQA 240
 DB 181 GSIRPKQNDQCLTSGRDSVSTVINVSQSGASGQWFTNKGALINLKNLWTVYQA 240
 QY 241 NPKLRRIITTPATGKNQWMLPVF 264
 DB 241 NPKLRRIITTPATGKNQWMLPVF 264

RESULT 7
 AAY25989

XX 03-FEB-1998; 98DE-1004210.
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI: 1999-44535/38.
 XX N-PSDB; AA209110.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Claim 9, Fig 8B; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (WLA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly of the
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX also described. In a preferred embodiment, the 28S subunit of
 XX represents a fragment of a mistletoe lectin B1 protein.
 XX Sequence 264 AA;
 XX
 XX Query Match 99.1%; Score 1403; DB 20; Length 264;
 XX Best Local Similarity 98.9%; Pred. No. 6.3e-127;
 XX Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 1 DDTVCASSEPPTRIYVGNMGVAVDDDDPFDGNDQIQLPKSKNNDPNQLWTIKDGTIR 60
 XX 1 DDTVCASSEPPTRIYVGNMGVAVDDDDPFDGNDQIQLPKSKNNDPNQLWTIKDGTIR 60
 XX QY 61 NSCLTYGYTAGYVWIFDCNTRAVEATWQIMDNQTIIPRSNVLAAASGKGTIT 120
 XX 61 NSCLTYGYTAGYVWIFDCNTRAVEATWQIMDNQTIIPRSNVLAAASGKGTIT 120
 XX DB 61 NSCLTYGYTAGYVWIFDCNTRAVEATWQIMDNQTIIPRSNVLAAASGKGTIT 120
 XX QY 121 VQTLDTLGGQMLAGNDTAPFEVTVYIGRPOLCMESNGSVWVEETDSSQNGKALYGD 180
 XX 121 VQTLDTLGGQMLAGNDTAPFEVTVYIGRPOLCMESNGSVWVEETDSSQNGKALYGD 180
 XX DB 121 VQTLDTLGGQMLAGNDTAPFEVTVYIGRPOLCMESNGSVWVEETDSSQNGKALYGD 180
 XX QY 181 GSIRPKQNDQCLTSGSDSVSTINIVSCGASGSRWVFNBGAILNLKNSIAYDAQA 240
 XX 181 GSIRPKQNDQCLTSGSDSVSTINIVSCGASGSRWVFNBGAILNLKNSIAYDAQA 240
 XX DB 181 GSIRPKQNDQCLTSGSDSVSTINIVSCGASGSRWVFNBGAILNLKNSIAYDAQA 240
 XX QY 241 NPKLRRIIIPATGKQNMWLPVF 264
 XX 241 NPKLRRIIIPATGKQNMWLPVF 264
 XX DB 241 NPKLRRIIIPATGKQNMWLPVF 264
 XX
 XX RESULT 4
 XX AA25992
 XX ID AA25992 standard; Protein; 265 AA.
 XX AC AA25992;
 XX
 XX DT 18-OCT-1999 (first entry)
 XX DE Mistletoe lectin B1 variant protein fragment.
 XX KW Mistletoe lectin; antitumour; immunostimulant; A-chain; WLA; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 XX cancer; cytotoxicity; antigen; isoform; lectin B1.
 XX Viscum album.

PN DB19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI: 1999-44535/38.
 XX N-PSDB; AA209116.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 14B; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (WLA)
 XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly of the
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX also described. In a preferred embodiment, the 28S subunit of
 XX represents a fragment of a variant mistletoe lectin B1 protein.
 XX Sequence 265 AA;
 XX
 XX Query Match 99.1%; Score 1403; DB 20; Length 265;
 XX Best Local Similarity 98.9%; Pred. No. 6.3e-127;
 XX Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 1 DDTVCASSEPPTRIYVGNMGVAVDDDDPFDGNDQIQLPKSKNNDPNQLWTIKDGTIR 60
 XX 1 DDTVCASSEPPTRIYVGNMGVAVDDDDPFDGNDQIQLPKSKNNDPNQLWTIKDGTIR 60
 XX DB 1 DDTVCASSEPPTRIYVGNMGVAVDDDDPFDGNDQIQLPKSKNNDPNQLWTIKDGTIR 60
 XX QY 61 NSCLTYGYTAGYVWIFDCNTRAVEATWQIMDNQTIIPRSNVLAAASGKGTIT 120
 XX 61 NSCLTYGYTAGYVWIFDCNTRAVEATWQIMDNQTIIPRSNVLAAASGKGTIT 120
 XX DB 61 NSCLTYGYTAGYVWIFDCNTRAVEATWQIMDNQTIIPRSNVLAAASGKGTIT 120
 XX QY 121 VQTLDTLGGQMLAGNDTAPFEVTVYIGRPOLCMESNGSVWVEETDSSQNGKALYGD 180
 XX 121 VQTLDTLGGQMLAGNDTAPFEVTVYIGRPOLCMESNGSVWVEETDSSQNGKALYGD 180
 XX DB 121 VQTLDTLGGQMLAGNDTAPFEVTVYIGRPOLCMESNGSVWVEETDSSQNGKALYGD 180
 XX QY 181 GSIRPKQNDQCLTSGSDSVSTINIVSCGASGSRWVFNBGAILNLKNSIAYDAQA 240
 XX 181 GSIRPKQNDQCLTSGSDSVSTINIVSCGASGSRWVFNBGAILNLKNSIAYDAQA 240
 XX DB 181 GSIRPKQNDQCLTSGSDSVSTINIVSCGASGSRWVFNBGAILNLKNSIAYDAQA 240
 XX QY 241 NPKLRRIIIPATGKQNMWLPVF 264
 XX 241 NPKLRRIIIPATGKQNMWLPVF 264
 XX DB 241 NPKLRRIIIPATGKQNMWLPVF 264
 XX
 XX RESULT 5
 XX AA25998
 XX ID AA25998 standard; Protein; 264 AA.
 XX AC AA25998;
 XX
 XX DT 18-OCT-1999 (first entry)
 XX DE Mistletoe lectin B3 protein fragment.
 XX KW Mistletoe lectin; antitumour; immunostimulant; A-chain; immunity;
 XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

PI Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
PS Claim 9; Fig 12B; 78pp; German.
XX
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B5 protein.
SQ Sequence 264 AA;
Query Match 100.0%; Score 1416; DB 20; Length 264;
Best Local Similarity 100.0%; Pred. No. 3.5e-128;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DDTCSASBPPTVRIYVGNKGVYVDDPDHDDNQIQIMPSSKNDPNQLTITKQGTIRS 60
DB 1 DDTCSASBPPTVRIYVGNKGVYVDDPDHDDNQIQIMPSSKNDPNQLTITKQGTIRS 60
OY 61 NSGCLITVGYTAGVYVMPDCTAREATITQINDGTTINPSNVLAASSGIKGTILT 120
DB 61 NSGCLITVGYTAGVYVMPDCTAREATITQINDGTTINPSNVLAASSGIKGTILT 120
OY 121 VQTLIDYTLQGGWLAGNDTAREVITVGFEDLCMSNGSVAWETDSSQNGKALYGD 180
DB 121 VQTLIDYTLQGGWLAGNDTAREVITVGFEDLCMSNGSVAWETDSSQNGKALYGD 180
OY 181 GSIRPKQNDQCLTSGRDSVSTVINVSCGASGSGQWTFTEGAILNLSIMWVQA 240
DB 181 GSIRPKQNDQCLTSGRDSVSTVINVSCGASGSGQWTFTEGAILNLSIMWVQA 240
OY 241 NPELRRITIVPATGKKNQMLPEVF 264
DB 241 NPELRRITIVPATGKKNQMLPEVF 264
RESULT 2
AAZ5996
ID AAZ5996 standard; Protein; 265 AA.
XX
AC AAZ5996;
XX
DT 18-OCT-1999 (first entry)
XX
DE Mistletoe lectin B5 variant protein fragment.
XX
KW Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;
KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform; lectin B5.
XX
OS Viscum album.
XX
KM DEL19804210-A1.
XX
PD 12-AUG-1999.
XX
PF 03-FEB-1998; 98DE-1004210.
XX
PR 03-FEB-1998; 98DE-1004210.
XX
PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
XX

PI Morris P, Stiefel T, Voelster W, Welters P;
XX WPI; 1999-445336/38.
DR N-PSDB; AA03120.
XX
CC Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
PS Disclosure; Fig 18B; 78pp; German.
XX
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B5 protein.
SQ Sequence 265 AA;
Query Match 100.0%; Score 1416; DB 20; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.5e-128;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DDTCSASBPPTVRIYVGNKGVYVDDPDHDDNQIQIMPSSKNDPNQLTITKQGTIRS 60
DB 1 DDTCSASBPPTVRIYVGNKGVYVDDPDHDDNQIQIMPSSKNDPNQLTITKQGTIRS 60
OY 61 NSGCLITVGYTAGVYVMPDCTAREATITQINDGTTINPSNVLAASSGIKGTILT 120
DB 61 NSGCLITVGYTAGVYVMPDCTAREATITQINDGTTINPSNVLAASSGIKGTILT 120
OY 121 VQTLIDYTLQGGWLAGNDTAREVITVGFEDLCMSNGSVAWETDSSQNGKALYGD 180
DB 121 VQTLIDYTLQGGWLAGNDTAREVITVGFEDLCMSNGSVAWETDSSQNGKALYGD 180
OY 181 GSIRPKQNDQCLTSGRDSVSTVINVSCGASGSGQWTFTEGAILNLSIMWVQA 240
DB 181 GSIRPKQNDQCLTSGRDSVSTVINVSCGASGSGQWTFTEGAILNLSIMWVQA 240
OY 241 NPELRRITIVPATGKKNQMLPEVF 264
DB 241 NPELRRITIVPATGKKNQMLPEVF 264
RESULT 3
AAZ5986
ID AAZ5986 standard; Protein; 264 AA.
XX
AC AAZ5986;
XX
DT 18-OCT-1999 (first entry)
XX
DE Mistletoe lectin B1 protein fragment.
XX
KW Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;
KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform; lectin B1.
XX
OS Viscum album.
XX
KM DEL19804210-A1.
XX
PD 12-AUG-1999.
XX
PF 03-FEB-1998; 98DE-1004210.
XX

Thu Dec 11 16:09:47 2003

us-09-601-667c-11.reg

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 : Search time 26.0664 Seconds

(without alignments)
1606.345 Million cell updates/sec

Title: US-09-601-667C-11

Perfect score: 1416
Sequence: 1 DVTGCSASEPTVAVHNMK.....RRIIYPAQKPNQWMLPWF 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1416	100.0	264 20 AAY25990	Mistletoe lectin B
2	1416	100.0	264 20 AAY25996	Mistletoe lectin B
3	1403	99.1	264 20 AAY25986	Mistletoe lectin B
4	1403	99.1	264 20 AAY25992	Mistletoe lectin B
5	1397	98.7	264 20 AAY25988	Mistletoe lectin B
6	1397	98.7	264 20 AAY25994	Mistletoe lectin B
7	1390	98.2	264 20 AAY25989	Mistletoe lectin B
8	1390	98.2	264 20 AAY25995	Mistletoe lectin B
9	1384	96.3	264 20 AAY25987	Mistletoe lectin B

10	1364	96.3	265 20 AAY25993	Mistletoe lectin B
11	1324.5	93.5	263 20 AAY25985	Mistletoe lectin B
12	1324.5	93.5	264 20 AAY25991	Mistletoe lectin B
13	1324.5	93.5	531 20 AAY25979	Mistletoe lectin I
14	1324.5	93.5	532 20 AAY25982	Mistletoe lectin I
15	1318.5	93.1	263 19 AAM64662	Mistletoe rMLB var
16	1318.5	93.1	264 18 AAM10023	Prepro mistletoe I
17	1318.5	93.1	263 20 AAM90126	Mistletoe rMLB pro
18	1318.5	93.1	264 20 AAM17085	Mistletoe lectin I
19	1318.5	93.1	564 18 AAM90127	Mistletoe lectin I
20	1318.5	93.1	564 20 AAM90127	Mistletoe lectin B
21	1290	91.1	264 20 AAY25972	Mistletoe lectin B
22	1290	91.1	264 20 AAY25978	Mistletoe lectin B
23	1290	91.1	264 20 AAY25975	Mistletoe lectin B
24	1290	91.1	533 20 AAY25970	Mistletoe lectin P
25	1290	91.1	533 20 AAY25973	Mistletoe lectin P
26	1242.5	87.8	267 19 AAM4667	Mistletoe rMLB pro
27	1242.5	87.8	267 22 AAM47085	B-chain isoform fo
28	1184.5	76.9	263 22 AAM47085	B-chain isoform fo
29	1085.5	74.1	581 25 ABB7925	B-chain isoform fo
30	1049.5	70.4	266 22 ABB47083	Sequence of Prepro
31	997	63.8	565 6 AAY50166	Sequence of Prepro
32	903.5	63.8	565 22 AAG78300	Sequence of Prepro
33	903.5	63.8	565 22 AAG78304	Sequence of Prepro
34	901.5	63.7	574 8 AAY70325	Modified factor be
35	901.5	63.7	574 8 AAY70325	DNA sequence of ri
36	901.5	63.7	576 18 AAY25793	Caetor bean ricin
37	901.5	63.7	576 18 AAY25787	Caetor bean ricin
38	901.5	63.7	576 21 AAY55882	Ricinus communis r
39	901.5	63.7	576 22 AAY78502	Caetor bean prepro
40	891.5	63.3	565 7 AAB60240	Prepro of ricin B
41	891.5	63.3	262 10 AAB90200	B Chain of ricin D
42	895.5	63.0	262 10 AAB82896	Ricin B matured wit
43	885.5	62.5	576 8 AAY70326	Sequence of Ricinu
44	885.5	62.5	576 8 AAY70326	Sequence of Ricinu

ALIGNMENTS

PROFIT 1
ID AAY25990
AAY25990 standard; Protein, 264 AA.

AC AAY25990;
XX 18-OCT-1999 (first entry)

DE Mistletoe lectin B5 protein fragment.

KV Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
KW riboprotein 28S subunit; non-cytotoxic; T-cell activation; immune response;
KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KN cancer; cytotoxicity; antigen; isoform; lectin B5.

OS Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

XX Viscum album.

Query Match	52.9%;	Score 748.5;	DB 10;	Length 382;
Best Local Similarity	53.9%;	Pred. No. 2.6e-55;		
Matches 139; Conservative	44;	Mismatches 73;	Indels 1;	Gaps 1;

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QY      9  EPLTAVIGNKAPVTDHDDHPDQKNOQLTQMSKSNDDPOLMTIPEGTISENOSGLTLY 66
Db      128 EPLTAVIGNRGDCVQSDBEANRGNPILIMKRCQDREKQMLTTSKPIIKSKKGLTLY 187
QY      69  GYAGAVYWIPIPCVYFBEATVIMQITNGTINFRSBNVILAAASGIGTILTVGIDYTL 128
Db      188 GIDPNCVWVIVICLTSVEPATEVITWNGIINLILKALSAASSAMGKGLTVKDDITRM 247
QY      129 GQGLTANDTAPRVTAVITVYGFZDI  CSENGSIVYVITCTSSQKQKQALYGDPS  IPEKON  186
Db      248 RQMTNDNDPSIFVYVITVYSDLCSEHBSNMMVLAQDNRKNG  QHVLPSYSLIPEKON  305
QY      189 QDPCCTGGRDSYVTVINIVSSQSGSQRWYETBKAALINKSLYDVQAMQETBRI  248
Db      307 TNNCLTSEKHQKSGSVTLVAGCSGMSQAPWFKNDSYVSLYDWDVVDVGSDELKCI  366
QY      249 IYFATKPNQMLFVPE  264
Db      367 IWEYGRKQNDILTR  382

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RESULT 14
Q9M6E9
ID Q9M6E9 PRELIMINARY; PRT; 547 AA

[illegible]

RP SEQUENCE FROM N.A.
 RX MEDLINE=3102702; PubMed=1063690;
 RA Llin C.L., Tsai C.C., Lin S.C., Wang L.S., Hsu C.I., Huang M.J.,
 PA Lin Y.Y.
 PT Primary Structure and Function Analysis of the Abrus precatorius
 RX Agglutinin A Chain: A Site-directed Mutagenesis Study of Amphiphilic
 RL J. Biol. Chem. 275(18):12011-12020.
 RL -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADONOSIN TO THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE PROTEOM-INACTIVATING PROTEIN FAMILY.

DR HSSP: Y1101; 1188; 1
DR InesP01: IER001772; R10n_3 lectin.
DR D10000: IER001772; R10n_3 lectin.
DR Pfam: pf00652; R10n_3 lectin; 6
DR Pfam: pf00161; R1p; 1
DR PRINTS: PRO0396; SHIGARCIN.
DR SMART: SMO0458; RCIN; 2
DR PROSITE: PSS0231; SHICIN_B; LECTIN; 2
DR PROSITE: PSS0275; SHICIN_RCIN; 1.
DR

50	SEQUENCE	547 AA; 61248 MM; 3563435023544ABD	CHC64;
Query March	5.8%; Score 748; DB 10;	Length 547;	
Best local	Similarity 52.0%;	Positives 44;	
Matches 140;	Conservative 43;	Mismatches 76;	Indels 2
Gap 2			
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288	CSSEHPEFPAIGSDGICADVSNVANNNGPFIIMKDKOILEVQVLTMSKPTKISKK	347	

QY 6 C L T T Y G T A G Y A Y M T F D C N A N E K T M O I W I D N G I I N P R S M I V I A A S G K R T T I T Y Q T 123
Db 348 C L T T Y G A G A Y A Y M D D S S A A R A Y M D I W D N G I I N P S S G I A S E S S G I T Y P Q A K 403
QY 124 D L T L G C H L A G M P A P E V T Y F R L L D S N S G S M V T P D S O S M A L N D G S T 183
Db 408 N Y K M G C M R G M D S P R V T S I A G P F L T A A R S N M L E V D I D I R E G Q M A Y D G S I 466
QY 184 R E K N O D C L T S R P S V T A Y I V T S C S A S G S O R W F F N S C A L I N L S N I A M P A O A P K 243
Db 467 R E V G N T N N L C E H R Q A I I W M S C S N A S O R W F K S D G T I V M L Y D M V M P K S D P S 526
QY 244 L R A I I I V A T E R K N O M L P V F 264
Db 527 L R Q I I I M F T I N A N O M M L F 547

RESULT 15	
08W2E8	
ID 08W2E8	PRELIMINARY;
08W2E8	PRT; 573 AA

D7 01-MAR-2009 (TRENHARVEL_20, last sequence update)
D8 01-MAR-2009 (TRENHARVEL_20, last annotation update)
DE Ribosome-inactivating protein IPAR (EC 3.2.2.2) (rRNA N-glycosidase)
DS
DS
DS
DS
DS
OC iris hollandica (lunch iris)
OC
OC Embryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
OX NCBI TaxID=35876;

RP SEQUENCE FROM N. A.
R van Damme B.J.M., Peumans W.J.;
RT "Wirs (Iris holandica var. Professor Blaau) plants express both type 1 and type 2 ribosome-inactivating proteins in bulb tissue." ;
CC 1. SPECIFIC ACTIVITY OF THE 28S RRNA
CC 2. CATALYTIC ACTIVITY
CC 3. SPECIFIC AMBOSOME ON THE 28S RRNA
CC 4. -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AF550841; AA55093.1; -

DR InterPro3, IPR001574; RIB.
DR Pfam, PF06527; RIB_n_lectin, 6.
DR Pfam, PF06527; RIB_n_lectin, 6.
DR PRINTS, PR00396; SHIGARG.CN.
DR SMART, SMO0458; RIBIN, 2.
DR PROSITE, PS00231, RIBIN & LECTIN, 2.
DR PROSITE, PS00231, SHIGARG.CN, 1.
DR PROSITE, PS00231, SHIGARG.CN, 1.
FT NON TER. 1
SQ SEQUENCE 573 Aa: 63759 MW; 1441439ABCDAPSC CRC64;

QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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D6	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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Dy	3 71	MEKCTBIIHAKAIIAIIYCCACBAMATLITM - KOSII, IIRKISSA, I5A8B56K5G1IT	4
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Dy	430	KYTHHAKOCBACIIPATPEBITYCIBI, I5I5I5I5CIBIIOKOCBACIYK - KYTHIIG	4 66
Dy	180	DO5IIPKOCBACIICACBACIYK IIVINIC5C5ACIIOKOCBACIYK IIRKISSA IIMDYO	2 39
Dy	489	DO5IIPKOCBACIICACBACIYK IIVINIC5C5ACIIOKOCBACIYK IIRKISSA IIMDYO	5 48

"Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomol proteins and study of their expression patterns.";
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: AY039801; AKS2458.1; Ricin_B_lectin.
DR EMBL: AY039802; AKS2459.1; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00652; Ricin_B_lectin; 5.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
KV Hydrolase; signal; toxin.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 1 32 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
SQ SEQUENCE 581 AA; 64215 MW; 6853587FBA0D196 CRC64;
Query Match 58.0%; Score 821.5; DB 10; Length 581;
Best Local Similarity 59.2%; Pred. No. 2.9e-61;
Matches 157; Conservative 34; Indels 3; Gaps 2;
Db 1 DDTCSASEPTVATVSGNGRVVDDDPDPCNQIQLMPKSNNDPQMLTIRKDTIRSG 60
317 NDDTCADPEPTVATVSGNGRVVDDDPDPCNQIQLMPKSNNDPQMLTIRKDTIRSG 376
QY 61 NSGLTGTGAGVYVMTFPCNTAVRENTIQLMDNGTINPNSNYLAASSGIGKTTLYQT 120
Db 377 NGKLTNGTSGMDVMTDRTVTAISIKQFANGTIIIPGSAVLVLSGSGPTTLIF 436
QY 121 VQTLDTLQGLAGNDPAPEVITVGFPCNLCSNGSVVETCDSSQKNGMALVGD 180
Db 437 VQNTVTSRQGLAGNDPAPEVITVGFPCNLCSNGSVVETCDSSQKNGMALVGD 495
QY 181 GSIRPKQND--QCLTSGRDSVTYINIVSCGASGSGQRFVFNBAIIMKSLMTDVA 238
Db 496 GSIRPKQND--QCLTSGRDSVTYINIVSCGASGSGQRFVFNBAIIMKSLMTDVA 555
QY 239 GNPTRRIITVATGKQVQWLPV 263
Db 556 GNPTRRIITVATGKQVQWLPV 580
RESULT 12
Q06076 PRELIMINARY; PRT; 528 AA.
ID Q06076
AC Q06076
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
OS Abrus precatorius (Indian licorice) (Crab's eye).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eucosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OX NCBI_TaxID:3816;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE:933798; PubMed:642133.
RA HUNG C.-H., Lee N.-C., Lin J.-Y.;
RA "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomol proteins and study of their expression patterns.";
RA submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RT -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: M98346; AAA3262.1; -.
DR HSRP; P11140; IABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.

DR Pfam: PF00652; Ricin_B_lectin; 6.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KV Hydrolase; toxin.
FT SIGNAL 1 1
FT CHAIN 1 1
SQ SEQUENCE 528 AA; 58870 MW; 62BD42FB8FF60F8 CRC64;
Query Match 53.8%; Score 762; DB 10; Length 528;
Best Local Similarity 54.4%; Pred. No. 2.8e-56;
Matches 142; Conservative 47; Mismatches 70; Indels 2; Gaps 2;
Db 5 CASL-EPVATVATVSGNGRVVDDDPDPCNQIQLMPKSNNDPQMLTIRKDTIRSG 63
269 CASL-EPVATVATVSGNGRVVDDDPDPCNQIQLMPKSNNDPQMLTIRKDTIRSG 328
QY 64 CLTGTGTGAGVYVMTFPCNTAVRENTIQLMDNGTINPNSNYLAASSGIGKTTLYQT 123
Db 329 CLTGTGTGAGVYVMTFPCNTAVRENTIQLMDNGTINPNSNYLAASSGIGKTTLYQT 386
QY 124 DDTLQGLAGNDPAPEVITVGFPCNLCSNGSVVETCDSSQKNGMALVGD 183
Db 389 DDTLQGLAGNDPAPEVITVGFPCNLCSNGSVVETCDSSQKNGMALVGD 447
QY 184 RKQNDQCLTSGRDSVTYINIVSCGASGSGQRFVFNBAIIMKSLMTDVA 243
Db 448 RKQNDQCLTSGRDSVTYINIVSCGASGSGQRFVFNBAIIMKSLMTDVA 507
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Db 508 LRKIIITVATGKQVQWLPV 528
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AC Q08943
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
OS Abrus precatorius (Indian licorice) (Crab's eye).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eucosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OX NCBI_TaxID:3816;
RN
RP SEQUENCE FROM N.A.
RX COOK J.P., Roberts L.N., Lord M.;
RA "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomol proteins and study of their expression patterns.";
RA submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RT -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL: M98346; AAA3262.1; -.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00652; Ricin_B_lectin; 5.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KV Hydrolase; toxin.
FT SIGNAL 1 1
FT CHAIN 1 1
SQ SEQUENCE 382 AA; 42743 MW; B0B8B341813AD2B8 CRC64;

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us-09-601-667c-11.rsp

Page 5

DB 496 GSIRPHODRCLSTNDHSCGSIISCSFSGRWPNDSITLAKGLWVAG 555
QY 240 ANPKRLIIPATGKPKOMWLPV 263
DB 556 SNPSHQLIIPATGKPKOMWLPV 579

RESULT 9

Q94BM3 PRELIMINARY; PRT; 580 AA.
AC Q94BM3; (TREMUREL.19, Created)
DT 01-DEC-2001 (TREMUREL.19, Last sequence update)
DE Type 2 ribosome-inactivating protein cinnamomol III precursor
DE EC 3.2.2.22 (RNA N-glycosidase).
OC Cinnamomum camphora (Camphor tree).
OC Spermatophyta; Viridiplantae; Embryophyta; Tracheophyta;
OC Eukaryota; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI_TaxID=13429;

RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomol proteins and study of their expression
RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
RL -1- CATALYTIC ACTIVITY: ENDOPHYLOXIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AY039803; AAK82460.1; -.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR SMART; S00048; RLP1; 1.
DR PROSITE; PS00231; Ricin_B_lectin; 2.
KW Hydroxylase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMOL III.
SQ SEQUENCE 580 AA; 64421 MW; 940D0F0LE7B558 CRC64;

Query Match 50.7% Score 860; DB 10; Length 580;
Best Local Similarity 52.1%; Pred. No. 1,66-63;
Matches 164; Conservative 35; Mismatches 63; Indels 2; Gaps 2;

QY 1 DVTCSASEPTVIVGKGVVDDPHDQIOLPCKSNQDPMQATIKGGTGR 60
DB 317 NBDTCADPEPTVIRISRNGLCDVDDKNNKNGIOLPCKSNQDPMQATIKGGTGR 376
QY 61 NSGCLTGYGTAGVYVAFPCNTAVRENTIWIQINDGIIINPSNVLAASSGIGTTLT 120
DB 377 NSGCLTNGISAGDPTVADCTPTVTAISVQFWANGLIINQSAVLAASSGIRPTTLT 436
QY 121 VQTLDTLQGLANQDTPAPRETIYGFEDLCQESNGSVVETCGSGKQKXALVGD 180
DB 437 VQADIVASRGVLAGNNEPEPTVTSVGFNDLCQANQANMVAVERESSAQQ-KNALYD 495
QY 181 GSIRPHODRCLSTNDHSCGSIISCSFSGRWPNDSITLAKGLWVAG 239
DB 496 GSIRPHODRCLSTNDHSCGSIISCSFSGRWPNDSITLAKGLWVAG 555
QY 240 ANPKRLIIPATGKPKOMWLPV 263
DB 556 SNPSHQLIIPATGKPKOMWLPV 579

RESULT 10
Q94BM3 PRELIMINARY; PRT; 549 AA.
ID Q94BM3
AC Q94BM3; (TREMUREL.19, Created)
DT 01-DEC-2001 (TREMUREL.19, Last sequence update)
DE Type 2 ribosome-inactivating protein cinnamomol I precursor
DE EC 3.2.2.22 (RNA N-glycosidase).
OC Cinnamomum camphora (Camphor tree).
OC Spermatophyta; Viridiplantae; Embryophyta; Tracheophyta;
OC Eukaryota; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI_TaxID=13429;

AC Q94BM3; (TREMUREL.19, Created)
DT 01-DEC-2001 (TREMUREL.19, Last sequence update)
DE Type 2 ribosome-inactivating protein cinnamomol I precursor
DE EC 3.2.2.22 (RNA N-glycosidase).
OC Cinnamomum camphora (Camphor tree).
OC Spermatophyta; Viridiplantae; Embryophyta; Tracheophyta;
OC Eukaryota; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI_TaxID=13429;

RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT Molecular cloning of cinnamomol A-, B-chain and the expression,
RT purification, characterization and mutagenesis of the A-chain.
RT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
RL -1- CATALYTIC ACTIVITY: ENDOPHYLOXIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF295548; AAF68378.2; -.
DR HSP; P02879; 2A1.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 5.
DR SMART; S00048; RLP1; 1.
DR PROSITE; PS00231; Ricin_B_lectin; 2.
KW Hydroxylase; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 549
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMOL I.
SQ SEQUENCE 549 AA; 60648 MW; 02607F607CA4480 CRC64;

Query Match 58.0% Score 821.5; DB 10; Length 549;
Best Local Similarity 59.2%; Pred. No. 2,76-61;
Matches 157; Conservative 34; Mismatches 71; Indels 3; Gaps 2;

QY 1 DVTCSASEPTVIVGKGVVDDPHDQIOLPCKSNQDPMQATIKGGTGR 60
DB 285 NBDTCADPEPTVIRISRNGLCDVDDKNNKNGIOLPCKSNQDPMQATIKGGTGR 344
QY 61 NSGCLTGYGTAGVYVAFPCNTAVRENTIWIQINDGIIINPSNVLAASSGIGTTLT 120
DB 345 NSGCLTNGISAGDPTVADCTPTVTAISVQFWANGLIINQSAVLAASSGIRPTTLT 404
QY 121 VQTLDTLQGLANQDTPAPRETIYGFEDLCQESNGSVVETCGSGKQKXALVGD 180
DB 405 VQADIVASRGVLAGNNEPEPTVTSVGFNDLCQANQANMVAVERESSAQQ-KNALYD 463
QY 181 GSIRPHODRCLSTNDHSCGSIISCSFSGRWPNDSITLAKGLWVAG 238
DB 464 GSIRPHODRCLSTNDHSCGSIISCSFSGRWPNDSITLAKGLWVAG 523
QY 239 ANPKRLIIPATGKPKOMWLPV 263
DB 524 SNPSHQLIIPATGKPKOMWLPV 548

DR PFAM: PF00161; R1P; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
DR Hydrolase; Toxin.
KM NON_TER
FT SEQUENCE 541 AA; 60281 MW; 28782CDSEFIETZ9D9 CRC64;
SQ

Query Match 63.8%; Score 903.5; DB 10; Length 541;
Best Local Similarity 63.5%; Pred. No. 36-68;
Matches 165; Conservative 35; Mismatches 59; Indels 1; Gaps 1;

OY 5 CSASEPTVRIYVGNKGVVDVDDDFDQNOIQUMPSKSNNDPNQMTIKEDGTIRSGSC 64
DB CMDEPIYRIYVGNGLCVVDGDFHNGNAIQUMPSKSNNDPNQMTIKEDGTIRSGSC 342
OY 65 LITVGYTAGVYVIMFDCTAVREKATVQINDGTINPESNLVLAASSGKFTLVQTL 124
DB LITVGYSPGVYVIMFDCTAVREKATVQINDGTINPESNLVLAASSGKFTLVQTL 402
OY 125 DYTLAGQWLAGNDTAREVITVIGFDLCNDSNGSVWETCCSQKQKRMALYDGSIR 184
DB IVAVSQWLPNNTPQFVITVIGYGLCLQNSGGVWIEDC-TSEKASQWALYDGSIR 461
OY 185 PKQNDQCLTSGRDVSTVINIVCSGASGQRFWETGALINRSLAWDYAQNAPL 244
DB PQNRNDCLTSDNIRFETVYKLSGPAASGQRFWETGALINRSLAWDYAQNAPL 521
OY 245 RRIITVPATGKPNQMTLPV 264
DB RRIITVPATGKPNQMTLPV 541

RESULT 7
OY 041143 PRELIMINARY; PRT; 263 AA.
AC 041143
DT 01-NOV-1996 (TRENBERG). 01. Created
DT 01-NOV-1996 (TRENBERG). 01. Last sequence update
DT 01-MAR-2003 (TRENBERG). 23. Last annotation update
DE RICIN B beta chain (Fragment).
OS Homo sapiens
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
OC Eucosids I; Malpighiales; Euphorbiaceae; Ricinus
OX NCBI_Taxid:3988;
RN
RP SEQUENCE FROM N.A.
RA Ladin B.F., Murray E.E., Halling A.C., Halling K.C., Tlakarata N.,
RA Long G.L., Houston L.L., Weaver R.F.;
RT Characterization of a cDNA encoding ricin E, a hybrid ricin-Ricinus
RT communis agglutinin gene from the castor plant Ricinus communis";
RT J Biol Chem 273(1997):9511-9517.
DR EMBL: M1631; AA:G3506.1; .
DR HESP: P02879; 2AA1.
DR InterPro: IPR000772; Ricin_B_Lectin.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF00652; Ricin_B_Lectin; 6.
DR SMART: SM00458; RICIN; 2.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
FT NON_TER
SQ SEQUENCE 263 AA; 29134 MW; A4880FDIDDL14 CRC64;
Query Match 61.5%; Score 871; DB 10; Length 263;
Best Local Similarity 61.3%; Pred. No. 6-66;
Matches 160; Conservative 38; Mismatches 61; Indels 2; Gaps 2;

DB 4 CMDEPIYRIYVGNGLCVVDGDFHNGNAIQUMPSKSNNDPNQMTIKEDGTIRSGSC 63
OY 65 LITVGYTAGVYVIMFDCTAVREKATVQINDGTINPESNLVLAASSGKFTLVQTL 124
DB LITVGYSPGVYVIMFDCTAVREKATVQINDGTINPESNLVLAASSGKFTLVQTL 402
OY 125 DYTLAGQWLAGNDTAREVITVIGFDLCNDSNGSVWETCCSQKQKRMALYDGSIR 184
DB IVAVSQWLPNNTPQFVITVIGYGLCLQNSGGVWIEDC-TSEKASQWALYDGSIR 461
OY 185 PKQNDQCLTSGRDVSTVINIVCSGASGQRFWETGALINRSLAWDYAQNAPL 244
DB PQNRNDCLTSDNIRFETVYKLSGPAASGQRFWETGALINRSLAWDYAQNAPL 521
OY 245 RRIITVPATGKPNQMTLPV 264
DB RRIITVPATGKPNQMTLPV 541

RESULT 8
OY 0948M4 PRELIMINARY; PRT; 580 AA.
AC 0948M4
DT 01-DEC-2001 (TRENBERG). 19. Created
DT 01-DEC-2001 (TRENBERG). 19. Last sequence update
DT 01-MAR-2003 (TRENBERG). 23. Last annotation update
DE Type 2 ribosome-inactivating protein in cinnamon II precursor
DE (EC 3.2.2.22) (rRNA N-glycosidase).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_Taxid:13429;
RN
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamonin proteins and study of their expression
RT patterns";
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DE EMBL: A039802; A0482459.1; .
DR InterPro: IPR000172; Ricin_B_Lectin.
DR Pfam: PF00652; Ricin_B_Lectin; 6.
DR PRINTS: PR00161; R1P; 1.
DR SMART: SM00458; SHIGARICIN.
DR PROSITE: PS00231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00338; SOMATOTROPIN_2; 1.
FT NON_TER
FT SIGNAL 33 580
KM Hydrolase; Signal; Toxin.
SQ SEQUENCE 580 AA; 64265 MW; 37544289CECECF CRC64;
Query Match 61.2%; Score 867; DB 10; Length 580;
Best Local Similarity 62.5%; Pred. No. 48-65;
Matches 165; Conservative 34; Mismatches 63; Indels 2; Gaps 2;

OY 5 CSASEPTVRIYVGNKGVVDVDDDFDQNOIQUMPSKSNNDPNQMTIKEDGTIRSGSC 64
DB CMDEPIYRIYVGNGLCVVDGDFHNGNAIQUMPSKSNNDPNQMTIKEDGTIRSGSC 342
OY 65 LITVGYTAGVYVIMFDCTAVREKATVQINDGTINPESNLVLAASSGKFTLVQTL 124
DB LITVGYSPGVYVIMFDCTAVREKATVQINDGTINPESNLVLAASSGKFTLVQTL 402
OY 125 DYTLAGQWLAGNDTAREVITVIGFDLCNDSNGSVWETCCSQKQKRMALYDGSIR 184
DB IVAVSQWLPNNTPQFVITVIGYGLCLQNSGGVWIEDC-TSEKASQWALYDGSIR 461
OY 185 PKQNDQCLTSGRDVSTVINIVCSGASGQRFWETGALINRSLAWDYAQNAPL 244
DB PQNRNDCLTSDNIRFETVYKLSGPAASGQRFWETGALINRSLAWDYAQNAPL 521
OY 245 RRIITVPATGKPNQMTLPV 264
DB RRIITVPATGKPNQMTLPV 541

DB 4 CMDEPIYRIYVGNGLCVVDGDFHNGNAIQUMPSKSNNDPNQMTIKEDGTIRSGSC 63
OY 65 LITVGYTAGVYVIMFDCTAVREKATVQINDGTINPESNLVLAASSGKFTLVQTL 124
DB LITVGYSPGVYVIMFDCTAVREKATVQINDGTINPESNLVLAASSGKFTLVQTL 402
OY 125 DYTLAGQWLAGNDTAREVITVIGFDLCNDSNGSVWETCCSQKQKRMALYDGSIR 184
DB IVAVSQWLPNNTPQFVITVIGYGLCLQNSGGVWIEDC-TSEKASQWALYDGSIR 461
OY 185 PKQNDQCLTSGRDVSTVINIVCSGASGQRFWETGALINRSLAWDYAQNAPL 244
DB PQNRNDCLTSDNIRFETVYKLSGPAASGQRFWETGALINRSLAWDYAQNAPL 521
OY 245 RRIITVPATGKPNQMTLPV 264
DB RRIITVPATGKPNQMTLPV 541

Matches 244; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY 1 DDTTCSAEPYVAVKNGKAVVDDDPDHDGNCIOLMPSKSNNDPNQMTWKIKDGTIRS 60
DB 269 DDTTCSAEPYVAVKNGKAVVDDDPDHDGNCIOLMPSKSNNDPNQMTWKIKDGTIRS 328

QY 61 NSGCTTYGTAGYVWIFDCNNAVEKATITWQJNDGTTINPSNMLVLAASSGKGTIT 120
DB 329 NSGCTTYGTAGYVWIFDCNNAVEKATITWQJNDGTTINPSNMLVLAASSGKGTIT 388

QY 121 VQTLDTLGGGLAGNDTAPREVTIYGFRLCMESNGSVWETCVSGSQNQ-EMALYGD 180
DB 389 VQTLDTLGGGLAGNDTAPREVTIYGFRLCMESNGSVWETCVSGSQNQ-EMALYGD 447

QY 181 GSIRPKONODCLTSGDSVSTVINIVSCSAGSGQWFTNEGALINKSLMVDVAQA 240
DB 448 GSIRPKONODCLTSGDSVSTVINIVSCSAGSGQWFTNEGALINKSLMVDVAQA 507

QY 241 NPKLRILITTPATGKPNQWMLPV 263
DB 508 NPKLRILITTPATGKPNQWMLPV 530

RESULT 2

ID Q8LK02 PRELIMINARY; PRT; 263 AA.

AC Q8LK02; TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Lactin chain B isoform 2 (fragment).

OS Viscum album subsp. coloratum.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Eudicotyledons; Core eudicot;
Rosales; Viscaceae; Viscum.

NCBI_TaxID=159976;

RP SEQUENCE FROM N.A.

RX MEDLINE=2156752; PubMed=11710524;

RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-U., Kim J.-B.,
Do M.-S., Song S.K.,
"cDNA cloning and sequence analysis of the lectin genes of the Korean
mistletoe (Viscum album coloratum).";
Mol. Cells 12:215-220(2001).

RT

RM

RN SOURCE FROM N.A.

RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-U., Kim J.-B.,
Do M.-S., Song S.K.,
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF509318; AA46936.1; -
Interpco; IP8000772; Ricin_B_lectin.
Pfam; PF00652; Ricin_B_lectin; 5.
DR SMART; SM00458; RICIN_2; LECTIN_2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
FT NON-TER 1
FT NON-TER 263
SQ SEQUENCE 263 AA; 23150 MW; B685BCB7C49CDDIF CRC64;

Query Match 78.8%; Score 116.5; DB 10; Length 263;
Best Local Similarity 78.7%; Pred. No. 1,le-86;
Matches 207; Conservative 23; Mismatches 32; Indels 1; Gaps 1;

QY 1 DDTTCSAEPYVAVKNGKAVVDDDPDHDGNCIOLMPSKSNNDPNQMTWKIKDGTIRS 60
DB 269 DDTTCSAEPYVAVKNGKAVVDDDPDHDGNCIOLMPSKSNNDPNQMTWKIKDGTIRS 328

QY 61 NSGCTTYGTAGYVWIFDCNNAVEKATITWQJNDGTTINPSNMLVLAASSGKGTIT 120
DB 329 NSGCTTYGTAGYVWIFDCNNAVEKATITWQJNDGTTINPSNMLVLAASSGKGTIT 388

QY 121 VQTLDTLGGGLAGNDTAPREVTIYGFRLCMESNGSVWETCVSGSQNQ-EMALYGD 180
DB 389 VQTLDTLGGGLAGNDTAPREVTIYGFRLCMESNGSVWETCVSGSQNQ-EMALYGD 447

QY 181 GSIRPKONODCLTSGDSVSTVINIVSCSAGSGQWFTNEGALINKSLMVDVAQA 240
DB 448 GSIRPKONODCLTSGDSVSTVINIVSCSAGSGQWFTNEGALINKSLMVDVAQA 507

QY 241 NPKLRILITTPATGKPNQWMLPV 263
DB 508 NPKLRILITTPATGKPNQWMLPV 530

QY 181 GSIRPKONODCLTSGDSVSTVINIVSCSAGSGQWFTNEGALINKSLMVDVAQA 240
DB 180 GSIRPKONODCLTSGDSVSTVINIVSCSAGSGQWFTNEGALINKSLMVDVAQA 239

QY 241 NPKLRILITTPATGKPNQWMLPV 263
DB 240 NPKLRILITTPATGKPNQWMLPV 262

RESULT 3

ID Q8W243 PRELIMINARY; PRT; 565 AA.

AC Q8W243; TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE VCA precursor (BC 3.2.2.22) (rRNA N-glycosidase).

OS Viscum album subsp. coloratum.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Eudicotyledons; Core eudicot;
Rosales; Viscaceae; Viscum.

NCBI_TaxID=159976;

RP SEQUENCE FROM N.A.

RX Park W.-B., Lyu S.-I.
"Cloning of Viscum album subsp. coloratum (Korean mistletoe).";
Biochem. Biophys. Res. Commun. 0:0(2002).

RT -1- CARPATIC ACTIVITY: ENOXYHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

DR EMBL; AF509318; AA46936.1; -
Interpco; IP8000772; Ricin_B_lectin.
Pfam; PF00652; Ricin_B_lectin; 6.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN_2; LECTIN_2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
KV Hydrolyase; Signal; Toxin.
FT SIGNAL 1
FT SIGNAL 22
FT CHAIN 23
FT CHAIN 273
SQ SEQUENCE 565 AA; 62401 MW; 991E3994D005F11 CRC64;

Query Match 77.9%; Score 110.5; DB 10; Length 565;
Best Local Similarity 79.8%; Pred. No. 3,6e-85;
Matches 210; Conservative 17; Mismatches 31; Indels 5; Gaps 2;

QY 1 DDTTCSAEPYVAVKNGKAVVDDDPDHDGNCIOLMPSKSNNDPNQMTWKIKDGTIRS 60
DB 307 DDTTCSAEPYVAVKNGKAVVDDDPDHDGNCIOLMPSKSNNDPNQMTWKIKDGTIRS 362

QY 61 NSGCTTYGTAGYVWIFDCNNAVEKATITWQJNDGTTINPSNMLVLAASSGKGTIT 120
DB 329 NSGCTTYGTAGYVWIFDCNNAVEKATITWQJNDGTTINPSNMLVLAASSGKGTIT 388

QY 121 VQTLDTLGGGLAGNDTAPREVTIYGFRLCMESNGSVWETCVSGSQNQ-EMALYGD 180
DB 389 VQTLDTLGGGLAGNDTAPREVTIYGFRLCMESNGSVWETCVSGSQNQ-EMALYGD 447

QY 181 GSIRPKONODCLTSGDSVSTVINIVSCSAGSGQWFTNEGALINKSLMVDVAQA 240
DB 448 GSIRPKONODCLTSGDSVSTVINIVSCSAGSGQWFTNEGALINKSLMVDVAQA 507

QY 241 NPKLRILITTPATGKPNQWMLPV 263
DB 542 NPKLRILITTPATGKPNQWMLPV 564

RESULT 4

ID Q8LK01 PRELIMINARY; PRT; 263 AA.

FT CARBOHYD 131 131 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 343 343 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 444 444 N-LINKED (GLCNAc. . .) (POTENTIAL).
 SQ SEQUENCE 545 AA; 60148 MW; 2DC5A710C95D59C CRC64;

Query Match 6.7%; Score 94.5; DB 1; Length 545;
 Best Local Similarity 19.5%; Pred. No. 1.1;
 Matches 45; Conservative 43; Mismatches 98; Indels 45; Gaps 8;

QY 22 VDVRRDDPFDGNGIQMPKSNNDPNQWTKRKGIRNSGLTYGYTA----- 72
 DB 342 LDILTRSLANGDRLATVINKNR-----IVTRDIPVQWGLTEYDCTTAEDLDGKTQ 395
 QY 73 ---GVYMLFDGNTAVREATNG-----INDGIIIPRSMILAAAGIKTILTYQT 124
 DB 396 KISDHKIELASHATVFRSLPQGSQVPRGLVPTASGNTLRAS--NSVAFQSC 452
 QY 125 DYLGGGLAGNDTPAPREVTIYGRDLQMSNGSVWETCDSSQKQKMAIYGDGSR 184
 DB 453 NGERSCIWVTSSGIRFVS--QITQCLAADGNLYELQACDSTDSQDKATYPTGNLK 509
 QY 185 PRONQOCTTSRDSVSTVINIVSCGASGQWVTFNEGAIIINKSLNV 235
 DB 510 -NKTGGLTSS-----VQKMSC-----LFRDQVRLPSGVOL 544

Search completed: December 11, 2003, 14:09:07
 Job time : 4.6201 secs

[illegible]

Dr	Pfam: PF00652; Ricin B lectin; 3.
Dr	SMART: SM00458; RICIN: 1.
Dr	PROSITE: PS50231; Ricin B LECTIN: 1.
KM	Hydrolase; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.
FT	SIGNAL 1
FT	POTENTIAL 36
FT	CHAIN 37 548
FT	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE.
FT	RICIN B-TYPE LECTIN.
FT	POSSIBS BETA-GLUCANASE ACTIVITY, BUT IS
FT	UNABLE TO LYSE VIABLE CELLS.
FT	ESSENTIAL FOR THE LYtic ACTIVITY, BUT NOT
FT	FOR THE BETA-GLUCANASE FUNCTION.
FT	DOMAIN 472 548
FT	SEQUENCE 548 AA; 58088 MW; 41858AA454068D CnCR43.
FT	
Query Match	9.1%; Score 114; DP 1; Length 548;
Best local similarity	9.13% Pident. No. 0.023; 52; Indels 20; Gaps 7
Matches	41; Conservative 18; Mismatches 52; Indels 20; Gaps 7
Dr	16 GRNGRNV-----DVDDDFDNDNDIOIAMPSSNSNPONLWTKKDGIRSGSL--TT 67
Dr	422 GTGARLRIGSLDLVYPMADPFDNNOVL--ATCSGNAACQWRTGTDGVYALGKLDVLR 479
Dr	68 YGTGAYGVYFDQN--TAVRATVQIOWDNG--IINPSNVLVLAASG--KQITLAV 121
Dr	480 SGADGAAVAVTNGNSGTAKQMT--YVSATKALSNPSSKGLDAQGAPLRQSRQVQL 535
Dr	122 QTLDTVTLGGGM 132
Dr	536 WTQNTLEARNW 546

ID	ABBP_STRL1	STANDARD;	PRT;	475 AA.
AC	P96463;			
DT	15-DEC-1998	(Rel. 37, Created)		
DT	15-DEC-1998	(Rel. 37, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Alpha-L-arabinofuranoside precursor (EC 3.2.1.55) (arabinosidase).			
OS	Streptomyces lividans.			
OC	Bacteria; Actinobacteridae; Actinobacteriales; Actinomycetales;			
OC	Streptomycinae; Streptomycetaceae; Streptomycetes.			
OX	NCBI_Taxid:1916;			
PN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STEINHAUS, J. / 1126; PubMed:9149759;			
RC	STEINHAUS, J. / 1126; PubMed:9149759;			
RC	Vincent, P., Sharrack, P., Dupont, C., Morosoli, R., Kluepfel, D.;			
RT	"New alpha-L-arabinofuranosidase produced by Streptomyces lividans:			
RT	cloning and DNA sequence of the abfp gene and characterization of the			
RT	enzyme.";			
RL	Biochem. J. 322:845-852 (1997).			
RN	[2]			
RN	REVISIONS:			
RN	1. (1998) (1998) (1998) (1998) (1998) (1998) (1998) (1998) (1998) (1998)			
RA	Sharrack, P. / 1126;			
RL	Submitted (UTL-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: HAS A SPECIFIC ARABINOFURANOSIDE-BRANCHING ACTIVITY ON			
CC	XYLAN FROM GRAMINAE. ACTS SYNERGISTICALLY WITH THE XYLANASES AND			
CC	BINDS SPECIFICALLY TO XYLAN. FROM SMALL ARABINOSYLO-OLIGOSIDES,			
CC	IT LIBERATES ARABINOSIDE AND, AFTER PROLONGED INCUBATION, THE			
CC	CRYSTALLINE ENZYME EXHIBITS SOME KATALYTIC ACTIVITY AS WELL.			
CC	-1- CATALYZES THE RELEASE OF ARABINOSIDE FROM ARABINOSYLO-OLIGOSIDES.			
CC	-1- ARABINOFURANOSIDASE RESIDUES IN ALPHA-L-ARABINOSIDES.			
CC	-1- PATHWAY: Xylan degradation.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL HYDROLASES.			
CC	-1- SIMILARITY: CONTAINS 1 Ictin B-type lectin domain.			
CC	-----			
CC	This Swiss-Prot entry is copyrighted. It is produced through a collaborative			
CC	effort between the EMBL, GenBank and DDBJ databases. It is the property of			
CC	the European Bioinformatics Institute. There are no restrictions on its use			
CC	by non-profit institutions as long as its content is in the public domain.			

InterPro: IPRO00772; Ricin B lectin.
 Pfam: PF00633; Glycohydrolase 10.
 PRINTS: PR00134; GHYDRLAS10.
 SMART: SM00458; RICHN1.1.
 PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
 PROSITE: PS50231; RICHN_B_LECTIN; 1.
 KX: Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
 KX: Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
 FT: CHAIN 1 41 ENDO-1,4-BETA-XYLANASE A.
 FT: DOMAIN 361 477 RICHN_B-TYPE LECTIN.
 FT: ACT_SITE 169 169 PROTON DONOR.
 FT: ACT_SITE 277 277 NUCLEOPHILE.
 SQ: SEQUENCE 477 AA; 51162 MW; E14VFE37EDC6CC CRC64;
 Query Match 8.9%; Score 125.5; DB 1; Length 477;
 Best Local Similarity 23.9%; Pred. No. 0.002; 61; Indels 13; Gaps 6;
 Matches 40; Conservative 20; Mismatches 61; Indels 13; Gaps 6;
 QY 7 ASPP-----TVRIYGNKNGRYVDVDDDFDQNGIOIOWPSKSNNDPNQMTIKEDGTRISN 61
 DB 346 SSEPAPDGOIKVQ-SFPCIDVPDSTSGTOLMDGSGT--NCPAANDAGSLVY 402
 QY 62 G-SCLTYGYTAGYVIMFDQNTAVKATWQIMDMETINPSMLYLA--SSGKQTT 118
 DB 403 GPKCLDAKTSKNSKVSITSCGQDNQK--WELNSDSYVQSGSLCLDVNGTAKTL 460
 QY 119 LTVQGLDYTLGGQW 132
 DB 461 ICLYTCNSGNSGW 474
 RESULT 9
 AFBF STFCO STANDARD: PRT; 475 AA.
 ID AFBF STFCO STANDARD: PRT; 475 AA.
 DT 15-DEC-1996 (Rel. 37, Created)
 DT 15-DEC-1996 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).
 GN AFBF OR SC05932 OR SC7H.02.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomyces; Streptomyces; Streptomyces.
 KX: taxid:1902;
 RP SEQUENCE FROM N.A.
 RC STRAIN:A3(2) / M45;
 RA MEDLINE:2196410; PubMed:1200953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleeer H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chan C.W., Collins M.,
 RA Cronin A., Fraser A., Gobie A., Hidalgo J., Horsey T., Howarth S.,
 RA Huang C.-H., Kleeer H., Larke L., Murphy D., Oliver K., O'Neill S.,
 RA Rabinowitz J., Rabinowitz J., Rabinowitz J., Rabinowitz J.,
 RA Seeger K., Sanders D., Sharp S., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrett B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomyces Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-
 arabinofuranoside residues in alpha-L-arabinosides.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLYCOSYL_HYDROLASES.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
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 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC EMBL: AL939125; CAL16189.1; .
 DR PIR: T35697; T35697.
 DR InterPro: IPRO00772; Ricin B lectin.
 DR Pfam: PF00633; Glycohydrolase 10.
 DR PRINTS: PR00134; GHYDRLAS10.
 DR SMART: SM00458; RICHN1.1.
 DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
 DR PROSITE: PS50231; RICHN_B_LECTIN; 1.
 KX: Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
 KX: Xylan degradation; Hydrolase; Glycosidase; Signal; Lectin;
 FT: CHAIN 1 37 POTENTIAL.
 FT: DOMAIN 38 475 ALPHA-B-TYPE LECTIN.
 FT: ACT_SITE 169 169 PROTON DONOR.
 FT: ACT_SITE 277 277 NUCLEOPHILE.
 SQ: SEQUENCE 475 AA; 50045 MW; 473707F353C6AD CRC64;
 Query Match 8.2%; Score 115.5; DB 1; Length 475;
 Best Local Similarity 24.1%; Pred. No. 0.014;
 Matches 52; Conservative 35; Mismatches 104; Indels 25; Gaps 10;
 QY 6 SASEPPIVGNKNGRYVDVDDDFDQNGIOIOWPSKSNNDPNQMTIKEDGTRISN-SC 64
 DB 37 PASESALKSGNSNC-LVVLQSGQDDALDLDYDCGGT--NCPMTSTVSLVYSGKC 93
 QY 65 LTVGYTA-GVYVIMFDQNTAVKATWQIMDMETINPSMLYLA--SSGKQTT 120
 DB 94 LDVPHATAGFRVQVWSCSGANQK--WRVNSDGVVGVESCLCLAAAGTANQVAVQ 151
 QY 121 VQTLDYTLGGQW 132
 DB 152 LMTGNGGNGKWTGTPPTDGTALPSTWASSTGLVAPSSAVALKDPTVYNGR 211
 QY 175 WALNGSG-----IFKQVQDCLTSGSDYS 201
 DB 212 HVIYGTSSGSGYSGWPTPTWMDASNSGNNN 247
 RESULT 10
 E13B ARTSP STANDARD: PRT; 548 AA.
 ID E13B ARTSP STANDARD: PRT; 548 AA.
 DT 15-JUN-1998 (Rel. 36, Created)
 DT 15-JUN-1998 (Rel. 36, Last sequence update)
 DT 15-OCT-2003 (Rel. 46, Last annotation update)
 DE Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) (1->3)-beta-
 GN glucan endohydrolase ((1->3)-beta-glucanase).
 OS Athrobacter sp. (strain YC90).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcales; Micrococcales; Actinobacter.
 KX: taxid:1667;
 RP SEQUENCE FROM N.A.
 RC STRAIN:YC90;
 RA Watanabe T., Hasegawa H., Tanaka H., Doi A., Doi K.,
 RA Subitelli (DEC-1993) to the EMBL/GenBank/DBJ databases.
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
 CC IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
 CC in 1,3-beta-D-glucans; periplasmic (by similarity).
 CC -1- SUBCELLULAR LOCATION: periplasmic (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
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ID	ABRC	ABRP	STANDARD	PRT	562 AA.
REPEAT 5					
AD	ABRC	ABRP			
AC	P28570				
DT	01-DEC-1992	(Rel. 24, Created)			
DT	01-DEC-1992	(Rel. 24, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DS	Abt1-c precursor [comains: Abt1-c A chain (cRNA N-glycosylase)]				
D3	Abt1-c.1 (c222) [Abt1-c B chain]				
OS	Abt1-c.2 (c222) [Abt1-c B chain]				
OC	Eukaryotes: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta; Eudicotyledons: Magnoliopsida; eudicotyledons: core eudicots: Rosidae; eudicots 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abt1-c				
NCBI	Taxid=3816				
REPEAT 6					
AD	ABRC	ABRP			
AC	P28570				
DT	01-DEC-1992	(Rel. 24, Created)			
DT	01-DEC-1992	(Rel. 24, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DS	Abt1-c precursor [comains: Abt1-c A chain (cRNA N-glycosylase)]				
D3	Abt1-c.1 (c222) [Abt1-c B chain]				
OS	Abt1-c.2 (c222) [Abt1-c B chain]				
OC	Eukaryotes: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta; Eudicotyledons: Magnoliopsida; eudicotyledons: core eudicots: Rosidae; eudicots 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abt1-c				
NCBI	Taxid=3816				
REPEAT 7					
AD	ABRC	ABRP			
AC	P28570				
DT	01-DEC-1992	(Rel. 24, Created)			
DT	01-DEC-1992	(Rel. 24, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DS	Abt1-c precursor [comains: Abt1-c A chain (cRNA N-glycosylase)]				
D3	Abt1-c.1 (c222) [Abt1-c B chain]				
OS	Abt1-c.2 (c222) [Abt1-c B chain]				
OC	Eukaryotes: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta; Eudicotyledons: Magnoliopsida; eudicotyledons: core eudicots: Rosidae; eudicots 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abt1-c				
NCBI	Taxid=3816				
REPEAT 8					
AD	ABRC	ABRP			
AC	P28570				
DT	01-DEC-1992	(Rel. 24, Created)			
DT	01-DEC-1992	(Rel. 24, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DS	Abt1-c precursor [comains: Abt1-c A chain (cRNA N-glycosylase)]				
D3	Abt1-c.1 (c222) [Abt1-c B chain]				
OS	Abt1-c.2 (c222) [Abt1-c B chain]				
OC	Eukaryotes: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta; Eudicotyledons: Magnoliopsida; eudicotyledons: core eudicots: Rosidae; eudicots 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abt1-c				
NCBI	Taxid=3816				
REPEAT 9					
AD	ABRC	ABRP			
AC	P28570				
DT	01-DEC-1992	(Rel. 24, Created)			
DT	01-DEC-1992	(Rel. 24, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DS	Abt1-c precursor [comains: Abt1-c A chain (cRNA N-glycosylase)]				
D3	Abt1-c.1 (c222) [Abt1-c B chain]				
OS	Abt1-c.2 (c222) [Abt1-c B chain]				
OC	Eukaryotes: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta; Eudicotyledons: Magnoliopsida; eudicotyledons: core eudicots: Rosidae; eudicots 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abt1-c				
NCBI	Taxid=3816				
REPEAT 10					
AD	ABRC	ABRP			
AC	P28570				
DT	01-DEC-1992	(Rel. 24, Created)			
DT	01-DEC-1992	(Rel. 24, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DS	Abt1-c precursor [comains: Abt1-c A chain (cRNA N-glycosylase)]				
D3	Abt1-c.1 (c222) [Abt1-c B chain]				
OS	Abt1-c.2 (c222) [Abt1-c B chain]				
OC	Eukaryotes: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta; Eudicotyledons: Magnoliopsida; eudicotyledons: core eudicots: Rosidae; eudicots 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abt1-c				
NCBI	Taxid=3816				
REPEAT 11					
AD	ABRC	ABRP			
AC	P28570				
DT	01-DEC-1992	(Rel. 24, Created)			
DT	01-DEC-1992	(Rel. 24, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DS	Abt1-c precursor [comains: Abt1-c A chain (cRNA N-glycosylase)]				
D3	Abt1-c.1 (c222) [Abt1-c B chain]				
OS	Abt1-c.2 (c222) [Abt1-c B chain]				
OC	Eukaryotes: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta; Eudicotyledons: Magnoliopsida; eudicotyledons: core eudicots: Rosidae; eudicots 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abt1-c				
NCBI	T				

PT	DISULFID	281	303		INTERCHAIN (BY SIMILARITY)
PT	DISULFID	320	339		BY SIMILARITY.
PT	DISULFID	363	380		BY SIMILARITY.
PT	DISULFID	451	464		BY SIMILARITY.
PT	DISULFID	490	507		BY SIMILARITY.
PT	NOL_ABS	35	35		BENZOIC ACID (BY SIMILARITY)
FT	CANOHND	234	234		N-LINKED (GLNAC...) (POTENTIAL).
FT	CANOHND	395	395		N-LINKED (GLNAC...) (POTENTIAL).
FT	CANOHND	435	435		N-LINKED (GLNAC...) (POTENTIAL).
SQ	SEQUENCE	562 AA	6281 NT	1PFOA30CJDT9A65279 CREG4.	
<hr/>					
Query Match		54.0%	Score 765.	DB 1.6	Length 562;
E-value		1e-51	Raw M. 1.3	E= -71.	Gaps 2.
<hr/>					
Matches 142/ Conservative 46; Mismatches 96					
<hr/>					
Oy	CSAS-BETAYRIVGNAMRVAVDDDFHDGNOIQIAPMSKSNDPQNLTXDKGTYSNGS	63			
Db	303 CSAREPEYRIGRDSDVVDVDCDYNBNRIIAWKCKELBRLMLTKSDTHTSHSG	362			
Oy	CLTTGYRAGNYWIFPCNTAAVEATITWINDGNIINPSNLTALASGCISKGITIT	123			
Db	64 CLTTGVAKGMYWIFDCTSAVALEATITWINDGNIINPSNLTALSSMSGSTLQG	422			
Oy	134 LDVTGGWLKANDVPREYTYGRDLCKSNSGSWVFCDSSQKNGKVALVGDSGI	183			
Db	423 NRYLRMGRRGNSTSPVTSISGSDLCMPQSVMWDCKNKKEO-OHMLYTDISI	481			
Oy	184 RPKNODICTIRSRDSVSYVIYVINGSGASGSGORVFTFGAILTLKSLAWDTQAHPK	243			
Db	482 RSVQTNLTLSKDHQGSFVLVASCNSMASHPLFDNGSITVLDLDNWVQVSPPS	541			
Oy	244 LRLTIYPATKPKPMQWLPF	264			
Db	542 LKEIIHFPHKRPQWTLLTF	562			
<hr/>					
NCBI TAXID:	STANDARD:	PRT:	563 AA.		
AD	NIGB SAMOI				
ID	P3183; P3184; P3342;				
DT	01-OCT-1993 (Rel. 27, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DE	28-FEB-2003 (Rel. 41, Last annotation update)				
DR	NIGRB B proteinase (Agglutinin 2) (SMNV) (Contactin: Nigrin b A chain				
OS	Sambucus nigra (European elder); [2]; Nigrin b A chain).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophytes;				
CC	Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;				
CC	Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.				
NCBI Taxid:	4202;				
SN	(11)				
SN	SEQUENCE FROM N.A.				
SN	SEU28362				
RX	MEDLINE=96215449; PubMed=8647092;				
RX	Van Damme E.J., Barre A., Rouge F., Van Leuven F., Peumans W.J.;				
RT	"Characterization and molecular cloning of Sambucus nigra agglutinin V				
RT	(nigrin b), a GALNAc-specific type-2 ribosome-inactivating protein				
RT	from the bark of elderberry (Sambucus nigra)."				
RL	Eur. J. Biochem. 237:505-513(1996).				
RL	EU				
RC	SEQUENCE OF 26-49 AND 296-321.				
RC	TISSUE=Bark;				
RC	MEDLINE=94003077; PubMed=8400133;				
RA	Gibbes T., Cloues L., Ferreras J.M., Rojo M.R., Iglesias R.,				
RA	Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.				
RT	"Isolation and partial characterization of nigrin b, a non-toxic				
RT	novel type 2 ribosome-inactivating protein from the bark of Sambucus				
RL	nigra M.; Biol. 22:1181-1186(1993).				
CC	-1- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHERITS ANIMALIAN				
CC	PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN				
CC	SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN				

	DR	EMBL; M98345; AAA32625.1; .	
	DR	PIR; S32430; S32430.	
	DR	HSPF; P11140; IABF.	
	DR	InterPro; IPRO00772; Ricin_E_lectin.	
	DR	InterPro; IPR001574; RFP.	
	DR	Pfam; PF00662; Ricin_E_lectin; 6.	
	DR	Pfam; PF00662; Ricin_E_lectin; 6.	
	DR	PRINTS; PR00336; SHGARICIN.	
	DR	SMART; SMO0456; RCIN; 2.	
	DR	PROSITE; PS00231; RCIN B_LECTIN; 2.	
	DR	PROSITE; PS00275; SHIG_RICIN; 1.	
KV	KM	Plant dectase, Hydrolase, Protein synthesis inhibitor, Toxin; Repeat;	
KV	KM	Glycoprotein; Lectin; Pyridoxine carboxylic acid.	
FT	FT	CHAIN	1 250
FT	FT	PERITIDE	231 260
FT	FT	LINKER PEPTIDE	231 260
FT	FT	Ricin_B_Type LECTIN	231 393
FT	FT	DOMAIN	231 393
FT	FT	RCIN B_Type LECTIN 1.	402 526
FT	FT	1-ALPHA.	402 526
FT	FT	REPEAT	282 324
FT	FT	REPEAT	325 365
FT	FT	REPEAT	388 400
FT	FT	REPEAT	413 448
FT	FT	REPEAT	452 491
FT	FT	REPEAT	494 527
FT	FT	ACT_SITE	163 163
FT	FT	DISULFID	246 268
FT	FT	DISULFID	246 268
FT	FT	DISULFID	378 345
FT	FT	DISULFID	416 429
FT	FT	DISULFID	455 472
FT	FT	MOD_RES	1 1
FT	FT	CARBOHYD	110 110
FT	FT	CARBOHYD	360 360
FT	FT	CARBOHYD	400 400
FT	FT	CARBOHYD	402 402
FT	FT	CONFLICT	323 381
FT	FT	CONFLICT	350 351
FT	FT	CONFLICT	378 378
FT	FT	CONFLICT	426 426
FT	FT	CONFLICT	428 428
FT	FT	CONFLICT	431 431
FT	FT	CONFLICT	484 484
FT	FT	CONFLICT	491 491
FT	FT	CONFLICT	493 493
FT	FT	CONFLICT	502 502
FT	FT	CONFLICT	502 502
FT	FT	CONFLICT	513 513
FT	FT	CONFLICT	516 516
SQ	SEQUENCE	527 AA; 5911 MW; 3253AF90CE94A CRC64;	
Query Match	54.3%; Score 769; DB 1; Length 527;		
Best Local Similarity	51.8%; Pred. No. 8,96-59;		
Matches	Conservative 45; Mismatches 71; Indels 2; Gaps 2		
OY	5 CAS; EPMRIYVNGKRGWEDPDDPNOLGMPSSNNPNOWTIRPGRTISNS	63	
Db	CSRSRETPRIGSNMGCCVDYDHGNRLIMKCDPLENOGLTLKDPKRISNKK	327	
OY	64 CLTVGTAGAYGVAMPDCNVAEKATIMQMNONTIINSRAVLAASSGIQTLLVT	123	
Db	32E CLTTGVAENRWAIWDCTSAVEKTYWEHMONETIINPKSLVLAESSVGQTIIVT	387	
OY	124 IDTLCGGWACADNTAPREVITYGRDLNESGSSVAVETCSSQXGOKALLYGDSI	193	
Db	38E NETLRGAKMTANTSTTFPVLSIGSDCNQSCSNVALYCNKGKQ ⁺ ONALUUGSI	446	
OY	184 RPKNPDGCGLTSGHSDSVATYNVSGASGSQKVFNEGAIIILKSLNLDVAQNKK	243	
Db	447 RSVQTNLNLCKSKDKHQSSPIVLVANCNMBAQGMFLINDOSLYLHDVMDVKSPDS	506	
OY	244 LRITITPATKRNQMQLPVF 264		

FT	STRAND	4.06	4.08
FT	STRAND	4.10	4.11
FT	HELIIX	4.13	4.15
FT	STRAND	4.17	4.21
FT	STRAND	4.22	4.23
FT	STRAND	4.24	4.25
FT	TURM	4.32	4.33
FT	HELIIX	4.35	4.37
FT	STRAND	4.39	4.41
FT	TURM	4.43	4.44
FT	STRAND	4.47	4.49
FT	TURM	4.50	4.51
FT	STRAND	4.52	4.59
FT	TURM	4.64	4.65
FT	STRAND	4.67	4.75
FT	HELIIX	4.78	4.80
FT	STRAND	4.83	4.84
FT	TURM	4.86	4.87
FT	STRAND	4.90	4.92
FT	TURM	4.93	4.96
FT	STRAND	4.97	5.01

	Query Match	55.8%	Score 779	DB 1	Length 528	
	Best Local Similarity	55.8%	Pred. No. 1,2e-59			
	Matches 144	Conservative	46	Mismatches 69	Indels 2	Gaps 2
Qy	5	CSAS-EPTAVIVGKNGKRVYRDDDFDQNOQLMSEKSNNDNDQVLTATDGTISNNS	63			
Dy	269	CSASREPTAVIVGKNGKRVYRDDDFDQNOQLMSEKSNNDNDQVLTATDGTISNNS	328			
Qy	64	CLTYSAGSYVWVWIDCNSAVNATVWMTNTITNPKALVLSASSSGVGLTVGT	123			
Dy	329	CLTYSAGSYVWVWIDCNSAVNATVWMTNTITNPKALVLSASSSGVGLTVGT	368			
Qy	134	LDVTLGGOMLANNITLAPREVTIVGRFDLCMSNGSVMWTCOSSQKQKALVYGPSI	193			
Dy	389	NEVLMRQSGMTGNTSPFVSIYSYSDLCQKQSGSNVMAVCDCKSKKKQ-QNALVYDGGI	447			
Qy	184	RPKXNQDQCLTSGSDSVSTVINTVSCSASGSGVWFTTNEGATLNLKNSLMTVDAQNP	243			
Dy	448	RSVNTVNNCLSKTHKQCSSTLLMLDCSGNSGKSGVFWFNDSITYSVDQVWMDKASD	507			
Qy	244	LRRIITLYPATGPGQVQMLPV 264				
Dy	508	LKQILMPYTKSPKQVLTWLF 528				
RESULT 4						
ID	AGGL_RICCO	STANDARD:	PRT:	564	AA.	
DT	01-JUN-1988	(Rel. 06, Created)				
DT	01-JUN-1988	(Rel. 06, Last sequence update)				
DT	28-FEB-2003	(Rel. 41, Last annotation update)				
DE	653032048	(EC:92.2.22) (Contains: Agglutinin A chain (rRNA N-				
OS	Richiusa communis (Cactaceae)	Agglutinin B chain				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Richiusa					
NCBI_Taxid=3988;						
LN	[1]					
LN	SEQUENCE FROM N.A.					
RP	MEDLINE=36059449; PubMed=2399130;					
RT	"The primary sequence of Richiusa communis agglutinin. Comparison with ricin";					
RL	J. Biol. Chem. 260:15682-15686(1985).					
RP	SEQUENCE OF 303-564.					
RT	TISUE=Seed;					
RA	Araki T., Yoshioaka Y., Funatsu G.;					

[illegible]

FT VARIANT 231 231 N -> S OR T.
 FT VARIANT 231 233 NGU -> KSP.
 FT VARIANT 232 235 GLAM -> SLMT.
 SQ SEQUENCE 264 AA; 28981 MW; 7D0DC326CCEFF5A4 CRC64;
 Query Match 99.1%; Score 1403; DB 1; Length 264;
 Best Local Similarity 99.9%; Pred. No. 9, 9e-114;
 Matches 261; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVTCSASBPFTVIVGRNKRVDVADDDPHDQNGIQIOLPSSKNDPNQIATIKEDITRS 60
 DB 1 DVTCSASBPFTVIVGRNKRVDVADDDPHDQNGIQIOLPSSKNDPNQIATIKEDITRS 60
 QY 61 NSGCLTTFYTAGYVWTFPCDCAVREKATIKQWNGTIIINPSNVLAAASGKQITLT 120
 DB 61 NSGCLTTFYTAGYVWTFPCDCAVREKATIKQWNGTIIINPSNVLAAASGKQITLT 120
 QY 121 VOTLPTLGGWLNAGNDPAPREVTYGFRLQMSNGSVVETCDSSQKQGNALYGD 180
 DB 121 VOTLPTLGGWLNAGNDPAPREVTYGFRLQMSNGSVVETCDSSQKQGNALYGD 180
 QY 121 VOTLPTLGGWLNAGNDPAPREVTYGFRLQMSNGSVVETCDSSQKQGNALYGD 180
 DB 121 VOTLPTLGGWLNAGNDPAPREVTYGFRLQMSNGSVVETCDSSQKQGNALYGD 180
 QY 181 GSIRPKQKQDOCLTSGRDSVSTVIVIVSCGSGSGQWTFNEGALINLNGALMDVQA 240
 DB 181 GSIRPKQKQDOCLTSGRDSVSTVIVIVSCGSGSGQWTFNEGALINLNGALMDVQA 240
 QY 241 NPTLRITIIYPAKGNOMLPPF 264
 DB 241 NPTLRITIIYPAKGNOMLPPF 264
 QY 241 NPTLRITIIYPAKGNOMLPPF 264
 DB 241 NPTLRITIIYPAKGNOMLPPF 264

RESULT 2
 RICI RICCO STANDARD; PRT; 576 AA.
 ID RICI RICCO
 AC P02879; P02880;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-APR-1987 (Rel. 05, Last annotation update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE RICI precursor (Cecilians: Ricin A chain (trna N-glycosidase))
 DE RICI precursor (Cecilians: Ricin A chain (trna N-glycosidase))
 DE RICI precursor (Cecilians: Ricin A chain (trna N-glycosidase))
 OS Ricinus communis (Castor bean)
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucoside I; Malpighiales; Euphorbiaceae; Ricinus.
 OX NCBI_TaxID:3988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86067214; PubMed=2999712;
 RA Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,
 RA Weaver R.F.,
 RA "Cloning and characterization of a ricin gene from Ricinus
 RT communis"
 RT Nucleic Acids Res. 13:8019-8033(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9163016; PubMed=1371405;
 RA Tregear J.W., Roberts L.M.;
 RA "The lectin gene family of Ricinus communis: cloning of a functional
 RT ricin gene and three lectin pseudogenes."
 RT Plant Mol. Biol. 18:515-525(1992).
 RN [3]
 RP SEQUENCE OF 12-576 FROM N.A.
 RA MEDLINE=85179479; PubMed=3898723;
 RA Lamb A., Roberts L.M., Lord J.M.;
 RA "Nucleotide sequence of cloned cDNA coding for prepro-ricin."
 RT Eur. J. Biochem. 148:265-270(1985).
 RN [4]
 RP SEQUENCE OF 36-302.
 RA Yoshitake S., Punatsu G., Punatsu M.;
 RA "Isolation and sequences of peptic peptides, and the complete
 RT sequence of the chain of ricin-D."
 RT Agric. Biol. Chem. 42:1267-1274(1978).
 RN [5]
 RP SEQUENCE OF 315-576.

RA Punatsu G., Kimura M., Punatsu M.;
 RA "Primary structure of A1a chain of ricin D."
 RT Agric. Biol. Chem. 43:2221-2224(1979).
 RN [6]
 RP SEQUENCE OF 1-1000.
 RA MEDLINE=90144223; PubMed=136817;
 RA Kimura Y., Kusnoku H., Tada M., Takagi S., Punatsu G.;
 RA "Structural analyses of sugar chains from ricin A-chain variant."
 RT Agric. Biol. Chem. 54:157-162(1990).
 RN [7]
 RP REVIEW.
 RA MEDLINE=21480122; PubMed=11595634;
 RA Olsnes S., Kozlov J.V.;
 RA "Ricin." 39:1723-1728(2001).
 RN [8]
 RP TOXICOLOGY.
 RA MEDLINE=9152004; PubMed=1881881;
 RA Katzin B.J., Collins E.J., Robertus J.D.;
 RA "Structure of ricin A-chain at 2.5 A."
 RT Proteins 10:251-259(1991).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RA MEDLINE=9152004; PubMed=1881881;
 RA Katzin B.J., Collins E.J., Robertus J.D.;
 RA "Structure of ricin A-chain at 2.5 A."
 RT Proteins 10:251-259(1991).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
 RA MEDLINE=9152005; PubMed=1881882;
 RA Rutenber E., Robertus J.D.;
 RA "Structure of ricin B-chain at 2.5-A resolution."
 RT Proteins 10:260-269(1991).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
 RA MEDLINE=9082010; PubMed=7991030;
 RA Weston S.A., Tucker A.D., Thacker D.R., Deshpande D.J.,
 RA "Supplemental structure of recombinant ricin A-chain at 1.8-A resolution."
 RT J. Mol. Biol. 244:410-422(1994).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
 RA MEDLINE=96374222; PubMed=8780513;
 RA Day P.J., Ernst S.R., Frankel A.B., Monzingo A.F., Pascal J.M.,
 RA Molina-Svanech M.C., Robertus J.D.;
 RA "Structure and activity of an active site substitution of ricin A
 RT chain."
 RT Biochemistry 35:11098-11103(1996).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
 RA MEDLINE=97240820; PubMed=9086280;
 RA Yan X., Rojals T., Svanech M., Day P., Monzingo A.F., Milne G.W.,
 RA Robertus J.D.;
 RA "Structure-based identification of a ricin inhibitor."
 RT J. Mol. Biol. 266:1043-1049(1997).
 RN [14]
 RP MUTAGENESIS.
 RA MEDLINE=9165633; PubMed=1287657;
 RA Kim Y., Robertus J.D.;
 RA "Analysis of several key active site residues of ricin A chain by
 RT protein engineering."
 RT Protein Eng. 5:775-779(1993).
 RN [15]
 RP FUNCTION.
 RA "Ricin is highly toxic to animal cells and to a less
 CC extent to plant cells. The A chain is responsible for inhibiting
 CC protein synthesis through the catalytic inactivation of 60S
 CC ribosomal subunits. It acts as a glycosylase that removes a
 CC specific adenine residue from an exposed loop of 28S ribosomal
 CC RNA. As this loop is involved in the binding of elongation
 CC factors, the modified ribosomes are unable to support protein
 CC synthesis. The A chain can inactivate a few thousand ribosomes
 CC per minute, thus inactivating them faster than the cell can make
 CC new ones. A single A-chain molecule can therefore kill an animal

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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 4.53677 Seconds

Title: US-09-601-667C-11

Sequence: 1 DDVTCASASEPTVRIVGRNGM.....RRIIYPATGKPNQMWLPVF 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum DB seq length: 20000000000

Post-processing: Minimum Match. 0.9

Listing first 45 summaries

Database : SwissProt_41:*

Preſ. No. is the number of reſults predicted by chance to have a ſcore greater than or equal to the ſcore of the reſult being printed and is derived by analysis of the total ſcore diſtribution.

SUMMARIES

No.	Score	Query Match	Length	DB	ID	Description
1	94.00	89.1	254	1	ME1_VISAL	P81830 vlsam_albu
2	93.00	87.4	254	1	ME1_VISAL	P81830 vlsam_albu
3	91.00	87.1	254	1	ME1_VISAL	P81830 vlsam_albu
4	77.9	55.0	528	1	ABR1_ABRP	P11101 abrp_ricm
5	77.5	54.0	544	1	AGL1_RICCO	P06750 ricm_con
6	76.9	54.0	527	1	ABR1_ABRP	P06077 abrp_prec
7	76.5	54.0	562	1	ABR1_ABRP	P28590 abru_prec
8	72.6	37.2	563	1	NIGR_STAM1	P31313 stambus_co
9	72.5	37.2	563	1	NIGR_STAM1	P31313 stambus_co
10	71.5	8.9	477	1	XVYA_STAM1	P25514 streptomyc
11	71.5	8.2	485	1	ABR1_STRO	O51611 streptomyc
12	71.4	8.1	481	1	ABR1_STRO	O51611 streptomyc
13	71.4	8.1	481	1	ABR1_STRO	O51611 streptomyc
14	71.3	7.9	495	1	ABR1_STRI1	P36463 streptomyc
15	71.1	7.8	525	1	SP1_RABPA	O50308 rabpacar
16	70.8	6.9	612	1	PAG3_CHEE1	P34678 caemostrad
17	69.5	6.7	545	1	AGL1_ASPIN	P28331 aspergillu
18	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
19	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
20	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
21	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
22	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
23	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
24	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
25	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
26	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
27	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
28	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
29	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
30	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
31	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
32	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi
33	69.2	6.6	4074	1	PERD_HUMAN	O81639 homo_sapi

ALIGNMENTS

	RESULT 1	
ID	MIB_VISAL	STANDARD; PRT; 264 AA.
D1	28-FEB-2003 (Ref. 4) (Created)	
D7	28-FEB-2003 (Ref. 4) last sequence update)	
D7	15-SEP-2003 (Ref. 4) last annotation update)	
DE	Galactose specific lectin I B chain (MIB) (ML-I-B).	
OC	Viscum album (European mistletoe).	
CC	Ephemeroptera; Vitisidaceae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Santalales; Santalaceae; Viscum.	
RX	NBFI_Taxids93972;	
RX	SEQUENCE	
RX	MEDLINE=96289595; PubMed=9618256;	
RT	Soler M.H., Steele S., Voelter W.;	
RL	"Complete amino acid sequence of the B chain of mistletoe lectin I."/	
CC	Biochem. Biophys. Res. Commun. 246:196-201(1998).	
CC	-I- FUNCTION: The A chain is responsible for inhibiting protein synthesis by removing adenine from position 4,324 of 28S rRNA. The B chain binds to cell receptors and probably facilitates the entry of cell agglutination (lectin activity). Both chains are also responsible for cell agglutination (lectin activity).	
CC *	* -II- SUBUNIT: Disulfide-linked dimer of A and B chains.	
CC	-I- PHARMACEUTICAL: Due to its immunomodulative effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid tumors.	
CC	-I- MISCELLANEOUS: Several isoforms of MIB exist.	
CC	C1. STRUCTURAL: Contains 2 ricin B-type lectin domains.	
DR	PDB: 1CE7; 2O-MAR-00.	
DR	PDB: 2WLL; 2O-MAR-00.	
DR	InterPro: IPRO001772; Ricin B lectin.	
DR	Pfam: PF00652; Ricin B lectin; 6.	
DR	SMART: SMO0458; Ricin; 2.	
KR	PROSITE; PS02031; Ricin B Lectin; 2.	
DM	Plant defense; Glycoprotein; Lectin; Repeat; 3D-structure.	
FT	DOMAIN	
FT	1..136	Ricin B-type lectin 1.
FT	136..224	Ricin B-type lectin 2.
FT	BINDING	225 GALACTOSE.
FT	BINDING	236 5 INTERCHAIN.
FT	DISULFID	64 81 BY SIMILARITY.
FT	DISULFID	152 165 BY SIMILARITY.
FT	DISULFID	192 209 BY SIMILARITY.
FT	CARBOND	61 61 N-TERMINED (GLNRC..) (POTENTIAL).
FT	CARBOND	136 136 N-TERMINED (GLNRC..) (POTENTIAL).
FT	VARIANT	18 18 N -> S.
FT	VARIANT	56 56 G -> Q.
FT	VARIANT	157 157 G -> O.
FT	VARIANT	195 195 S -> V.
FT	VARIANT	224 224 G -> Y.

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DB 309 GDNCLDLAGTNGSNVQIVSCWGNOK--WHLNDSGSGVSGSLGLDANVGNNTANOTL 366
QY 119 LTVQTLIDVTLGGW 132
DB 367 IOLYTCNSGNCNW 380

RESULT 14

arabinofuranosidase - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Dec-1999
C/Accession: T35697
R/Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A/Reference number: T35697
A/Accession: T35697
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-475 <MUR>
A/Cross-references: EMBL:AL021411; PDB:CAL6189.1; GSPDB:GN00070; SCODEB:SC9B5.23c
A/Experimental source: strain A3(2)
C/Genetics:
A:Gene: abfB; SCODEB:SC7H1.02

Query Match 8.28; Score 115.5; DB 2; Length 475;
Best local similarity 24.18; Fred. No. 0.054;
Matches 52; Conservative 35; Mismatches 104; Indels 25; Gaps 10;

QY 6 SASPEPTVIVGNNGRYVDRODDPDHGNOLMFPSKNNDDNQLTKRDTIRSNQ-SC 64
DB 37 AAGSGALRGAGSNRC-LDVLGSGQDGLALQLYDCWGT--NOCWTSTDTGALVYGDKC 93
QY 65 LTVGYTLA--GYVWIPDNTAVRENTIOWIDNGTINPSNVL--ANSSC-IKSTTLT 120
DB 94 LDVGGHAPETRVQVWVSGSAGANQ--WRVNSDGVGVESGLCPAGAGTANVQ 151
QY 121 VQTLIDVTLGGWLAAGNTPAREVY----LYGPRDLQMSNGSVWETCP-SQGNOK 174
DB 152 LMTONGGNGQVWGLNTPPTDGTALPPTVNSSTGVLAQPSGVWALKDPITVHNGR 211
QY 175 WALYDQS-----IRKQNDQCLTSGRDSVS 201
DB 212 HLYVGYTSSGSSYSGNWFSPFTNWDMAAGQNNRN 247

RESULT 15

T35943
probable hydrolytic protein - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C/Accession: T35943
R/Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1999
A/Reference number: T35943
A/Accession: T35943
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-464 <SEB>
A/Cross-references: EMBL:AL035206; PDB:CAA22765.1; GSPDB:GN00070; SCODEB:SC9B5.23c
A/Experimental source: strain A3(2)
C/Genetics:
A:Gene: SCODEB:SC9B5.23c

Query Match 8.13; Score 114; DB 2; Length 464;
Best local similarity 28.13; Fred. No. 0.07;
Matches 38; Conservative 27; Mismatches 52; Indels 18; Gaps 8;

QY 139 APREV---TLYGF-RDLQMSNGSVW----VETCDSSQKQNGWALYDQSGIRPKN 188
DB 332 AEPVAPGVITVGHASNRCEIV--AGHKVRDGAFLQINDCTGRWQKQDFPFDGTR--S 387
QY 189 QPQCL--TSGRDSVTVLVIVSGSGSGQRWFTNBNALNLSLMDVA--QANPKLR 245

DB 388 LGLCDNATNGTNGTNGVQVAVCSG--HPAQPTIAGPRDLVWVQANKCTDVDEKTNAGA 446
QY 246 RIIIVPATKPKQW 260
DB 447 RLQIWECSGRDIVQW 461

Search completed: December 11, 2003, 13:55:46
Job time : 9.20622 secs

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	Matches	116	Conservative	35;	Mismatches	94;	Indels	12;	Gaps	6;
Qy	5	CSASRPYAIYVGNKMRVYRDDDDPHQNDQIQMESKSDNPQALMTKIDQITIRNSQC	64							
Dy	316	CSVEVETRIISGMDGLCAVDYRGHYIDGNVPOLAR--CGNECQQLMTFRDITIRNLGKC	373							
Qy	65	LTYYGTAQYVWTEPCNPAEENATKQIMQMDGTTIMPSSNVLAASSGLKGTIVYTL	124							
Dy	374	-----TASSVHLDQYIPFPAKIRVYSDITITNHSGLVYPPQAGKSLVLSNN	428							
Qy	125	LYTGGCGMAGNDPAPEVYITVGRPOLCSAGS--WVETSGDVSQKQKALYSQSS	182							
Dy	429	IPARAGMTVG-DVEPLVETIYGVKQCLRENSKNFVPLECYTLNRVQ--EMLYVDGT	486							
Qy	183	TFKPNQDQCTIGSDSYSTVINVSCSAGASQWVFTEGALTLNLNLAIVQANAP	242							
Dy	487	IKVNSRSLCYTSEDSHSDLLVLKCRS-SKQKRVFVNTGNTISNPARTLMVDQADV	545							
Qy	243	KLRITIIYPATGSKPNQML	261							
Dy	546	SKRLIIYKPTGSKPNQML	564							

RESULT 11

UC7535

Chitinase (EC 3.2.1.14) 35 - Streptomyces thermoviolaceus

C/Species: Streptomyces thermoviolaceus

C/Date: 30-Jun-2001 #sequence_rev10n 30-Jun-2001 #ext_change 30-Jun-2001

C/Acession: UC7535

R/Unpubl: H., Okamoto, T., Hatan, N., Miyano, K., Maranabe, T., Mitsutomi, M.; Inano

Biosci. Biotechnol. Biochem. 64, 2445-2453, 2000

A>Title: Family 19 chitinases from Streptomyces thermoviolaceus OGC-520: Molecular cloning

A/Reference number: UC7535; PMID:21036907; PMID:11193414

A/Acession: UC7535

A/Molecule type: DNA

A/Residues: 1-377 <TSU>

A/Cross-references: DDBJ:AB016842

A/Experimental source: strain OGC-520

C/Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin degradation. It is a glycosyl hydrolase with a catalytic domain that is important in the efficient hydrolysis of insoluble a

A/Details:

A/Name: ch15

A/Keywords: glycosidase; hydrolase

[illegible]

RESULT 12
DS0589
endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - *Streptomyces lividans*
Milestone names: xylanase A

C.Species: Streptomyces lividans
C.Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #ext_change 26-Feb-1999
C.Reference: JUS0589; F80338
C.Author: E. Aoyagi, T. Yaguchi, M. Moroselli, R. Kluweff, D. Schaefer
C.Title: Sequences of three genes specifying xyloses in Streptomyces lividans.
A.Reference number: JUS0589; MUID:92077439; PMID:1743551
A.Accession: JUS0589
A.Molecule type: DNA
A.Residues: 1-477 <SHA>
A.Cross-references: GB:W64551
A.Molecule type: protein
A.Residues: 42-92 <SRZ>
A.Ceomics: 42-92 <SRZ>
A.Gene: xlnA
A.Function:
A.Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A.Pathway: xylan degradation and/or 1,4-beta-xylosylase A; Streptomyces endo-1,4-beta-xylan
A.Keywords: extracellular protein; glycosylase; hydrolase; polysaccharide degradation
A.Domain: signal sequence #status predicted <SIG>
A.12-477/Product: endo-1,4-beta-xylosylase A #status experimental <MMT>
A.74-341/Product: Streptomyces endo-1,4-beta-xylosylase A homology <SXY>
A.169-27/Active site: Glu #status predicted

Query Match	8.9%; Score 125.5; DB 1; Length 477;
Best local	Similarity 29.98%; Pval. No 0.0078; Indels 13; Gaps 6
Matches	40; Conservative 20; Mismatches 61;
QY	7 ASEP-----TVAIYGNASGRADVDDEPHDGNQQLAMSSKSNIDNPLMTIRRCQITIRSN 61
Db	346 SSEPFDAGQKIVGVG--SGECIDVPASTSTDTGLQMDHSGT--NQOAMATDAGELRY 402
OY	62 G--SCITTYITKYGKIVGMIPEONTAIREATITINDGCTINPSLSYLA--SSGICKGT 118
Db	403 GPKCIDAGTSGKATQIYSSWCGENQX--VALNSQSVWGVSGCLDADVNGTANGTL 460
OY	119 LTVOTLDYTLGGW 132
Db	461 IQLYTCNSNSQNR 474

```

RESULT 13
T34603
Xylanase A - Streptomyces coelicolor (fragment)
Species: Streptomyces coelicolor
CDate: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 28-Jul-2000
Accession: T34603
RefSeq: T34603
R:Harpury, L.; Harris, D.; Parkhill, J.; Barrett, B.G.; Rajadream, M.A.
B:Reference number: EMBL Data Library, January 1998
A:Accession: T34603
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-381 <RNR>
A:Cross-references: EMBL:AL021529; PDB: 1CAL6468.1; GSPDB:GNO0070; SCEEBA:SC10A5.36C
A:Experimental source: strain AJ12
C:Genetics:
A:Gene: xlnA; SCEEBA:SC10A5.36C
S:Superfamily: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-xylanase A homology <X>
P:1-247/Domain: Streptomyces endo-1,4-beta-xylanase A homology <X>

```

Query Match	8.7%	Score 12.5	DB 2	Length 383
Best Local Similarity	29.3%	Prod. No.	0.011	62
Matches	407	Mismatches		13
				6
QY	7	ASP-----TVRIQNGNCHVVEDEDFDNDGIDOLAFMSNNNDLNTTKRQYISRN	61	
		252	SSSPADGGQIKGVG-SRCLTADPASTDTDTOLMDCHSGT--NQQAATDAGELAVY	308
DB				
QY	62	G-SCITTYGTVAGVYMTFCNCAVREATITQWMDNGIINRSNLVLA--SSGIGKTT	118	

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Page 3

506330
Ricin B - castor bean (fragment)
N:Contains: chain B; rRNA N-glycosidase (EC 3.2.2.22) (chain A)
C/Species: Ricinus communis (castor bean)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Aug-1999
C/Accession: 506330; J05381
Plant Mol. Biol. 9, 287-295, 1987
Plant Mol. Biol. 9, 287-295, 1987
A>Title: Characterization of a cDNA encoding ricin B, a hybrid ricin-Ricinus communis ag
A/Accession: 506330
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-263 <IAD>
A/Cross-references: EMBL:M17631; NID:G169714; PIRN:AA63506.1; PTD:G169715
R/Atk: T.; Funatsu, G.
Biochim. Biophys. Acta 911, 191-200, 1987
A/Note: The B-chain of the B-chain of ricin B isolated from small
A/Reference number: J05381; MIMD:87101186; PMID:3801493
A/Accession: J05381
A/Molecule type: protein
A/Residues: 1-69, 'P8', '72-209', 'A', '211-241', '243-250', 'V', '252-263' <ARA>
A/Experimental source: seed
A/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase
E/1-263/Product: ricin B chain B status experimental <BCH>
F/1-263/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/20-39/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/95-115/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 61.5%; Score 871; DB 2; Length 263;
Best Local Similarity 61.3%; Pred. No. 7.66-66;
Matches 160; Conservative 38; Mismatches 61; Indels 2; Gaps 2;
QY 5 GSASEPTATVGNKRVVDVDDPHDQICLWPSKNDPQVLTAKDGTIRSGSC 64
DB 4 QMDPPTVAVGSGKCDVWGRFRKKNKIDLPKCSMDPKDMVLRKDK 63
QY 65 LITVGYAGVYVMPDONTAVBEKTIQWIDNGIINPNSULVLAASGKATLVQY 124
DB 64 LITVGYSPGVYVMPDONTAVBEKTIQWIDNGIINPNSULVLAASGKATLVQY 123
QY 125 DVLGGSMAGNDTPREVITYVGRNDICMSNGSFWETZDSOKQKQKALYGGSI 184
DB 124 IYNSQMLPNTVPFVTTIVGICGICDANSGRVWEDC-TSRKADQMLADSGIR 182
QY 165 PKHQDQCLTSGEDSVTYVNIYVSGSGSGSGRWTFPNEGAIINPKSLMYVVAQAN-R 243
DB 163 PQRHNDCLITTPANKTGVVKKLSQPVSSQGRWPFNDGIIINLVGVLVDVRSDDSS 242
QY 244 LERITVPTGKKNQMTPEP 264
DB 243 LKQIVHPKSNLQIMPLP 263

RESULT 5
T2LSA
Abirin-a precursor - Indian licorice (fragment)
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C/Species: Abrus precatorius (Indian licorice)
C/Date: 31-Dec-1993 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C/Accession: 506330; J05381
Plant Mol. Biol. 9, 287-295, 1987
Plant Mol. Biol. 9, 287-295, 1987
A>Title: Primary structure of three distinct isoforms determined by cDNA sequencing. C
A/Accession: S32429; MIMD:93123798; PMID:842113
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA <RNA>
A/Cross-references: GB:W8344; NID:G169294; PIRN:AA32524.1; PTD:G169295
A/Note: the coding region for the sequence shown is preceded by an ATG codon
A/Note: residues 1-8 were derived from the synthesized primer
R/Punnett, G.; Taguchi, Y.; Kamegawa, M.; Yanaka, M.
Biochem. Biophys. Res. Commun. 193, 1097-1097, 1988
A>Title: The complete amino acid sequence of the A-chain of abirin-a, a toxic protein
A/Reference number: J0202
A/Accession: J0202
A/Molecule type: protein
A/Residues: 1-201, 201-351 <FNU>
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we ha
R/Kjenseth, G.; Mathiesen, A.; Sigaa, A.
Biochem. Biophys. Res. Commun. 193, 1097-1097, 1988
A>Title: Direct molecular cloning and expression of two distinct abirin A-chains.
A/Reference number: A39761; MIMD:9120323; PMID:2016300
A/Accession: A39761
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-2-251 <EVE>
A/Cross-references: DB:J05492
A/Note: The A-chain of abirin-a was derived from the synthesized primer
R/Kjenseth, G.; Mathiesen, A.; Sigaa, A.
Biochem. Biophys. Res. Commun. 193, 1097-1097, 1988
A>Title: The complete amino acid sequences of the B-chains of abirin-a and abirin-b, tox
A/Reference number: J01398; MIMD:93169023; PMID:7763422
A/Accession: J01398
A/Status: seeds
A/Molecule type: protein
A/Residues: 261-341, 'P', '349-351', 'A', '353-357', 'V', '359-528' <KIN>
A/Experimental source: seed
A/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase
E/1-263/Product: ricin B chain B status experimental <BCH>
F/1-263/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/20-39/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/95-115/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 55.0%; Score 779; DB 1; Length 528;
Best Local Similarity 55.2%; Pred. No. 1e-57;

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Page 1

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 11, 2003, 13:53:18 / Search time 8.20222 seconds

1093.317 Million cell updates/sec

Title: US-09-601-667C-11

Perfect score: 1416

Sequence: 1 DVVTCASSEPTVRIYVGNK...RRIIVPATCKENQWLPVF 264

Scoring table: BLOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 283308 segs, 9616662 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: PIR 76:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1401	98.1	264	PD0010	MACTEALCIN I
2	1392.5	98.1	265	U00090	MACTEALCIN I
3	1391.5	98.1	265	U00090	MACTEALCIN I
4	871	61.5	263	1 RUCSD	ricin B precursor
5	779	55.0	228	1 TELA	abrin-a precursor
6	777.5	54.9	227	1 RUCSD	abrin-b precursor
7	769	54.3	227	1 RUCSD	abrin-b precursor
8	765	54.0	228	1 RUCSD	abrin-b precursor
9	764	54.0	228	1 RUCSD	abrin-b precursor
10	764	54.0	228	1 RUCSD	abrin-b precursor
11	764	54.0	228	1 RUCSD	abrin-b precursor
12	764	54.0	228	1 RUCSD	abrin-b precursor
13	764	54.0	228	1 RUCSD	abrin-b precursor
14	764	54.0	228	1 RUCSD	abrin-b precursor
15	764	54.0	228	1 RUCSD	abrin-b precursor
16	764	54.0	228	1 RUCSD	abrin-b precursor
17	764	54.0	228	1 RUCSD	abrin-b precursor
18	764	54.0	228	1 RUCSD	abrin-b precursor
19	764	54.0	228	1 RUCSD	abrin-b precursor
20	764	54.0	228	1 RUCSD	abrin-b precursor
21	764	54.0	228	1 RUCSD	abrin-b precursor
22	764	54.0	228	1 RUCSD	abrin-b precursor
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26	764	54.0	228	1 RUCSD	abrin-b precursor
27	764	54.0	228	1 RUCSD	abrin-b precursor
28	764	54.0	228	1 RUCSD	abrin-b precursor
29	764	54.0	228	1 RUCSD	abrin-b precursor

30	91	6.4	1723	2	H85557	polymorphic membra
31	91	6.4	1723	2	H85557	polymorphic membra
32	91	6.4	1723	2	H85557	polymorphic membra
33	90.5	6.4	1723	2	H85557	polymorphic membra
34	90.5	6.4	1723	2	H85557	polymorphic membra
35	89.5	6.4	1723	2	H85557	polymorphic membra
36	89.5	6.4	1723	2	H85557	polymorphic membra
37	89.5	6.4	1723	2	H85557	polymorphic membra
38	89.5	6.4	1723	2	H85557	polymorphic membra
39	89.5	6.4	1723	2	H85557	polymorphic membra
40	88.5	6.2	1577	2	A35140	hemolysin vmba pre
41	88.5	6.2	1577	2	A35140	hemolysin vmba pre
42	88	6.2	623	2	A42245	probable polypepti
43	88	6.2	1083	2	AH2493	hypothetical prote
44	87.5	6.2	1526	2	AC2235	WD-40 repeat prote
45	87	6.1	2273	2	T09083	hemagglutinin/hemo

ALIGNMENTS

RESULT 1

PD0019

C:Species: Viscum album (fragment)

C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999

C:Accession: PD0019

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

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C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

C:Accession: U00090

C:Species: Viscum album (European mistletoe)

C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000

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us-03-601-667c-10.rai

Qy 22 VDVRODDPHDGNQIOLMPSKNNNDENQOLWIKRQGTISNGS-CITTYGTAGVYMFD 80
Db 379 IDVPRKNTADGTVOLOYDCHSGS--NOOWTYSSEGFHIFGNKCLDAGSSNGANVOIYS 436
Qy 81 CNTAVRENTIWOINDNGTIIIPRSNLYLAASSGINKITLTVO 122
Db 437 GNGGNOK--WELRADGIIWVOSGLCDIVGSGTNGTRLO 476

Search Completed: December 11, 2003, 14:11:35
Job Time : 9.14026 secs

Thu Dec 11 16:09:45 2003

us-09-601-667c-10.ra1

Page 7

QY 56 GTRISNG-SCLTGYGTAGYVWIFDCNTAVREATTWQIMNGTINPNSLVLA--SS 112
DB 411 GELAVYVVKCLDPAAGTNSGNSVQVYISCGWGDHOK--WRINSDSVGVGSGLCDVANG 468
QY 113 GIKGTYLWOTLDYTLGGCM 132
DB 469 TANGTILQVTCNSGNRW 488

RESULT 14

US-09-770-621-8
Sequence 8, Application US/09770621

Patent No. 6506593

GENERAL INFORMATION:

APPLICANT: M RYU, Arja

APPLICANT: Peltamäper, Jari

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

TITLE OF INVENTION: Production and Secretion of Proteins of

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09770, 621

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/590, 563

FILING DATE:

CLASSIFICATION: DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/332, 412

FILING DATE: 31-OCT-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/282, 001

FILING DATE: 29-JUL-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Peltamäki, Jari

REGISTRATION NUMBER: 1050, 0340003

REFERENCE/DOCKET NUMBER: 1050, 0340003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2640

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 101 amino acids

STRANDNESS: No. 6506593 Relevant

STRANDNESS: linear

MOLECULE TYPE: peptide

POSITION IN GENOME:

CHROMOSOME/SEGMENT: M64551

US-09-770-621-8

Query Match

Best Local Similarity 28.6%, Score 122.5, DB 4, Length 492,

Matches 40, Conservative 20, Mismatches 61, Indels 19, Gaps 6,

QY 7 ASP-----TVIRVGRKGVYRDDDEPHQDQGLQMPKSNNDNQVLTIRK 55
DB 354 SSSPXXXXXXXXXADGQIQKVG-SGRCLDPDASTSDTQLQMPCHSGT--NQWMAATDA 410
QY 56 GTRISNG-SCLTGYGTAGYVWIFDCNTAVREATTWQIMNGTINPNSLVLA--SS 112
DB 411 GELAVYVVKCLDPAAGTNSGNSVQVYISCGWGDHOK--WRINSDSVGVGSGLCDVANG 468
QY 113 GIKGTYLWOTLDYTLGGCM 132
DB 469 TANGTILQVTCNSGNRW 488

RESULT 15

US-08-468-812-4
Sequence 4, Application US/08468812

Patent No. 6506593

GENERAL INFORMATION:

APPLICANT: Peltamäper, Jari

APPLICANT: M RYU, Arja

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

APPLICANT: Lantto, Raimo

APPLICANT: Peltomäki, Marja

APPLICANT: Suominen, Pirkko

APPLICANT: Lantinen, Taina

US-08-468-812-4

Query Match

Best Local Similarity 32.4%, Score 122.5, DB 2, Length 492,

Matches 33, Conservative 16, Mismatches 48, Indels 5, Gaps 3,

Thu Dec 11 16:09:45 2003

us-09-601-667c-10.ra1

Page 6

Db 437 CWGANOK--WELRADOTIVAGSGLCLDAVGGTNGTFRDQ 476

RESULT 12
US-08-468-812-8
Sequence 8, Application US/08468812
Patent No. 5950114
GENERAL INFORMATION:
APPLICANT: Vennamper, Jari
APPLICANT: M nyl, Aija
APPLICANT: Pegerst m, Richard
APPLICANT: Lantto, Ralja
APPLICANT: Paloheimo, Maria
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
APPLICANT: Kristo, Paula
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US/08/468,812
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 05-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION/DOCKET NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-08-468-812-8

Query Match 8.6%, Score 122.5; DB 2; Length 491;
Best Local Similarity 28.6%; Pred. No. 0.00035;
Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;

Db 354 SSSPXXXXXXXXXADGGQIKNGV-SGRCLDVPDASTGSDGQJLMDCHSGT--NQMAAATDA 410
QY 56 GTIRANG-SCLTYGYTAGVYVAFPCNCTVAENATTMOIMNGTITMPSNLYAA--SS 112
DB 411 GELRYADKCLDAAGTSGNSKVOIYSCMGIDNOK--WELNDSGVYGVSGGLCLDAVNG 468

QY 113 GIKETLTWQTLDTLTLOGGM 132
DB 469 TANGTLTCLTCNSNGNR 468

RESULT 13
US-08-590-563-8
Sequence 8, Application US/08590563
Patent No. 6300114
GENERAL INFORMATION:
APPLICANT: nyl, Aija
APPLICANT: Vennamper, Jari
APPLICANT: Pegerst m, Richard
APPLICANT: Lantto, Ralja
APPLICANT: Paloheimo, Maria
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 08/08/590,563
APPLICATION NUMBER: 536
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 05-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION/DOCKET NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-08-590-563-8

Query Match 8.6%, Score 122.5; DB 4; Length 491;
Best Local Similarity 28.6%; Pred. No. 0.00035;
Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;

QY 7 ASRP-----TTLVGRNKNRVYRDDDFHGNQIOLAPSKSNNDPQWLTKRD 55
DB 354 SSSPXXXXXXXXXADGGQIKNGV-SGRCLDVPDASTGSDGQJLMDCHSGT--NQMAAATDA 410

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Page 5

DB 437 CWGANKK-WELPADDITVGVSGSLCLAVGGSTNRRLQ 476

RESULT 10

US-08-590-563-5
Sequence 5, Application US/08590563
Patent No. 6506593
Germ. No. 1994-0000000
Germ. Information:
Applicant: M. Nyl, Aja
Applicant: Vehmaender, Jari
Applicant: Paegerst m, Richard
Applicant: Lantto, Ralja
Applicant: Paloheimo, Maria
Applicant: Suominen, Pirkko
Applicant: Lantinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STEPHEN KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bagelsky, Lawrence B.
REGISTRATION NUMBER: 35,085
REFERENCE/DOCKET NUMBER: 1050, 0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPER: amino acid
STRANDBESS: no
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50

Query Match 8.6%; Score 122.5; DB 4; Length 480;
Best Local Similarity 32.4%; Fred. No. 0.00034;
Matches 33; Conservative 16; Mismatches 46; Indels 5; Gaps 3;

Qy 22 VVRRDDPHGNGQLPFSKNDPVLWTIRKGTIRSNCS-CTTYGYTGYVMIFD 80
Db 379 IDVPMNNTADGTVQVLIDCHSGS--NQOWTYSSEGRIFPKKCLDAGSSSGAVVYIS 436
Qy 81 CNTAVKATWQIMWNGTIIIPRSNLVLAASGKRTLTVO 122

DB 437 CWGANKK-WELPADDITVGVSGSLCLAVGGSTNRRLQ 476

RESULT 11

US-09-770-621-5
Sequence 5, Application US/09770621
Patent No. 6506593
Germ. No. 1994-0000000
Germ. Information:
Applicant: M. Nyl, Aja
Applicant: Vehmaender, Jari
Applicant: Paegerst m, Richard
Applicant: Lantto, Ralja
Applicant: Paloheimo, Maria
Applicant: Suominen, Pirkko
Applicant: Lantinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STEPHEN KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bagelsky, Lawrence B.
REGISTRATION NUMBER: 35,085
REFERENCE/DOCKET NUMBER: 1050, 0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPER: amino acid
STRANDBESS: no
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50

Query Match 8.6%; Score 122.5; DB 4; Length 480;
Best Local Similarity 32.4%; Fred. No. 0.00034;
Matches 33; Conservative 16; Mismatches 46; Indels 5; Gaps 3;

Qy 22 VVRRDDPHGNGQLPFSKNDPVLWTIRKGTIRSNCS-CTTYGYTGYVMIFD 80
Db 379 IDVPMNNTADGTVQVLIDCHSGS--NQOWTYSSEGRIFPKKCLDAGSSSGAVVYIS 436
Qy 81 CNTAVKATWQIMWNGTIIIPRSNLVLAASGKRTLTVO 122

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us-09-601-667c-10.ra1

FILE REFERENCE: 4693.204-US
CURRENT APPLICATION NUMBER: US/09/159.106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: 127/DK97/00160
EARLIER FILING DATE: 1997-04-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 132
TYPE: PRT
ORGANISM: Oerskovia xanthineolytica
US-09-159-106-15

Query Match
Similarity 9.6%; Score 136; DB 3; Length 132;
Best Local 38.3%; Pred. No. 2,1e-06;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;

18 NGRVDPDDPHGNOIQIIMPESKNDPNOIATIKGGTIRNSGCTTT--GTAGV 75
14 NMCVDVPAADPTDGNVOIVTCSGN--AAQWTRSDGVYALKKIDVDSSTTRAA 71
76 VMIPTDCTAVREATIQIV--DNGT--IINPSNLVLAASSGI--KGTTLTQTLDYTL 128
72 VQVWTCN-----GTGAKMAYDAGSKALRNFGSLCLDITGAGLPRDQRLQVTCNGTT 126
129 GCGW 132
127 AQQW 130

RESULT 8
US-09-159-106-11
Sequence 11, Application US/09159106
Patent No. 6284509
GENERAL INFORMATION:
APPLICANT: Petzer, Pau
APPLICANT: Halko, Tapan
APPLICANT: Hedegard, Lisbeth
TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
FILE REFERENCE: 4693.204-US
CURRENT APPLICATION NUMBER: US/09/159.106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: 127/DK97/00160
EARLIER FILING DATE: 1997-04-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 11
LENGTH: 435
TYPE: PRT
ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11

Query Match
Similarity 9.6%; Score 136; DB 3; Length 435;
Best Local 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;
18 NGRVDPDDPHGNOIQIIMPESKNDPNOIATIKGGTIRNSGCTTT--GTAGV 75
317 NMCVDVPAADPTDGNVOIVTCSGN--AAQWTRSDGVYALKKIDVDSSTTRAA 374
76 VMIPTDCTAVREATIQIV--DNGT--IINPSNLVLAASSGI--KGTTLTQTLDYTL 128
72 VQVWTCN-----GTGAKMAYDAGSKALRNFGSLCLDITGAGLPRDQRLQVTCNGTT 429

US-06-468-812-5
Sequence 5, Application US/06468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Vermaas, Jari
APPLICANT: Muly, Arja
APPLICANT: Rasmussen, Richard
APPLICANT: Lantto, Raimo
APPLICANT: Palomaho, Marja
APPLICANT: Suominen, Eiriko
APPLICANT: Laitinen, Tarja
TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
STREET: 1106 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: 09/08/468.812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
TITLE OF INVENTION: 435
AUTHOR/INVENTOR INFORMATION:
NAME: Bugelsky, Larry B.
REGISTRATION NUMBER: 15,086
REFERENCE/DOCKET NUMBER: 1050.0340002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
FEATURES: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-06-468-812-5

Query Match
Similarity 8.6%; Score 122.5; DB 2; Length 480;
Best Local 32.4%; Pred. No. 0.00034;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;

22 VVDRDDPHGNOIQIIMPESKNDPNOIATIKGGTIRNSG--CLTGYGTAGVYVMPD 80
379 IDVFNKSNADGTQVQVLDCHSGS--NQQWTRTSSGEFIFNKCLDAGSSNGAVVQIS 436
81 CNVAVREATIQIVMDNGTIIINPSNLVLAASSGIKGTTLTQ 122

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RESULT 2
US-08-776-059-33
Sequence 33, Application US/087760598
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: ZINKE, Axel
APPLICANT: ZINKE, Jörg
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOURCE: Patent In Ver. 2.0
SEQ ID NO: 33
LENGTH: 264
TYPE: PRT
ORGANISM: Viscum album
US-08-776-059-33
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Query Match
Best Local Similarity 94.7%; Pred. No. 4.1e-128;
Matches 249; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
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QY 1 DDTYCSASEPTVRIYVGNMCRVDDDFDQNGIQLMPSKSNNDPQLMTTKRDTIS 60
DB 2 DDTYCSASEPTVRIYVGNMCRVDDDFDQNGIQLMPSKSNNDPQLMTTKRDTIS 61
QY 61 NSCLTGYTAGYVNIQDNTAVREATTQIMDNGTINPRSNVLAASSGICGTTLT 120
DB 62 NSCLTGYTAGYVNIQDNTAVREATTQIMDNGTINPRSNVLAASSGICGTTLT 121
QY 121 VQILDYTLGGMLAGNDTAPREVTIYGFRLCNESNGSVWETCDSSQKQKALYGD 180
DB 122 VQILDYTLGGMLAGNDTAPREVTIYGFRLCNESNGSVWETCDSSQKQKALYGD 180
QY 181 GSIRPKMODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGAILNLKGPADVQA 240
DB 181 GSIRPKMODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGAILNLKGPADVQA 240
QY 241 NPKLRRIIYPATGKNQMLPV 263
DB 241 NPKLRRIIYPATGKNQMLPV 263
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RESULT 3
US-08-776-059-35
Sequence 35, Application US/087760598
Patent No. 6271368
GENERAL INFORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jürgen
APPLICANT: ZINKE, Axel
APPLICANT: ZINKE, Jörg
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776, 059B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SOURCE: Patent In Ver. 2.0
SEQ ID NO: 35
LENGTH: 564
TYPE: PRT
ORGANISM: Viscum album
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US-08-776-059-35
Query Match
Best Local Similarity 94.7%; Pred. No. 1.3e-127;
Matches 249; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
QY 1 DDTYCSASEPTVRIYVGNMCRVDDDFDQNGIQLMPSKSNNDPQLMTTKRDTIS 60
DB 302 DDTYCSASEPTVRIYVGNMCRVDDDFDQNGIQLMPSKSNNDPQLMTTKRDTIS 361
QY 61 NSCLTGYTAGYVNIQDNTAVREATTQIMDNGTINPRSNVLAASSGICGTTLT 120
DB 362 NSCLTGYTAGYVNIQDNTAVREATTQIMDNGTINPRSNVLAASSGICGTTLT 421
QY 121 VQILDYTLGGMLAGNDTAPREVTIYGFRLCNESNGSVWETCDSSQKQKALYGD 180
DB 422 VQILDYTLGGMLAGNDTAPREVTIYGFRLCNESNGSVWETCDSSQKQKALYGD 480
QY 481 GSIRPKMODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGAILNLKGPADVQA 240
DB 481 GSIRPKMODCLTSGRDSVSTVINIVCSGASGSGRWFTNKGAILNLKGPADVQA 540
QY 541 NPKLRRIIYPATGKNQMLPV 263
DB 541 NPKLRRIIYPATGKNQMLPV 563
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RESULT 4
US-08-378-761A-77
Sequence 77, Application US/08378761A
Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: MALSH, TERENCE A
APPLICANT: BSH, TIMOTHY D
APPLICANT: WILSON, ALBERT R
TITLE OF INVENTION: ANTICOPPER-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REFERENCE/DOCKET NUMBER: 36222B
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-761A-77
Query Match
Best Local Similarity 55.4%; Pred. No. 6.1e-74;
Matches 144; Conservative 41; Mismatches 74; Indels 1; Gaps 1;
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Page 6

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDNESS: NA
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M64551
US-09-770-621-8

Query Match 8.6%; Score 122.5; DB 9; Length 491;
Best Local Similarity 28.6%; Pred. No. 0.0007;
Matches 40; Conservative 20; Mismatches 61; Indels 19; Gaps 6;
DB 7 ASPP-----TAVVGRVGRVDDPHQVQLMPSKNDPQVLTIRSD 55
QY 354 SSEPXXXXXXADGGIKNG-SGRCLDPDASISDGLQMDCHSGT--NQMALDA 410
DB 56 GTRRANG-SCITTYGTAGVYVWIPDQNTAVREXATVQINDNTIIPNSNVLA--SS 112
QY 411 GELRYGDKCLDAGTNSGSKVQVQISCGADNCK--WELNSDSVYVSGCLDAVNG 468
DB 113 GIKGTLTWQNTIDVTLGGQW 132
QY 469 TANGTILQATGNSGNGRW 468
DB

RESULT 15
US-09-770-621-4
Sequence 4, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M ncy1, Arja
APPLICANT: Velmampster, Jari
APPLICANT: Fagerstrom, Richard
APPLICANT: Lantto, Ralf
APPLICANT: Soderstrom, Ralf
APPLICANT: Soderstrom, Ralf
APPLICANT: Lantto, Ralf
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
FILING DATE: 29-JUL-1994
COMPUTER: IBM PC COMPATIBLE
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
STRANDNESS: NA
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-770-621-4

Query Match 8.6%; Score 122.5; DB 9; Length 492;
Best Local Similarity 32.4%; Pred. No. 0.0007;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;
DB 22 VVPRDDPHQVQLMPSKNDPQVLTIRSDS-CLTTGYTAGVYVWIPDQNTAV 80
QY 379 IYVNRNTAGQVQLDCHSGS--NQMNTYSSGRFLPSKCLDAGSSNCAVYVLS 436
DB 81 CRTVREXATVQINDNTIIPNSNVLA--SSGIGKTLTWQ 122
QY 437 CWGAGNCK--WELRADGTVVSGCLDAVNGSGTNGTRIQ 476
DB

Search completed: December 11, 2003, 14:48:50
Job time: 17.0129 secs

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Page 5

Db 578 SASTADAKRIQYDCH-----GTAAQWBN-----ASTQDYVNTADKCLDY 620
Qy 127 TLGGMLAGNDAPRAVTVYGFADICMENGSGSWWETCSQKQKQKAL 177
Db 621 T-----GNSA-----NBAQWNSC-TGANO-KYKL 646

RESULT 12
US-09-770-621-5
Sequence 18 Application US/10137077
Publication No. US20030092109A1
GENERAL INFORMATION:
APPLICANT: Goldstein, Irwin J.
APPLICANT: Winter, Harry C.
APPLICANT: Kueger, Robert P.
TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin
FILE REFERENCE: UM-07124
CURRENT APPLICATION NUMBER: US/10/137,077
PRIORITY FILING DATE: 2002-05-02
PRIORITY FILING NUMBER: 47,882,596
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/354,322
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent in version 3.1
SEQ ID NO 18
LENGTH: 41
TREE: PKT
ORGANISM: Ricinus communis
US-10-137-077-18

Query Match 8.8%; Score 125; DB 15; Length 41;
Best Local Similarity 53.7%; Pred. No. 1.3e-05;
Matches 22; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 224 GATLWKKGPNDVQANPKRRIITYPATCPQWQMLPWF 264
Db 1 GTLWVXGALVDVPSADPSIKQILVPLHSPQIMLPWF 41

RESULT 13
US-09-770-621-5
Sequence 5, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vehmameper, Jari
APPLICANT: Pegerster m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Suominen, Pirko
APPLICANT: Suominen, Pirko
APPLICANT: Lantinen, Taina
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRIORITY FILING DATE: 2002-02-04
APPLICATION NUMBER: US/09/770,621
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REFERENCE/DOCKET NUMBER: 1050, 0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
STRANDNESS: NO
TOPOLOGY: linear
US20010024815A1 Relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-09-770-621-5

Query Match 8.8%; Score 123.5; DB 9; Length 480;
Best Local Similarity 32.4%; Pred. No. 0.00068;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;

Qy 22 VVDDPDHFGNGCQLMPKSNNDPRLATIRFQGITRNSG-CITTYGTGYWIPD 80
Db 379 IDVNMNADGTVQVLDYCHGSG-NOQWYSSGDFRPNKCLAGSGSSGAVQIYS 436

Qy 81 CMTAVERATQIMDNGTITNPSNLVLAASSGIRGTLTVQ 122
Db 437 CMGSAWOK-MELRADSTIVQSGICLDVGGTNGTRIQ 476

RESULT 14
US-09-770-621-8
Sequence 8, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M nyl, Arja
APPLICANT: Vehmameper, Jari
APPLICANT: Pegerster m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Suominen, Pirko
APPLICANT: Suominen, Pirko
APPLICANT: Lantinen, Taina
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRIORITY FILING DATE: 2002-02-04
APPLICATION NUMBER: US/09/770,621
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:

Thu Dec 11 16:09:45 2003

us-09-601-667c-10.rapb

Page 4

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; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8170
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8170

Query Match
; Score 134; DB 15; Length 536;
Best Local Similarity 30.1%; Pred. No. 5,2e-05;
Matches 40; Conservative 18; Mismatches 59; Indels 16; Gaps 6;

QY 14 IVGNNGMR-VVADDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--SCUTTY-- 68
DB 409 LVGASNNCLDAVDNQTAPGTATIRVDC--GGANQAVITIADELATLGGTCLDANR 465
QY 69 GTTAGVYVAFDQNTAVREKTIWQINDGTTINPSNVLV-----NAGSITKTLTQ 122
DB 466 GTTGTGKTVQVLTGNGANQ--NSLNPNTVYGTQSLCLDVTGSDQSNVVGTALELM 523
QY 123 TDDYTGCGKLAG 135
DB 524 TNGGANQWELG 536

RESULT 9
US-09-973-457-5
; Sequence 5, Application US/09973457
; Patent No. US20020164746A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: 47174, A NOVEL HUMAN GLYCOSYLTRANSFERASE
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 10448-099001
; CURRENT APPLICATION NUMBER: US/09/973,457
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/228,849
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match
; Score 127; DB 10; Length 135;
Best Local Similarity 25.7%; Pred. No. 4.1e-05;
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;

QY 14 IVGNNGMR-VV--RDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--CLTT 67
DB 7 IGVNNGMR-VV--RDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--CLTT 64
QY 68 YGTAGVYVAFDQNTAVREKTIWQINDGTTINPSNVLVLAASGIGKTLTVOITLD 125
DB 65 NG-----TVLYSCDGTGDKNDQKQEVNDGTRNPK-NKKGVDG----- 106
QY 126 YTLGGWLAGNDTAPREVTIYGRDLQNE-SNGSIVWETIDSSQNGKXV 175
DB 107 -----LCIDVKGKXQVMTNKSDBAPKQXV 132

RESULT 10
US-10-074-527-6
; Sequence 6, Application US/10074527
; Patent No. US20020142426A1
; GENERAL INFORMATION:
; APPLICANT: Olandt, Peter J.
; APPLICANT: Meyers, Rachel E.
```

```

; APPLICANT: Galvin, Katherine A.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: 33948, A HUMAN GLYCOSYLTRANSFERASE AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: WP2001-018P(BPCLIM)
; CURRENT APPLICATION NUMBER: US/10/074,527
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/269202
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: consensus
US-10-074-527-6

Query Match
; Score 127; DB 14; Length 135;
Best Local Similarity 25.7%; Pred. No. 4.1e-05;
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;

QY 14 IVGNNGMR-VV--RDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--CLTT 67
DB 7 IGVNNGMR-VV--RDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--CLTT 64
QY 68 YGTAGVYVAFDQNTAVREKTIWQINDGTTINPSNVLVLAASGIGKTLTVOITLD 125
DB 65 NG-----TVLYSCDGTGDKNDQKQEVNDGTRNPK-NKKGVDG----- 106
QY 126 YTLGGWLAGNDTAPREVTIYGRDLQNE-SNGSIVWETIDSSQNGKXV 175
DB 107 -----LCIDVKGKXQVMTNKSDBAPKQXV 132

RESULT 11
US-10-156-761-10246
; Sequence 10246, Application US/10156761
; Patent No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMR, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: HORIYAMA, JUN
; APPLICANT: HORIYAMA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, TOSHIYUKI
; APPLICANT: HIRAKAWA, HISAKI
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10246
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10246

Query Match
; Score 126; DB 15; Length 647;
Best Local Similarity 26.3%; Pred. No. 0.00044;
Matches 45; Conservative 20; Mismatches 60; Indels 46; Gaps 8;

QY 9 EPTVAVIYGNNGMR-VVADDDPHDGNQIQWPSKSNNDPQMLTKIKDITRNSG--CLTT 66
DB 520 DQTSFVGLAKKCLDVAASSSANGTAVQVLT--DQGSTAPKATYKADSVQVQAKCLVLT 577
QY 67 TGTGTAGVYVAFDQNTAVREKTIWQINDGTTINPSNVLVLAASGIGKTLTVOITLD 126
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Publication No. US20020142426A1
GENERAL INFORMATION:
APPLICANT: Olandt, Peter J.
APPLICANT: Meyers, Rachel E.
APPLICANT: Galvin, Katherine A.
APPLICANT: Millennium Pharmaceuticals Inc.
TITLE OF INVENTION: Uses of a human glycosyltransferase and
the encoded protein (US/01/074,537)
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: US/10/074,537
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/269202
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 145
TYPE: PRN
DESCRIPTION: Artificial Sequence
ORIGIN: INFORMATION: consensus
US-10-074-537-5
Query Match 12.0% Score 171; DB 14; Length 145;
Best Local Similarity 32.8%; Pred. No. 1.3e-09;
Matches 45; Conservative 20; Mismatches 58; Indels 14; Gaps 4;
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QY 11 TTVAVNGNMGVYRDDPHDQNOQLMPKSNNDPQMLTI--KRDGTIR--NSGC 64
DB 7 TTVAVNGNMGVYRDDPHDQNOQLMPKSNNDPQMLTI--KRDGTIR--NSGC 66
QY 65 LTTGYAGYVWIPDCNTAVKATITWQINDGTITP-----KSNLV--AASGSG 116
DB 67 LTVANSPGSEVLYCQDSATSDQKWEINDLISKTLILVNTGLVLDVKSADTONG 126
QY 117 TTVVOTLDTYLTGCGW 133
DB 127 TTVVOTLDTYLTGCGW 143
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RESULT 6
US-10-156-761-14970
Sequence 14970, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OKURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBATA, YOSHIO
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14970
LENGTH: 420
TYPE: PRN
ORIGIN: INFORMATION: Streptomyces avermitilis
US-10-156-761-14970
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Query Match 10.9% Score 155; DB 15; Length 420;
Best Local Similarity 32.8%; Pred. No. 2.4e-06;
Matches 44; Conservative 19; Mismatches 68; Indels 10; Gaps 5;
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DB 284 DQVKTGDSGSAITGLAKGVYVASSNANPQVLV--DQNTTAKXTVADPDL 341
QY 59 RNSGCL--TTGYAGYVWIPDCNTAVKATITWQINDGTITP--LVLASGGI 114
DB 342 RALGKLDVTENGTDGSDTVOIMDCGSAKOK--WVTAAGDIPVQAKDLVYGNNA 399
QY 115 KETVLTVOTLDTYLTGCGW 135
DB 400 MGRVLTGKSGANQKXKG 420
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RESULT 7
US-10-156-761-9724
Sequence 9724, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OKURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBATA, YOSHIO
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9724
LENGTH: 658
TYPE: PRN
ORIGIN: INFORMATION: Streptomyces avermitilis
US-10-156-761-9724
Query Match 9.8% Score 138.5; DB 15; Length 658;
Best Local Similarity 32.1%; Pred. No. 2.4e-05;
Matches 44; Conservative 17; Mismatches 57; Indels 19; Gaps 7;
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QY 11 TTVAVNGNMGVYRDDPHDQNOQLMPKSNNDPQMLTI--KRDGTIR 59
DB 523 TTVAVNGNMGVYRDDPHDQNOQLMPKSNNDPQMLTI--KRDGTIR 580
QY 60 SNGSCLTY--GYVAGYVWIPDCNTAVKATITWQINDGTITP--LVLASGGI 115
DB 581 GKKLKLNLNLTGNTKTYTATVWQKQANOK--NVLNSDGLTNNVNSGLDLNVAALN 638
QY 116 GTTVLTGKSGANQKXKG 132
DB 639 GTTVLTGKSGANQKXKG 420
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QY 121 VQTLDTLGGWMLAGNDTAREVITVGFRLCMESNGSGSVWETCDSSQXKQKALVAD 180
DB 121 VQTLDTLGGWMLAGNDTAREVITVGFRLCMESNGSGSVWETCDSSQXKQKALVAD 179
QY 181 GSIRPKONDOCLTSGRDSVSTVINIVSGSGASGQRMWFTNKGALINLKKGPMADVAQA 240
DB 180 GSIRPKONDOCLTSGRDSVSTVINIVSGSGASGQRMWFTNKGALINLKKGPMADVAQA 239
QY 241 NPKLRRIIIPATCKNQMLPV 263
DB 240 NPKLRRIIIPATCKNQMLPV 262

RESULT 2
US-09-347-064-4
Sequence 4, Application US/09347064A
Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Eek, Jürgen
APPLICANT: Schmidt, Arno
APPLICANT: Zinke, Holger
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
FILE OF INVENTION: album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
EARLIER APPLICATION NUMBER: EP/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 4
LENGTH: 267
TYPE: PRT
ORGANISM: Viscum album
US-09-347-064-4

Query Match
Best Local Similarity 94.7%; Pred. No. 1.5e-127;
Matches 249; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
QY 1 DVTCSASBETVRIYGRNKNKVDVDDPHDNGQIOLWPSKSNPNQMLTKKDTIRTS 60
DB 1 DVTCSASBETVRIYGRNKNKVDVDDPHDNGQIOLWPSKSNPNQMLTKKDTIRTS 60
QY 61 NSGCLTGTGTAAGVYVIFDONTAVREAITWQINDGTTINPSMLVLAASGIGKTTLT 120
DB 61 NSGCLTGTGTAAGVYVIFDONTAVREAITWQINDGTTINPSMLVLAASGIGKTTLT 120
QY 121 VQTLDTLGGWMLAGNDTAREVITVGFRLCMESNGSGSVWETCDSSQXKQKALVAD 180
DB 121 VQTLDTLGGWMLAGNDTAREVITVGFRLCMESNGSGSVWETCDSSQXKQKALVAD 179
QY 181 GSIRPKONDOCLTSGRDSVSTVINIVSGSGASGQRMWFTNKGALINLKKGPMADVAQA 240
DB 180 GSIRPKONDOCLTSGRDSVSTVINIVSGSGASGQRMWFTNKGALINLKKGPMADVAQA 239
QY 241 NPKLRRIIIPATCKNQMLPV 263
DB 240 NPKLRRIIIPATCKNQMLPV 262

RESULT 3
US-10-083-336A-1
Sequence 1, Application US/1008336A
Patent No. US2003018165A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Kamenecner, Robert W

FILE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P6745200, R11D 01-58
CURRENT APPLICATION NUMBER: US/10/083,336A
EARLIER APPLICATION NUMBER: US/02-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 576
TYPE: PRT
ORGANISM: Ricinus communis
US-10-083-336A-1

Query Match
Best Local Similarity 63.3%; Score 899.5; DB 12; Length 576;
Matches 165; Conservative 32; Mismatches 62; Indels 1; Gaps 1;
QY 5 CSASEPTVRIYGRNKNKVDVDDPHDNGQIOLWPSKSNPNQMLTKKDTIRTSKGC 64
DB 318 CSASEPTVRIYGRNKNKVDVDDPHDNGQIOLWPSKSNPNQMLTKKDTIRTSKGC 377
QY 63 LTTGYTAGVYVIFDONTAVREAITWQINDGTTINPSMLVLAASGIGKTTLT 124
DB 378 LTTGYTAGVYVIFDONTAVREAITWQINDGTTINPSMLVLAASGIGKTTLT 437
QY 125 DTTLGGWMLAGNDTAREVITVGFRLCMESNGSGSVWETCDSSQXKQKALVAD 184
DB 438 DTTLGGWMLAGNDTAREVITVGFRLCMESNGSGSVWETCDSSQXKQKALVAD 196
QY 185 PKONDOCLTSGRDSVSTVINIVSGSGASGQRMWFTNKGALINLKKGPMADVAQA 244
DB 497 PKONDOCLTSGRDSVSTVINIVSGSGASGQRMWFTNKGALINLKKGPMADVAQA 556
QY 245 RRIIIPATCKNQMLPV 264
DB 557 RRIIIPATCKNQMLPV 576

RESULT 4
US-10-137-077-17
Sequence 17, Application US/10137077
Patent No. US20030092109A1
GENERAL INFORMATION:
APPLICANT: Goldstein, Irwin J.
APPLICANT: Krueger, Robert P.
TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin
FILE OF INVENTION: 01-12-98, US/01/0137,077
CURRENT APPLICATION NUMBER: US/02-05-02
EARLIER FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/288,596
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 17
LENGTH: 44
TYPE: PRT
ORGANISM: Ricinus communis
US-10-137-077-17

Query Match
Best Local Similarity 77.3%; Pred. No. 7.4e-12;
Matches 34; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 12 VAIVGKGRVYVDDPHDNGQIOLWPSKSNPNQMLTKKDTIRTSKGC 55
DB 1 VAIVGKGRVYVDDPHDNGQIOLWPSKSNPNQMLTKKDTIRTSKGC 44

RESULT 5
US-10-074-527-5
Sequence 5, Application US/10074527

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Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 14:01:14 (Search time 17.0129 seconds
(without alignments)
2886.029 Million cell updates/sec

Title: US-09-601-667C-10

Perfect score: 1420

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Searched: 684280 seqs, 185931659 residues

Total number of hits satisfying chosen parameters: 684280

Maximum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1320.5	93.0	263	9	US-09-347-064-10
2	1320.5	93.0	267	9	US-09-347-064-4
3	889.5	63.3	576	12	US-10-063-336A-1
4	186	13.1	44	15	US-10-137-077-17
5	171	12.0	145	14	US-10-074-527-5
6	155	10.9	420	15	US-10-156-761-14970
7	138.5	9.4	658	15	US-10-156-761-9724
8	134	9.4	536	15	US-10-156-761-8170
9	127	8.9	135	15	US-09-973-457-3
10	126	8.9	135	15	US-10-156-761-10246
11	125	8.8	643	15	US-10-137-077-18
12	125	8.6	480	9	US-09-770-621-5
13	122.5	8.6	491	9	US-09-770-621-8
14	122.5	8.6	492	9	US-09-770-621-4
15	122.5	8.6	492	9	US-09-770-621-4

16	122.5	8.6	492	9	US-09-770-621-7	Sequence 7, Appl 1
17	122.5	8.6	492	12	US-10-286-993-4	Sequence 4, Appl 1
18	112	7.9	625	15	US-10-156-761-1508	Sequence 1508, A
19	108	7.6	41	15	US-10-137-077-20	Sequence 20, Appl 1
20	104	7.3	45	15	US-10-137-077-19	Sequence 19, Appl 1
21	102	7.0	612	14	US-10-001-851-25	Sequence 25, Appl 1
22	99.5	6.7	464	15	US-10-156-761-9647	Sequence 9647, A
23	93	6.7	1723	9	US-09-841-132-353	Sequence 3547, A
24	92	6.5	1271	10	US-09-808-602-82	Sequence 3947, A
25	92	6.5	2771	10	US-09-808-602-82	Sequence 82, Appl 1
26	92	6.5	2771	10	US-09-808-602-82	Sequence 70, Appl 1
27	92	6.5	2771	10	US-09-808-602-82	Sequence 8037, A
28	90.5	6.4	340	15	US-10-128-714-8037	Sequence 10, Appl 1
29	89	6.3	1706	12	US-10-229-066-10	Sequence 119, A
30	87	6.1	2732	12	US-10-238-075-119	Sequence 15, Appl 1
31	86.5	6.1	1032	11	US-09-133-643-16	Sequence 16, Appl 1
32	86.5	6.1	1032	12	US-10-133-643-16	Sequence 130, A
33	85.5	6.0	1082	12	US-10-133-643-16	Sequence 130, A
34	85.5	6.0	608	10	US-09-824-358-28	Sequence 8, Appl 1
35	85.5	6.0	1079	12	US-10-193-764-43	Sequence 45, Appl 1
36	85.5	6.0	1079	12	US-10-193-764-43	Sequence 45, Appl 1
37	85.5	6.0	1079	12	US-10-193-764-43	Sequence 15, Appl 1
38	84.5	6.0	239	10	US-09-839-996-6	Sequence 6, Appl 1
39	84	5.9	1848	15	US-10-080-505-6	Sequence 6, Appl 1
40	84	5.9	207	9	US-09-780-717-26	Sequence 26, Appl 1
41	83	5.8	2253	10	US-09-777-862-33	Sequence 33, Appl 1
42	83	5.8	2668	12	US-10-246-320-4	Sequence 4, Appl 1
43	82.5	5.8	871	10	US-09-858-525A-2	Sequence 2, Appl 1
44	82.5	5.8	871	10	US-09-858-525A-2	Sequence 2, Appl 1
45	82.5	5.8	871	10	US-09-858-525A-2	Sequence 2, Appl 1

ALIGNMENTS

RESULT 1	US-09-347-064-10
/ Sequence 10, Application US/09347064A	
/ Length: 263	
/ Residue Number: 1-263	
/ Applicant: Eck, Jurgen	
/ Applicant: Schmidt, Arno	
/ Applicant: Zinke, Holger	
/ TITLE OF INVENTION: Recombinant Fusion Proteins Based on	
/ TITLE OF INVENTION: Ribosome-inactivating proteins of the m12cease Viscum	
/ TYPE OF INVENTION: Album	
/ FILE REFERENCE: 09282-3	
/ CURRENT APPLICATION NUMBER: US/09347064A	
/ EARLIER FILING DATE: 1998-01-02	
/ EARLIER APPLICATION NUMBER: PCT/E99/00099	
/ EARLIER FILING DATE: 1997-01-02	
/ EARLIER APPLICATION NUMBER: EP 97 10 0012.0	
/ NUMBER OF SEQ ID NOS: 38	
/ SOFTWARE: Patent Ver. 2.1	
/ SEQ ID NO 10	
/ LENGTH: 263	
/ TYPE: Nucleic Acid	
/ ORGANISM: Viscum album	
US-09-347-064-10	
Query Match	93.0%; Score 1320.5; DB 9; Length 263;
Best Local Similarity	94.7%; Pred. No. 1.5e+127;
Matches 249; Conservative	2; Mismatches 11; Indels 1; Gaps 1;
QY	1 DVTGCSAEPTVRIYERNM.....RRIIVPATKPKMPLVF 264
DB	1 DVTGCSAEPTVRIYERNM.....RRIIVPATKPKMPLVF 264
QY	6 NSGCTTGTAGTGYTMMIDONTAVREATWIDNGTINPSSNLYTAAAGCTKTTT 120
DB	6 NSGCTTGTAGTGYTMMIDONTAVREATWIDNGTINPSSNLYTAAAGCTKTTT 120
QY	6 NSGCTTGTAGTGYTMMIDONTAVREATWIDNGTINPSSNLYTAAAGCTKTTT 120
DB	6 NSGCTTGTAGTGYTMMIDONTAVREATWIDNGTINPSSNLYTAAAGCTKTTT 120

ribosomes. Non-cytotoxic forms of (1) activate T-cell and lymphokine-producing macrophages, so stimulate immunity. (1) and its fragments are used to treat uncontrolled cell growth (particularly cancers) and if they lack cytotoxicity, to increase the strength of the immune response, particularly to a co-administered antigen production of immunomodulators. (1) is particularly useful in the treatment of metastatic disease, and its individual chains in many different isoforms and on a large scale, at any time of the year. Recombinant products are free from toxins present in natural mistletoe extracts. This sequence represents a fragment of a mistletoe lectin I protein variant.

XX Sequence 532 AA;

Query Match 93.4%; Score 1326.5; DB 20; Length 532;

Best Local Similarity 95.1%; Pred. No. 7,5e-123;

Matches 250; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

1 DDTGASAPPTVIVGNKNDVDDPHGNDQGLAPSKNDPQGLMTIKDGTIS 60

269 DDTGASAPPTVIVGNKNDVDDPHGNDQGLAPSKNDPQGLMTIKDGTIS 328

61 NSCLTYGTAGYVMI FDCNFAVEATIQWINDGIIINPSNLVLAASSGKXTLT 120

329 NSCLTYGTAGYVMI FDCNFAVEATIQWINDGIIINPSNLVLAASSGKXTLT 388

121 VQTLDTLGGMLAGNDTPBEVTIYGRDLCSNQSQWVEFCDSQNGKALYD 180

389 VQTLDTLGGMLAGNDTPBEVTIYGRDLCSNQSQWVEFCDSQNGKALYD 447

181 GSIRPKNDQCLTGRDSVSTVINIVSGASGQRPWFNFGALINLKLAMDVAQA 240

448 GSIRPKNDQCLTGRDSVSTVINIVSGASGQRPWFNFGALINLKLAMDVAQA 507

241 NPKLRILIIYPATKPNQWMLPV 263

508 NPKLRILIIYPATKPNQWMLPV 530

DB 508 NPKLRILIIYPATKPNQWMLPV 530

RESULT 15

ID AAW64662 standard; Protein; 263 AA.

XX AAW64662;

XX 23-OCT-1998 (first entry)

XX Mistletoe rMLB variant protein.

XX Lectin B-chain; mistletoe; rMLB; fusion protein; effector; cytotoxic;

XX intracellular; processing module; protease recognition; targeting module;

XX intracellular; treatment; disorder; cell proliferation; activation;

XX autoimmune disease; allergy; tumour; ricin; translocation.

XX Viscum album.

XX Key Location/Qualifiers

XX Protein 1..263

XX /note= "partial protein"

XX MO9629540-A2.

XX 09-JUL-1998.

XX 02-JAN-1998; 98WC-EP00009.

XX 02-JAN-1997; 97EP-0100012.

XX (BRAT-) BRAIN BIOTECHNOLOGY RES & INFORMATION KE.

XX Eck J, Schmidt A, Zinke H;

XX WPI; 1998-38812/23.

XX N-PSDB; AAVS1344.

DR

XX Nucleic acid encoding fusion protein containing mistletoe lectin A

PT chain - useful for treatment of proliferative and autoimmune

PT diseases, allergies and tumours

XX disclosure: Fig 11b; 115pp; German.

XX This sequence represents a variant mistletoe lectin B-chain, rMLB. This

XX sequence can be used in the construction of a fusion protein which

XX comprises an effector module that is cytotoxic intracellularly, a

XX processing module covalently bonded to the effector module and

XX containing a protease recognition sequence, and a targeting module

XX covalently bonded to the processing module, able to bind specifically to

XX the surface of a cell so as to mediate internalisation of the fusion

XX protein. Such a fusion protein can be used for treating disorders

XX involving proliferation and/or elevated activation of cells, especially

XX at 1 ng to 500 mg/kg/day, or for ex vivo use at 1 pg to 500 ng/ml.

XX Fusion proteins can develop toxic activity in a wide range of target

XX cells. The processing module prevents extracellular dissociation, and

XX fusion proteins based on mistletoe lectin A-chain are far more active

XX than those based on ricin and do have the associated problems of

XX non-specific toxicity. The protein may be expressed in a non-glycosylated

XX form that does not bind to sugar receptors in the liver, and which has a

XX long half-life in the blood, thereby the mistletoe lectin B-chain is used,

XX as a "carrier" for the "active" chain. The rMLB A-chain from the

XX endoplasmic reticulum to the cytoplasm.

XX Sequence 263 AA;

Query Match 93.0%; Score 1320.5; DB 19; Length 263;

Best Local Similarity 94.7%; Pred. No. 1.1e-122;

Matches 249; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

1 DDTGASAPPTVIVGNKNDVDDPHGNDQGLAPSKNDPQGLMTIKDGTIS 60

1 DDTGASAPPTVIVGNKNDVDDPHGNDQGLAPSKNDPQGLMTIKDGTIS 60

61 NSCLTYGTAGYVMI FDCNFAVEATIQWINDGIIINPSNLVLAASSGKXTLT 120

61 NSCLTYGTAGYVMI FDCNFAVEATIQWINDGIIINPSNLVLAASSGKXTLT 120

121 VQTLDTLGGMLAGNDTPBEVTIYGRDLCSNQSQWVEFCDSQNGKALYD 180

121 VQTLDTLGGMLAGNDTPBEVTIYGRDLCSNQSQWVEFCDSQNGKALYD 179

181 GSIRPKNDQCLTGRDSVSTVINIVSGASGQRPWFNFGALINLKLAMDVAQA 240

180 GSIRPKNDQCLTGRDSVSTVINIVSGASGQRPWFNFGALINLKLAMDVAQA 239

241 NPKLRILIIYPATKPNQWMLPV 263

240 NPKLRILIIYPATKPNQWMLPV 262

DB 240 NPKLRILIIYPATKPNQWMLPV 262

Search completed: December 11, 2003, 14:07:45

DB time : 26.0864 secs

XX Sequence 264 AA;
SQ
Query Match 93.4%; Score 1326.5; DB 20; Length 264;
Best Local Similarity 95.1%; Pred. No. 286-123;
Matches 250; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
OY 1 DVTCSASBETVRIYGNKRVYDADDDPHDNGIOIOLPSSKNNDPYQALTIKDGITRS 60
DB 1 DVTCSASBETVRIYGNKRVYDADDDPHDNGIOIOLPSSKNNDPYQALTIKDGITRS 60
OY 61 NSCLTTGYTAGYVYMIPOCNVREATTIWIQNGTINPNSNLYLAASSGIGKLTLL 120
DB 61 NSCLTTGYTAGYVYMIPOCNVREATTIWIQNGTINPNSNLYLAASSGIGKLTLL 120
OY 121 VOTLDYTLGQGLAENDTAPREVTIYGRDLQESNGSVYVETCSQKQNALYGD 180
DB 121 VOTLDYTLGQGLAENDTAPREVTIYGRDLQESNGSVYVETCSQKQNALYGD 180
OY 121 VOTLDYTLGQGLAENDTAPREVTIYGRDLQESNGSVYVETCSQKQNALYGD 179
DB 121 VOTLDYTLGQGLAENDTAPREVTIYGRDLQESNGSVYVETCSQKQNALYGD 179
OY 181 GSIRPKONPODCLTCGRDSVYVNIIVSCSAGSQRWFTNKGALINLKGPNADVQA 240
DB 181 GSIRPKONPODCLTCGRDSVYVNIIVSCSAGSQRWFTNKGALINLKGPNADVQA 239
OY 241 NPKLRRIIYPATGKPNQMLPV 263
DB 240 NPKLRRIIYPATGKPNQMLPV 262

RESULT 13

AAV25979
ID AAV25979 standard; Protein; 531 AA.

XX AAV25979;

XX 18-OCT-1999 (first entry)

XX Mistletoe lectin I protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;

XX cancer; cytotoxicity; antigen; isoform; lectin I.

XX Viscum album.

XX Viscum album.

XX DE19804210-A1.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P. Stiefel T. Voelter W. Walters P;

XX WPI; 1999-44535/38.

XX N-PSDB; AA209103.

XX Preparation of mistletoe lectins in heterologous systems.

XX Particularity for use as anticancer agents and immunostimulants

XX Claim 7; Fig 1B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments

XX which have antitumour and immunostimulatory activity. The A-chain (MIA)

XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of

XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and

XX lymphokine-producing macrophages, so stimulate immunity. (I) and its

XX fragments are used to treat uncontrolled cell growth (particularly

XX cancers) and if they lack cytotoxicity, to increase the strength of the

XX immune response, particularly to a co-administered antigen

CC (tumour-associated, bacterial or viral). The method allows production of

CC mistletoe lectin, and its A-chain, in many different isoforms

CC free from toxins present in natural mistletoe extracts. This sequence

CC represents a mistletoe lectin I protein fragment.

XX Sequence 531 AA;

SQ
Query Match 93.4%; Score 1326.5; DB 20; Length 531;
Best Local Similarity 95.1%; Pred. No. 736-123;
Matches 250; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

OY 1 DVTCSASBETVRIYGNKRVYDADDDPHDNGIOIOLPSSKNNDPYQALTIKDGITRS 60
DB 1 DVTCSASBETVRIYGNKRVYDADDDPHDNGIOIOLPSSKNNDPYQALTIKDGITRS 60
OY 269 DVTCSASBETVRIYGNKRVYDADDDPHDNGIOIOLPSSKNNDPYQALTIKDGITRS 328
DB 269 DVTCSASBETVRIYGNKRVYDADDDPHDNGIOIOLPSSKNNDPYQALTIKDGITRS 328
OY 61 NSCLTTGYTAGYVYMIPOCNVREATTIWIQNGTINPNSNLYLAASSGIGKLTLL 120
DB 61 NSCLTTGYTAGYVYMIPOCNVREATTIWIQNGTINPNSNLYLAASSGIGKLTLL 120
OY 121 VOTLDYTLGQGLAENDTAPREVTIYGRDLQESNGSVYVETCSQKQNALYGD 180
DB 121 VOTLDYTLGQGLAENDTAPREVTIYGRDLQESNGSVYVETCSQKQNALYGD 180
OY 121 VOTLDYTLGQGLAENDTAPREVTIYGRDLQESNGSVYVETCSQKQNALYGD 179
DB 121 VOTLDYTLGQGLAENDTAPREVTIYGRDLQESNGSVYVETCSQKQNALYGD 179
OY 181 GSIRPKONPODCLTCGRDSVYVNIIVSCSAGSQRWFTNKGALINLKGPNADVQA 240
DB 181 GSIRPKONPODCLTCGRDSVYVNIIVSCSAGSQRWFTNKGALINLKGPNADVQA 240
OY 241 NPKLRRIIYPATGKPNQMLPV 263
DB 240 NPKLRRIIYPATGKPNQMLPV 262

RESULT 14

AAV25982
ID AAV25982 standard; Protein; 532 AA.

XX AAV25982;

XX 18-OCT-1999 (first entry)

XX Mistletoe lectin I (variant) protein fragment.

XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MIA; immunity;

XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;

XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;

XX cancer; cytotoxicity; antigen; isoform; lectin I.

XX Viscum album.

XX Viscum album.

XX DE19804210-A1.

XX DE19804210-A1.

XX 12-AUG-1999.

XX 03-FEB-1998; 98DE-1004210.

XX 03-FEB-1998; 98DE-1004210.

XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.

XX Morris P. Stiefel T. Voelter W. Walters P;

XX WPI; 1999-44535/38.

XX N-PSDB; AA209106.

XX Preparation of mistletoe lectins in heterologous systems.

XX Particularity for use as anticancer agents and immunostimulants

XX Disclosure; Fig 4B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments

XX which have antitumour and immunostimulatory activity. The A-chain (MIA)

XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of

QY 61 NSCLTGYTGATGYVWIFDCNTAVREATTQIWMNGTIIIPESNLYAAASGIGKTTLT 120
 DB 61 NSCLTGYTGATGYVWIFDCNTAVREATTQIWMNGTIIIPESNLYAAASGIGKTTLT 120
 QY 121 VQTLDTYLAGQGMAGNDTAPREVTIYGFADLCWESNGSVWETCDSSQKQGMALYGD 180
 DB 121 VQTLDTYLAGQGMAGNDTAPREVTIYGFADLCWESNGSVWETCDSSQKQGMALYGD 180
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQRFVFTNKAIIINLKGPANDVQA 240
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQRFVFTNKAIIINLKGPANDVQA 240
 QY 241 NPKLRRIIYPRATGKPNQMLPV 264
 DB 241 NPKLRRIIYPRATGKPNQMLPV 264

RESULT 11

AAZ5985
 ID AAZ5985 standard; Protein: 263 AA.

XX AAZ5985;
 DT 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin B protein fragment.
 XX
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MHA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B.

XX Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 PA Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI, 1999-445335/38.
 XX N-PSDB; AA209109.
 XX
 PT Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 PS Claim 9; Fig 7B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MHA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to viral. The method allows production of
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B protein.

XX Sequence 263 AA;
 XX Query Match 93.4%; Score 1326.5; DB 20; Length 263;
 XX Best Local Similarity 95.1%; Pred. No. 2,76-123;

Matches 250; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
 QY 1 DDTVCSASBPVAVIYGRNGRVDVDDDFHDGNOIQIIMPESKNNDPNOIATIKROGTIR 60
 DB 1 DDTVCSASBPVAVIYGRNGRVDVDDDFHDGNOIQIIMPESKNNDPNOIATIKROGTIR 60
 QY 61 NSCLTGYTGATGYVWIFDCNTAVREATTQIWMNGTIIIPESNLYAAASGIGKTTLT 120
 DB 61 NSCLTGYTGATGYVWIFDCNTAVREATTQIWMNGTIIIPESNLYAAASGIGKTTLT 120
 QY 121 VQTLDTYLAGQGMAGNDTAPREVTIYGFADLCWESNGSVWETCDSSQKQGMALYGD 180
 DB 121 VQTLDTYLAGQGMAGNDTAPREVTIYGFADLCWESNGSVWETCDSSQKQGMALYGD 180
 QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQRFVFTNKAIIINLKGPANDVQA 240
 DB 181 GSIRPKONODCLTSGRDSVSTVINIVSCGASGSGQRFVFTNKAIIINLKGPANDVQA 240
 QY 241 NPKLRRIIYPRATGKPNQMLPV 263
 DB 241 NPKLRRIIYPRATGKPNQMLPV 263

RESULT 12

AAZ5991
 ID AAZ5991 standard; Protein: 264 AA.

XX AAZ5991;
 DT 18-OCT-1999 (first entry)
 XX
 XX Mistletoe lectin B variant protein fragment.
 XX
 XX Mistletoe lectin; antitumour; immunostimulant; A-chain; MHA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B.

XX Viscum album.
 XX DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 PA Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI, 1999-445335/38.
 XX N-PSDB; AA209115.
 XX
 PT Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 PS Disclosure; Fig 13B; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MHA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancers) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B protein.

Db 181 GSIRPKNDPQCLTSGRDSVSTVINIVCSGASGSRVFTNEGAILNKSLMDVQA 240
QY 241 NPKLRRIIYPATGKNGQWLPVF 264
Db 241 NPKLRRIIYPATGKNGQWLPVF 264

RESULT 9

AAZ5987 ID AAZ5987 standard; Protein; 264 AA.

AAZ5987; XX

18-OCT-1999 (first entry) XX

Mistletoe lectin B2 protein fragment. XX

Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity; XX

lymphokine-producing macrophage; uncontrolled cell growth; treatment; XX

cancer; cytotoxicity; antigen; isoform; lectin B2. XX

Viscum album. XX

DE19804210-A1. XX

12-AUG-1999. XX

03-FEB-1998; 98DE-1004210. XX

03-FEB-1998; 98DE-1004210. XX

(BIOS-) BIOSYN ARZNEIMITTEL GMBH. XX

Morris P, Sclafel T, Voelter W, Welters P. XX

WPI, 1999-44535/38. XX

N-P8DB; AA209111. XX

Preparation of mistletoe lectins in heterologous systems, XX

particularly for use as anticancer agents and immunostimulants XX

Claim 9; Fig 9B; 78pp; German. XX

This invention describes a novel mistletoe lectin (I) and its fragments XX

which have antitumor and immunostimulatory activity. The A-chain (MIA) XX

of the mistletoe lectin binds to (II) activate T-cell and (I) and XX

lymphokine-producing macrophages, so stimulate immunity. (I) and its XX

fragments are used to treat uncontrolled cell growth (particularly XX

cancers) and if they lack cytotoxicity, to increase the strength of the XX

immune response, particularly to a co-administered antigen (tumour-associated, XX

bacterial or viral). The method allows production of mistletoe lectin, XX

and on a large scale, at any time of the year. Recombinant products are XX

free from toxins present in natural mistletoe extracts. This sequence XX

represents a fragment of a mistletoe lectin B2 protein. XX

Sequence 264 AA. XX

Query Match 96.5%; Score 1371; DB 20; Length 264;

Best Local Similarity 97.3%; Pred. No. 1e-127; Matches 257; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 DDTVCASBPRTVIRVSGNKGWVVDVDDPFQDQNIQLMPSKSNNDPNGLWTIKDGTIRS 60

1 DDTVCASBPRTVIRVSGNKGWVVDVDDPFQDQNIQLMPSKSNNDPNGLWTIKDGTIRS 60

61 NSCLTGYTAGVYVWFDCNVAEALTIQIMNGTIIIPRSNLYLAASSGKIKTTLT 120

61 NSCLTGYTAGVYVWFDCNVAEALTIQIMNGTIIIPRSNLYLAASSGKIKTTLT 120

QY 121 VDTLDTLQGMAGNDAPREVITVYGFEDLCVNSGASVYVETCSQKQKQKALYGD 180
Db 121 VDTLDTLQGMAGNDAPREVITVYGFEDLCVNSGASVYVETCSQKQKQKALYGD 180
QY 181 GSIRPKNDPQCLTSGRDSVSTVINIVCSGASGSRVFTNEGAILNKSLMDVQA 240
Db 181 GSIRPKNDPQCLTSGRDSVSTVINIVCSGASGSRVFTNEGAILNKSLMDVQA 240

RESULT 10

AAZ5993 ID AAZ5993 standard; Protein; 265 AA.

AAZ5993; XX

18-OCT-1999 (first entry) XX

Mistletoe lectin B2 variant protein fragment. XX

Mistletoe lectin; antitumor; immunostimulant; A-chain; MIA; immunity; XX

lymphokine-producing macrophage; uncontrolled cell growth; treatment; XX

cancer; cytotoxicity; antigen; isoform; lectin B2. XX

Viscum album. XX

DE19804210-A1. XX

12-AUG-1999. XX

03-FEB-1998; 98DE-1004210. XX

03-FEB-1998; 98DE-1004210. XX

(BIOS-) BIOSYN ARZNEIMITTEL GMBH. XX

Morris P, Sclafel T, Voelter W, Welters P. XX

WPI, 1999-44535/38. XX

N-P8DB; AA209117. XX

Preparation of mistletoe lectins in heterologous systems, XX

particularly for use as anticancer agents and immunostimulants XX

Disclosure; Fig 15B; 78pp; German. XX

This invention describes a novel mistletoe lectin (I) and its fragments XX

which have antitumor and immunostimulatory activity. The A-chain (MIA) XX

of the mistletoe lectin binds to (II) activate T-cell and (I) and its XX

fragments are used to treat uncontrolled cell growth (particularly XX

cancers) and if they lack cytotoxicity, to increase the strength of the XX

immune response, particularly to a co-administered antigen (tumour-associated, XX

bacterial or viral). The method allows production of mistletoe lectin, XX

and on a large scale, at any time of the year. Recombinant products are XX

free from toxins present in natural mistletoe extracts. This sequence XX

represents a fragment of a variant mistletoe lectin B2 protein. XX

Sequence 265 AA. XX

Query Match 96.5%; Score 1371; DB 20; Length 265;

Best Local Similarity 97.3%; Pred. No. 1e-127; Matches 257; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 DDTVCASBPRTVIRVSGNKGWVVDVDDPFQDQNIQLMPSKSNNDPNGLWTIKDGTIRS 60

1 DDTVCASBPRTVIRVSGNKGWVVDVDDPFQDQNIQLMPSKSNNDPNGLWTIKDGTIRS 60

ID AAY25990 standard; Protein; 264 AA.
XX
AC AAY25990;
XX
DT 18-OCT-1999 (first entry)
XX
DE Mistletoe lectin B5 protein fragment.
XX
KW Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.
XX
OS Viscum album.
XX
PN DEJ9804210-A1.
XX
RD 12-AUG-1999.
XX
PF 03-FEB-1998; 98DE-1004210.
XX
PR 03-FEB-1998; 98DE-1004210.
XX
PA (BIO-) BIOSYN ARZNEIMITTEL GMBH.
XX
PI Morris P, Stiefel T, Voelter W, Welters P;
XX WP: 1999-445335/38.
XX DR N-PSDB; AA209114.
XX
PT Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
PS Claim 9; Fig 12B; 78pp; German.
XX
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
CC lymphokine-producing macrophages to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumor-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B5 protein.
XX
SQ Sequence 264 AA;
XX
Query Match 97.9%; Score 1390; DB 20; Length 264;
Best Local Similarity 98.1%; Pred. No. 1,46-129;
Matches 259; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 DDTYCSASEPTVRIVGRNGKRVVDVDDPHDQNOIQLPSPKSNDDPQMLWTIKKDGITIS 60
DB 1 DDTYCSASEPTVRIVGRNGKRVVDVDDPHDQNOIQLPSPKSNDDPQMLWTIKKDGITIS 60
QY 61 NSGCLTYGTAGTYVYVIMFDQNTAVREATTIWDNGITINPNSVLVLAASGIGKTTLT 120
DB 61 NSGCLTYGTAGTYVYVIMFDQNTAVREATTIWDNGITINPNSVLVLAASGIGKTTLT 120
QY 121 VQTLDTLGGWLAGNDTAPREVTYVGRDLQMSNGSVVETCDSSQKQGMALYED 180
DB 121 VQTLDTLGGWLAGNDTAPREVTYVGRDLQMSNGSVVETCDSSQKQGMALYED 180
QY 181 GSIRPKNOQCTNSGRDSVSTIVIVYSCASGSRWVFTNEGAILINKKQPMQVQA 240
DB 181 GSIRPKNOQCTNSGRDSVSTIVIVYSCASGSRWVFTNEGAILINKKQPMQVQA 240
QY 241 NPLERRIIYPATKXNOMLVPF 264
DB 241 NPLERRIIYPATKXNOMLVPF 264

ID AAY25996 standard; Protein; 265 AA.
XX
AC AAY25996;
XX
DT 18-OCT-1999 (first entry)
XX
DE Mistletoe lectin B5 variant protein fragment.
XX
KW Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.
XX
OS Viscum album.
XX
PN DEJ9804210-A1.
XX
RD 12-AUG-1999.
XX
PF 03-FEB-1998; 98DE-1004210.
XX
PR 03-FEB-1998; 98DE-1004210.
XX
PA (BIO-) BIOSYN ARZNEIMITTEL GMBH.
XX
PI Morris P, Stiefel T, Voelter W, Welters P;
XX WP: 1999-445335/38.
XX DR N-PSDB; AA209120.
XX
PT Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
PS Disclosure; Fig 18B; 78pp; German.
XX
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumor and immunostimulatory activity. The A-chain (MIA)
CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC fragments are used to treat uncontrolled cell growth (particularly of
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumor-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B5 protein.
XX
SQ Sequence 265 AA;
XX
Query Match 97.9%; Score 1390; DB 20; Length 265;
Best Local Similarity 98.1%; Pred. No. 1,46-129;
Matches 259; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 DDTYCSASEPTVRIVGRNGKRVVDVDDPHDQNOIQLPSPKSNDDPQMLWTIKKDGITIS 60
DB 1 DDTYCSASEPTVRIVGRNGKRVVDVDDPHDQNOIQLPSPKSNDDPQMLWTIKKDGITIS 60
QY 61 NSGCLTYGTAGTYVYVIMFDQNTAVREATTIWDNGITINPNSVLVLAASGIGKTTLT 120
DB 61 NSGCLTYGTAGTYVYVIMFDQNTAVREATTIWDNGITINPNSVLVLAASGIGKTTLT 120
QY 121 VQTLDTLGGWLAGNDTAPREVTYVGRDLQMSNGSVVETCDSSQKQGMALYED 180
DB 121 VQTLDTLGGWLAGNDTAPREVTYVGRDLQMSNGSVVETCDSSQKQGMALYED 180
QY 181 GSIRPKNOQCTNSGRDSVSTIVIVYSCASGSRWVFTNEGAILINKKQPMQVQA 240
DB 181 GSIRPKNOQCTNSGRDSVSTIVIVYSCASGSRWVFTNEGAILINKKQPMQVQA 240

KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform; lectin B3.
XX Viscum album.
XX DE19804210-A1.
XX 12-AUG-1999.
XX 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelker W, Welters P;
XX WPI, 1999-445335/38.
XX N-PSDB; AA209112.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Claim 9; Fig 10B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) stimulate immunity. (I) and its
XX lymphokine-producing macrophage associated antigen (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX of tumour-associated, bacterial or viral). The method allows production of
XX immune response, particularly to a co-administered antigen
XX (mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B3 protein.
XX Sequence 264 AA;
XX
XX Query Match 98.9%; Score 1404; DB 20; Length 265;
XX Identical Similarity 99.2%; Pred. No. 5,5e-131;
XX Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 DDTVCSASEPTVIRVGRNGRVVDNDPFDGNGIQOLWPSKSNPNQMTTKDGTIRS 60
DB 1 DDTVCSASEPTVIRVGRNGRVVDNDPFDGNGIQOLWPSKSNPNQMTTKDGTIRS 60
QY 61 NSGCLTYGYTGYVWIFPCNTAVREATTQIMNDGTTINPSSNVLAASSGKKTIT 120
DB 61 NSGCLTYGYTGYVWIFPCNTAVREATTQIMNDGTTINPSSNVLAASSGKKTIT 120
QY 121 VQTLDTLGGCHLANDTAPRETTVYGFRLQMSNGSVWVETDSSQNGKMALYGD 180
DB 121 VQTLDTLGGCHLANDTAPRETTVYGFRLQMSNGSVWVETDSSQNGKMALYGD 180
QY 181 GSIRPKXNODCLTSGRDSVSTVINIVSCGASGSGRWVFNKGALINLKGPAMDVAQA 240
DB 181 GSIRPKXNODCLTSGRDSVSTVINIVSCGASGSGRWVFNKGALINLKGPAMDVAQA 240
QY 241 NPKLRITITPATGKNGMWLPVF 264
DB 241 NPKLRITITPATGKNGMWLPVF 264
XX
XX RESULT 6
XX AAY25994
XX ID AAY25994 standard; Protein; 265 AA.
XX AC AAY25994;
XX XX
XX DT 18-OCT-1999 (first entry)

XX KW Mistletoe lectin B3 variant protein fragment.
XX KW Mistletoe lectin; antitumor; immunostimulant; A-chain; MA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophage; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B3.
XX Viscum album.
XX DE19804210-A1.
XX 12-AUG-1999.
XX 98DE-1004210.
XX 03-FEB-1998; 98DE-1004210.
XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelker W, Welters P;
XX WPI, 1999-445335/38.
XX N-PSDB; AA209118.
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX Disclosure; Fig 16B; 78pp; German.
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) stimulate immunity. (I) and its
XX lymphokine-producing macrophage associated antigen (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly
XX of tumour-associated, bacterial or viral). The method allows production of
XX immune response, particularly to a co-administered antigen
XX (mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B3 protein.
XX Sequence 265 AA;
XX
XX Query Match 98.9%; Score 1404; DB 20; Length 265;
XX Identical Similarity 99.2%; Pred. No. 5,6e-131;
XX Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 DDTVCSASEPTVIRVGRNGRVVDNDPFDGNGIQOLWPSKSNPNQMTTKDGTIRS 60
DB 1 DDTVCSASEPTVIRVGRNGRVVDNDPFDGNGIQOLWPSKSNPNQMTTKDGTIRS 60
QY 61 NSGCLTYGYTGYVWIFPCNTAVREATTQIMNDGTTINPSSNVLAASSGKKTIT 120
DB 61 NSGCLTYGYTGYVWIFPCNTAVREATTQIMNDGTTINPSSNVLAASSGKKTIT 120
QY 121 VQTLDTLGGCHLANDTAPRETTVYGFRLQMSNGSVWVETDSSQNGKMALYGD 180
DB 121 VQTLDTLGGCHLANDTAPRETTVYGFRLQMSNGSVWVETDSSQNGKMALYGD 180
QY 181 GSIRPKXNODCLTSGRDSVSTVINIVSCGASGSGRWVFNKGALINLKGPAMDVAQA 240
DB 181 GSIRPKXNODCLTSGRDSVSTVINIVSCGASGSGRWVFNKGALINLKGPAMDVAQA 240
QY 241 NPKLRITITPATGKNGMWLPVF 264
DB 241 NPKLRITITPATGKNGMWLPVF 264
XX
XX RESULT 7
XX AAY25990

PR	XX	03-FEB-1998;	98DE-1004210.
PA	XX	(BIO6-) BIOSYN ARZNEIMITTEL GMBH,	
PM	XX	Morris P., Stiefel T., Voelter W.,	Welters P;
PN	XX	WPI; 1999-44535/28.	
DR	XX	N-PSDB; AA209110.	
PT	XX	Preparation of mistletoe lectins in heterologous systems,	
PP	XX	particularly for use as anticancer agents and immunostimulants	
PS	XX	Claim 9; Fig 8B; 78pp; German.	
CC	XX	This invention describes a novel mistletoe lectin (I) and its fragments	
CC	XX	which have antitumor and immunostimulatory activity. The A-chain (MA)	
CC	XX	ribosome. Non-glycosylated forms of (I) activate immunity (II) and its	
CC	XX	fragments are used to treat uncontrolled cell growth (particularly	
CC	XX	cancers) and if they lack cytotoxicity, to increase the strength of the	
CC	XX	immune response, particularly to a co-administered antigen	
CC	XX	(tumour-associated, bacterial or viral). The method allows production of	
CC	XX	mistletoe lectin, and its individual chains, in many different isoforms	
CC	XX	and on a large scale, at any time of the year. Recombinant products are	
CC	XX	free from toxins present in natural mistletoe extracts. This sequence	
CC	XX	represents a fragment of a mistletoe lectin B protein.	
SQ	Sequence	264 AA;	
Q	Query Match:	98.9%; Score 1405; DB 20; Length 264;	
B	Best Local Similarity	99.2%; Pred. No. 4.4e-131;	
M	Matches	264; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
D	Db	1 DDTGSGSEPTTATVGNKGRVDTRDDDFDGNOLTMFSSSNMNDLTKRGGTIRS 60	
Q	Qy	61 NSGCTLTGTAGGYVYEDDNFAREATTWOIMDNSTINPNSNLYAAASGSKITLT 120	
D	Db	61 NSGCTLTGTGTGGYVYEDCNFAREATTWOIMDNSTINPNSNLYAAASGSKITLT 120	
Q	Qy	121 VOTLDYLGGMLAGNDPAETTYTGFRDLCSMSNGSWSWFSDSSONGSMALYCD 180	
D	Db	121 VOTLDYLGGMLAGNTNPHEFTYIGSRDLCSMSNGSWSWFETCSSONGSMALYCD 180	
Q	Qy	181 GSRRKONPGCGTSGSDSVATYTNVSCGASGSOPMTFNMGALINTKEAPANDVAQA 240	
D	Db	181 GSRRPONODCLTSGSDSVATYTNVSCGASGSOGWTFNMGALINTKEGLAMPDVAQA 240	
Q	Qy	241 NPLERLIITTEATKRPOMWTLPVF 264	
D	Db	241 NPLERLIITTEATKRPOMWTLPVF 264	
R	RESULT 4		
ID	AAZY5992	AAZY5992	
AC	AAZY5992;		
DT	18-OCT-1999	(first entry)	
XX			
XX	Mistletoe lectin B; variant protein fragment.		
XX	Mistletoe lectin; antitumor; immunostimulant; A-chain; MA; immunity;		
KW	lysozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;		
KM	lymphokine-producing macrophages; uncontrolled cell growth; treatment;		
XX	cancer; cytotoxicity; antigen; isoform; lectin B1.		
XX	Viscum album.		

PN	DEJ9804210~A1.
PD	12-AUG-1999.
FE	03-FEB-1998; 98DS-1004210.
EF	03-FEB-1998; 98DE-1004210.
PA	(BIO-) BIOSYN ARZENTMITTEL GMBH.
PX	Morris P, Stiefel T, Voelter W, Walters P,
P1	WPI; 1999-44535/78.
DR	N-PDBE; AA209116.
XX	
PT	Preparation of mistletoe lectins in heterologous systems,
PS	particularly for use as anticancer agents and immunostimulants
CC	Disclosure; Fig 1AB; 78pp; German.
CC	This invention describes a novel mistletoe lectin (I) and its fragments
CC	which have antitumour and immunostimulatory activity. The A-chain (MLA)
CC	of the mistletoe lectin binds to, and inactivates, the 28S subunit of
CC	r ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC	lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC	fragments are used to treat uncontrolled cell growth particularly of
CC	cancers and it they lack cytotoxicity, to increase the strength of the
CC	immune response against tumours. (I) can also be used to enhance production of
CC	(tumour-associated bacterial or viral) antigens and thus allow production of
CC	mistletoe lectin, and its individual chains, in many different isoforms
CC	and on a large scale, at any time of the year. Recombinant products are
CC	free from toxins present in natural mistletoe extracts. This sequence
CC	represents a fragment of a variant mistletoe lectin B1 protein.
XQ	
SQ	Sequence 265 AA:
Query Match	99.9%; Score 1405; DA 30; Length 265;
Blast local	Similarity 99.2%; Pred. No. 4.e-131;
Matches 262;	Conservative 0; Mismatches 2; Indels 0; Gaps 0
Oy	1 DVTGSASEFWYRVORGNKGVVADDDPHDNGOIQLPFSKNMPPQGLMTIKXDSTIS 60
Dd	1 DDTTGSASEFWYRVORGNKGVVADDDPHDNGOIQLPFSKNMPPQGLMTIKXDSTIS 60
Oy	61 NSGGCTTTGTGTCGYVFIFDCNTANREACTITNQINDGIIINPSSNVLVAASGIKKTLT 120
Dd	61 NSGGCTTTGTGTCGYVFIFDCNTANREACTITNQINDGIIINPSSNVLVAASGIKKTLT 120
Oy	121 VQLTYLTLSGWLAKNDRAPEVTVTFDELCMESNGSVWVEATDSSQGMALVGD 180
Dd	121 VQLTYLTLSGWLAKNDRAPEVTVTFDELCMESNGSVWVEATDSSQGMALVGD 180
Oy	181 GSIRPNMODQCLTSGRDSVSTIVNVCSGASGSGRWVPNEGAILINKGPAMDVQA 240
Dd	181 GSIRPNMODQCLTSGRDSVSTIVNVCSGASGSGRWVPNEGAILINKGPAMDVQA 240
Oy	241 NPLRRTIITPATCKNQMLPVF 264
Dd	241 NPLRRTIITPATCKNQMLPVF 264
RESULT 5	
AAZY5988	
ID	AAZY5988 standard; Proteoin; 264 AA.
XX	
XX	AAZY5988;
XX	
DT	18-OCT-1999 (first entry)
DE	
XX	Mistletoe lectin B1 protein fragment.
KM	Mistletoe lectin; antitumour; immunostimulant; A-chain; MLA; immunity;
KM	enzyme 28S subunit; non-cytotoxic; T-cell activation; immune response;

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Page 2

XX	XX	This invention describes a novel mistletoe lectin (I) and its fragments
XX	CC	which have antitumor and immunostimulatory activity. The A-chain (MA)
XX	CC	of the mistletoe lectin binds to, and inactivates T-cell and
XX	CC	ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX	CC	lymphokine-producing macrophages, so stimulate immunity. (II) and
XX	CC	fragments are used to treat uncontrolled cell growth (particularly
XX	CC	cancers) and if they elay cytotoxicity, to increase the strength of the
XX	CC	immune response, particularly to a co-administered antigen
XX	CC	(tumour-associated, bacterial or viral). The method of antigen production of
XX	CC	mistletoe lectin, and its use at the time of the year. Recombinant products are
XX	CC	free from toxins present in natural mistletoe extracts. This sequence
XX	CC	represents a fragment of a mistletoe lectin B4 protein.
XX	CC	Sequence 264 AA;
XX	CC	Query Match 100.0%; Score 1420; DB 20; Length 264;
XX	CC	Best Local Similarity 100.0%; Pred. No. 1.4e-13; Idents 0; Gaps 0;
XX	CC	Matches 264; Conservative 0; Mismatches 0;
Dy	1	DDVTGASAPPTVATVAGNENAVYVDSDPDHNDQIQMAPSKSNPNPMTITXDDTIRS 60
Dd	1	DDVTGSSEPTFATVAKGNKGVYDDEDDHDNQIQAMPKSNDDPQLWTKDGTIRS 60
Oy	61	NSSCLTYTGTVAGYYVMIPDCNAFARENTIWMIDNGTINPRSLVLAASSGGIKSTLT 120
Dd	61	NSGCTLYTGTVAGYYVIMIPDCNAFARENTIWMIDNGTINPRSLVLAASSGGIKSTLT 120
Oy	121	VQTLDYTIQGGMALANDVAPEVTIYGFRLCMESNSCSWETCDSSGONCKMALTD 180
Oy	121	VQTLDTYTIQGGMALANDVAPEVTIYGFRLCMESNSCSWETCDSSGONCKMALTD 180
Oy	181	GSRPPKNQOCICSPDSBVSSTVINVCSSGSSORWFNSCALINLKKGPANVDQA 240
Dd	181	GSIRPKNQOQCICSPDSBVSSTVINVCSSGSSORWFNSCALINLKKGPANVDQA 240
Oy	241	NPKLRRIITYPATGTPQPMLEPF 264
Dd	241	NPKLRRIITYPATGTPQPMLEPF 264
RESULT 2		
17	AAZY5995	Standard; Protein; 265 AA.
17	AAZY5995	Standard; Protein; 265 AA.
XX	XX	Mistletoe lectin B4 variant protein fragment.
XX	XX	Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;
XX	KM	libzyme 28S subunit; non-cytotoxic; antiproliferative; immune response;
XX	KM	lymphaemia; tumour; cancer; cytototoxicity; antigen; leucoderm; lectin B4.
XX	OS	Viscum album.
XX	XX	DELIS04210-AI.
XX	XX	DELIS04210-AI.
XX	XX	12-AUG-1999.
XX	XX	03-FEB-1998; 98DE-1004210.
XX	XX	03-FEB-1998; 98DE-1004210.
XX	PA	(BIOS-1) BIOSYN ARZNEIMITTEL GMBH.

PI	XX	PI	Morris P, Stiefel T, Voelker M, Welters P.
DR	XX	DR	WPI: 1999-44535/38.
DR	XX	DR	N-PSDB; AA029119.
PT	XX	PT	Preparation of mistletoe lectins in heterologous systems,
PT	XX	PT	particularly for use as anticancer agents and immunostimulants
PS	XX	PS	Disclosure; Fig 17B; 78pp; German.
XX	XX	XX	
CC	XX	CC	This invention describes a novel mistletoe lectin (I) and its fragments
CC	XX	CC	which have antitumor and immunostimulatory activity. The A-chain (WLA)
CC	XX	CC	of the mistletoe lectin binds to, and inactivates, the 2S6 subunit of
CC	XX	CC	lysochrome. Non-cytotoxic forms of (I) activate T-cell and (I) and its
CC	XX	CC	lysochrome-producing macrophages, stimulate T-cell growth. Particularly
CC	XX	CC	fragments are used to activate cytotoxicity to increase the strength of the
CC	XX	CC	immune response, particularly to a co-administered antigen
CC	XX	CC	(tumor-associated, bacterial or viral). The method allows production of
CC	XX	CC	mistletoe lectin, and its individual chains, in many different isoforms
CC	XX	CC	and on a large scale, at any time of the year. Recombinant products are
CC	XX	CC	free from toxins present in natural mistletoe extracts. This sequence
XX	XX	XX	represents a fragment of a variant mistletoe lectin 54 protein.
XX	XX	XX	
XX	XX	XX	Sequence 265 AA:
XX	XX	XX	
XX	XX	XX	Query Match 100.0%; Score 1420; DB 20; Length 265;
XX	XX	XX	Best Local Similarity 100.0%; Pred. No. 1,4e-12;
XX	XX	XX	Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	DB	QY	1 DVTGTSASEPVRVGRNKNRVEDDDPDNDGQIQLPKSNNDPNQMLTKDKGTIRS 60
DB	DB	DB	1 DVTGTSASEPVRVGRNKNRVEDDDPDNDGQIQLPKSNNDPNQMLTKDKGTIRS 60
QY	DB	QY	6: NSGCTTGTGTTGCTGTTAFOGTAATGATATGQINDGCTINPSTLVLAASGKGTILL 120
DB	DB	DB	6: NSGCTTGTGTTGCTGTTAFOGTAATGATATGQINDGCTINPSTLVLAASGKGTILL 120
QY	DB	QY	121 VQTLDTLTGGWGLKANDTAPREVTITGSRDLCKMSNGSWEVTECDSSQSNQGMALYD 180
DB	DB	DB	121 VQTLDTLTGGWGLKANDTAPREVTITGSRDLCKMSNGSWEVTECDSSQSNQGMALYD 180
QY	DB	QY	181 GSIRPKMONQDCTISRDSVSTINVCSSGASGSGKQVTFNEGLINTLKKPMMVQA 240
DB	DB	DB	181 GSIRPKMONQDCTISRDSVSTINVCSSGASGSGKQVTFNEGLINTLKKPMMVQA 240
QY	DB	QY	241 NPLKRIITVPKTRKPKQMLPVF 264
DB	DB	DB	241 NPLKRIITVPKTRKPKQMLPVF 264
XX	XX	XX	
XX	XX	XX	RESULT 3
XX	XX	XX	AAAY3596
XX	XX	XX	ID AAAY3596 standard; Protein; 264 AA.
XX	XX	XX	AAAY3596;
XX	XX	XX	18-OCT-1999 (first entry)
XX	XX	XX	Mistletoe lectin B1 protein fragment.
XX	XX	XX	Mistletoe lectin; antitumor; immunostimulant; A-chain; WLA; immutaly;
XX	XX	XX	lysozyme 2S6 subunit; non-cytotoxic; T-cell activation; immunolysis;
XX	XX	XX	lymphocyte-producing macrophages; oncogenic; antitumor growth; treatment;
XX	XX	XX	cancer; cytotoxicity; antigen; isoform; lectin B1.
XX	XX	XX	Viscum album.
XX	XX	XX	DE19804210-A1.
XX	XX	XX	12-AUG-1999.
XX	XX	XX	03-FEB-1998; 98DE-1004210.

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CM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 26.0664 Seconds

(without alignments)
1606.345 Million cell updates/sec

Title: US-09-601-667C-10

Sequence: 1 DDVTCASAPPTNATVGNQM.....RRIITPATGNQWLPVF 264

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Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100%
Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1420	100.0	264	20	AAV25989	Mistletoe lectin B
2	1420	100.0	265	20	AAV25995	Mistletoe lectin B
3	1405	98.9	264	20	AAV25986	Mistletoe lectin B
4	1405	98.9	265	20	AAV25992	Mistletoe lectin B
5	1404	98.9	264	20	AAV25988	Mistletoe lectin B
6	1404	98.9	265	20	AAV25994	Mistletoe lectin B
7	1390	97.9	264	20	AAV25990	Mistletoe lectin B
8	1390	97.9	265	20	AAV25996	Mistletoe lectin B
9	1371	96.5	264	20	AAV25987	Mistletoe lectin B

10	1371	96.5	265	20	AAV25993	Mistletoe lectin B
11	1326.5	93.4	263	20	AAV25985	Mistletoe lectin B
12	1326.5	93.4	264	20	AAV25991	Mistletoe lectin B
13	1326.5	93.4	511	20	AAV25979	Mistletoe lectin I
14	1326.5	93.0	512	20	AAV25982	Mistletoe lectin I
15	1320.5	93.0	263	19	AAV64662	Prepro mistletoe var
16	1320.5	93.0	264	18	AAV10023	Mistletoe rml B-cha
17	1320.5	93.0	264	20	AAV20126	Mistletoe rml B-cha
18	1320.5	93.0	564	18	AAV10021	Mistletoe lectin A
19	1320.5	93.0	564	20	AAV00127	Mistletoe lectin A
20	1320.5	93.0	564	20	AAV25978	Mistletoe lectin B
21	1289	90.8	264	20	AAV25972	Mistletoe lectin B
22	1289	90.8	264	20	AAV25975	Mistletoe lectin B
23	1289	90.8	533	20	AAV25970	Mistletoe lectin P
24	1289	90.8	533	20	AAV25973	Mistletoe lectin P
25	1289	90.8	533	20	AAV25976	Mistletoe lectin P
26	1246.5	87.8	267	19	AAV64667	Mistletoe rmlB pro
27	1142.5	78.3	263	22	AAV67094	B-chain isoform fo
28	1078.5	76.0	263	22	AAV67095	B-chain isoform fo
29	1078.5	76.0	511	22	AAV67096	B-chain isoform fo
30	982	63.6	511	22	AAV67097	B-chain isoform fo
31	982	63.6	511	22	AAV67098	B-chain isoform fo
32	901.5	63.5	565	22	AAV67099	B-chain isoform fo
33	901.5	63.5	565	22	AAV67100	B-chain isoform fo
34	899.5	63.3	565	22	AAV67101	B-chain isoform fo
35	899.5	63.3	574	8	AAV70325	Sequence of ricin
36	899.5	63.3	574	10	AAV70325	Sequence of ricin
37	899.5	63.3	576	18	AAV25787	Castor bean ricin
38	899.5	63.3	576	21	AAV25992	Castor bean ricin
39	899.5	63.3	576	21	AAV25992	Castor bean ricin
40	899.5	63.3	576	22	AAV25992	Castor bean ricin
41	893.5	63.3	576	22	AAV25992	Castor bean ricin
42	893.5	63.3	576	22	AAV25992	Castor bean ricin
43	893.5	63.3	576	22	AAV25992	Castor bean ricin
44	890.5	62.9	262	9	AAV28965	R chain of ricin D
45	879.5	61.9	251	9	AAV28965	R chain of ricin D

ALIGNMENTS

AAV25989	RESULT 1
AAV25989	AAV25989 standard; Protein; 264 Aa.
AAV25989	18-OCT-1999 (first entry)
AAV25989	Mistletoe lectin B4 protein fragment.
AAV25989	Mistletoe lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
AAV25989	lymphokine-288 subunit; non-cytotoxic; T-cell activation; immune response;
AAV25989	lymphokine-producing macrophage; uncontrolled cell growth; treatment;
AAV25989	cancer; cytotoxicity; antigen; isoform; lectin B4.
AAV25989	Viscum album.
AAV25989	DEL9804210-A1.
AAV25989	12-AUG-1999.
AAV25989	03-FEB-1998; 98DE-1004210.
AAV25989	03-FEB-1998; 98DE-1004210.
AAV25989	(BIOS-) BIOSYN ARZEMETITTEL GMBH.
AAV25989	Morris P, Stiefel T, Voelter W, Welters P;
AAV25989	WPI; 1999-445335/38.
AAV25989	N-PSDB; AA209113.

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Cy 240 ANPELRRIIYPATGKPNQWMLPVF 264
Db 549 SDPSLQCIILWSTGNPNQWFTTF 573

Search completed: December 11, 2003, 14:01:03
Job time : 20.3487 secs

Query Match 52.4%; Score 744.5; DB 10; Length 382;
Best Local Similarity 54.3%; Pred. No. 9,9e-55;
Matches 139; Conservative 40; Mismatches 76; Indels 1; Gaps 1;
QY 9 EPTVRIYGRNRRVYDDPHDQNOQLMRSKSNNDPQNLTKIKDGTIRSNQ 68
DB 128 EPTVRIYGRDQVSDVSDVSEAYNNGNPILMKCCQQLKSKDITIKSKKCLVY 187
QY 69 GTTAGVYVIMPCNTAVREATTIWOIWDNGTIIINFRSNLYLAASGIGKTLVQL 128
DB 188 GIDPKNVMTYDCKSAVEATWEIWDNGTIIINFKSALYLSASSAMGCKLTQKRDYEM 247
QY 129 GQGMAGNTAPREVITYGRDLCMESNGSVMWETCSSQKNGKALYGDGSIIRPKON 188
DB 248 RQMRKNDIISFTYSINGSDCKMHSNMALDCKRNKEQ-QMALIPDSISIRPVN 306
QY 189 QDQCLTSGRDSVSTVINVSQSGASQSPVTFNEGATLAKKGFANDPQAPLRLI 248
DB 307 TNNCLTSKDHKQSGTIVLMGCSNMALQSWTFKNDQSYVLVDPMWMDYKSDPSLKOII 366
QY 249 IYPATGKPNQMLPVE 264
DB 367 LWPYTKENQIWLTLF 382
RESULT 14
QWME9 PRELIMINARY; PRT; 547 AA.
AC QWME9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Preproagglutinin (EC 3.2.2.22) (RNA N-glycosidase).
GN Agg.
OS Abrys precatorius (Indian licorice) (Crab's eye).
OC Baktaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
OC U. rosaceae; Rubiales; Rubaceae; Fepililomolidae; Adreace; Abrys.
OX NCBI_TaxID=35976;
RN [1]_TaxID=35976;
RP SEQUENCE FROM N.A.
RX MEDLINE=20102702; PubMed=10636890;
RA Liu C.L., Teal C.C., Lin S.C., Wang L.I., Hsu C.I., Hwang M.J.,
LAH C.Y.,
RT "Primary Structure and Function Analysis of the Abrys precatorius
RT Agglutinin A Chain by Site-directed Mutagenesis: Pro199 of Amphiphilic
RT Alpha-Helix H Impacts Protein Synthesis Inhibitory Activity.";
RT J. Biol. Chem. 273(18):19011-19011(2000).
CC -1- CATALYTIC ACTIVITY: ENDODIOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL: AF190173; AAF2809.1; .
DR HSSP: P11440; IABR.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN_2.
DR PROSITE: PS00225; RICIN_B_LECTIN; 2.
DR PROSITE: PS00225; SHIGARICIN; 1.
KW Hydroxylase; Toxin.
SQ SEQUENCE 547 AA; 61246 MW; 355A32C0354A1BD CRC64;

Query Match 52.4%; Score 744; DB 10; Length 547;
Best Local Similarity 54.0%; Pred. No. 1.7e-54;
Matches 141; Conservative 39; Mismatches 79; Indels 2; Gaps 2;
QY 5 CSAS-EPTVRIYGRNRRVYDDPHDQNOQLMRSKSNNDPQNLTKIKDGTIRSNQ 63
DB 288 CSAS-EPTVRIYGRNRRVYDDPHDQNOQLMRSKSNNDPQNLTKIKDGTIRSNQ 347

QY 64 CLITGYTAGVYVIMPCNTAVREATTIWOIWDNGTIIINFRSNLYLAASGIGKTLVQL 123
DB 348 CLITGYTAGVYVIMPCNTAVREATTIWOIWDNGTIIINFRSNLYLAASGIGKTLVQL 407
QY 124 LDVTLQGMALANDAPREVITYGRDLCMESNGSVMWETCSSQKNGKALYGDGSI 183
DB 408 NQYMRQGMRTSNDISFTYSINGSDCKMHSNMALDCKRNKEQ-QMALIPDSISIRPVN 466
QY 184 RQMRKNDIISFTYSINGSDCKMHSNMALDCKRNKEQ-QMALIPDSISIRPVN 243
DB 467 RQMRKNDIISFTYSINGSDCKMHSNMALDCKRNKEQ-QMALIPDSISIRPVN 526
QY 244 LRRIIYYPATGKPNQMLPVE 264
DB 527 LKQIIIMPYTKENQIWLTLF 547
RESULT 15
QWME9 PRELIMINARY; PRT; 573 AA.
AC QWME9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribosome-inactivating protein IPak (EC 3.2.2.22) (RNA N-glycosidase) (Fragment).
GN LECTINAR.
OS Itis hollandica (Dutch iris).
OC Baktaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
OX NCBI_TaxID=35976;
RN [1]_TaxID=35976;
RP SEQUENCE FROM N.A.
RX Van Damme E.J.M., Peumans W.J.,
RT "Itis (Itis hollandica var. Professor Blaauw) plants express both type
RT 1 and type 2 ribosome-inactivating proteins in bulb tissue.";
RT Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDODIOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL: AF265990.1; AF26599.1; .
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SM00458; RICIN_2.
DR PROSITE: PS00221; RICIN_B_LECTIN; 2.
DR PROSITE: PS00225; SHIGARICIN; 1.
KW Hydroxylase; Toxin.
SQ SEQUENCE 573 AA; 63759 MW; 141A3B9AEC04F5C CRC64;
Query Match 47.6%; Score 676.5; DB 10; Length 573;
Best Local Similarity 50.2%; Pred. No. 9e-49;
Matches 133; Conservative 39; Mismatches 90; Indels 3; Gaps 3;
QY 1 DDTVCAEPTVRIYGRNRRVYDDPHDQNOQLMRSKSNNDPQNLTKIKDGTIRSNQ 60
DB 311 EDDTCASEPTVRIYGRNRRVYDDPHDQNOQLMRSKSNNDPQNLTKIKDGTIRSNQ 370
QY 61 NSGCLITGYTAGVYVIMPCNTAVREATTIWOIWDNGTIIINFRSNLYLAASGIGKTL 120
DB 371 NSGCLITGYTAGVYVIMPCNTAVREATTIWOIWDNGTIIINFRSNLYLAASGIGKTL 429
QY 121 VQTLDTLQGMALANDAPREVITYGRDLCMESNGSVMWETCSSQKNGKALYGDGSI 179
DB 430 VQTLDTLQGMALANDAPREVITYGRDLCMESNGSVMWETCSSQKNGKALYGDGSI 488
QY 180 DGSIRPNQDQCLTSGRDSVSTVINVSQSGASQSPVTFNEGATLAKKGFANDPQAPLRLI 239
DB 489 DGSIRPNQDQCLTSGRDSVSTVINVSQSGASQSPVTFNEGATLAKKGFANDPQAPLRLI 548

[illegible]

	DR	Pfam, EP00652; Ricin B lectin; 6
	DR	Fam, EF00161; RIP; 1
	DR	PRINTS; PR00936; RCTGARGCIN.
	DR	PROSITE; PS00282; RCTGARGCIN.
	DR	PROSITE; PS00281; RICIN B LECTIN; 2.
	DR	PROSITE; PS00275; SHIGA_RICIN; 1.
	KM	Hydrolase; Toxin.
	FT	NON_TER
	PT	TER
	SEQUENCE	528 AA; 5870 MW; 62ZD42B8FPE60F9 CRC64;
	Query Match	53.4%; Score 759; DB 10; Length 528;
	Blast Local Similarity	54.8%; Pctd No 1; E-55;
	Matches 143;	Conservative 43; Miscellaneous 73; Indels 2; Gaps 2;
Oy		
Dd		
Oy	5	CNSA-EPTVIRVGNGKGEVVDDEPDDPSNOGLCMFPSSNNKDPNOLTKTSDGTIFSNKS 63
Dd	269	CSAREPEYRVLGGSDMCVVVDGDHGNRNRIAMCKDLLEBNOLWTLSKLSTIFSNKG 348
Oy	64	CLTPVTGAGYYIVIPDCNPAVEANITWIDNGTIIIPSASNLVAASSQIKGTLTVTC 123
Dd	339	CLTEGAGAEENVALVIDCTSAVKETIEIIMWGNTIIIMPASLVASSSSMGSLTVCI 388
Oy	124	LDPYLQGGLANDTPAPELTIYGPRDIICMSNGSVVATCPSSGSGKKALVYSCSI 183
Dd	389	NELIWRGMRUNNSTPFSPVISISGYSDLCMAQSWSVLADCNKKKEQ-QWALYTDSGI 447
Oy	184	RPKNQDOQLCTGSADSVATYNIYNISVCGSSGSGQWFNFSGAILMLKKEPADVQAAPK 243
Dd	448	RSVNQTNNLTCLKSKHQKASPVLVACSMGASRWMLFNDQDISYSLYDDMVAVKSDPS 507
Oy	244	LRRLITIVANGNKMTLPF 264
Dd	508	LKQILMPFLVIGRPQNLITLF 528
	RESULT 13	
ID	OS8A43	PRELIMINARY; PAT; 382 AA.
AC	OS8A43;	
DT	01-JUN-2002	(TREMBLrel_21, Created)
DT	01-JUN-2002	(TREMBLrel_21, Last sequence update)
DT	01-MAR-2003	(TREMBLrel_23, Last annotation update)
DB	Ablin	18cortom G (EC 5.1.3.22) [RNA N-glycosylase]
OS	Ablin	18cortom G (EC 5.1.3.22) [RNA N-glycosylase]
OC	Ablin	18cortom G (EC 5.1.3.22) [RNA N-glycosylase]
CC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
CC	eumetazoa; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;	
CC	spermatids I; Fabales; Fabaceae; Papilionoideae; Abraceae; Abrus.	
NCBI	TaxId=816;	
XP	(1)	
RC	SEQUENCE FROM N.A.	
RC	TISSUE=leaf;	
RA	CDOK J.P., Roberts L.M., Lord M.;	
RA	New isolated cDNA from the leaf; G.	
RA	SHARP ET AL 2002 TO THE EMBL/genbank/DBJ databases.	
CC	- SPECIFIC ACTIVITY. ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE	
CC	SPECIFIC ADENSING ON THE 28S RNA.	
CC	-1. SMIPLARTY: BEONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
CC	EMBL: A479626; AL77434.1; -	
DR	Interpro; IPRO00773; Ricin B lectin.	
DR	Interpro; IPRO001574; RIP.	
DR	Pfam; PF00652; Ricin B lectin; 6.	
DR	Pfam; PF00161; RIP; 1.	
DR	SMART; SMART58; RICIN_B_LECTIN; 2.	
DR	SMART; SMART58; RICIN_B_LECTIN; 2.	
DR	PROSITE; PS00281; RICIN B LECTIN; 2.	
DR	PROSITE; PS00275; SHIGA_RICIN; 1.	
KW	Hydrolyase; Toxin.	
FT	NON TER	1
FT	CHAIN	>105
FT	CHAIN	116 >382
FT	NON TER	382
SEQUENCE	382 AA; 42743 MW; B06AB341B13AD2EE CRC64;	

Db 496 GSIRPHODRCLSTIDNHSQSIIISCSFSBSQRMVFMNDOTLNLKNGLVMDVKG 555
Qy 240 ANPKRLRIIIPATGKPMQWMLPV 263
Db 556 SNPSLHQIILIPATGKPMQWMLPV 579

RESULT 9

Q94BM3 PRELIMINARY; PRT; 580 AA.
ID Q94BM3
DT 01-MAR-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 22, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin III precursor
DE (EC 3.2.2.22) (RNA N-glycosidase)
OS Cinnamomum camphora (Camphor tree)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
genes encoding cinnamomin proteins and study of their expression
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL: AY039803; AK82460.1; -
DR Interpro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR PRINTS: PR00161; RIP; 1.
DR SMART: SM00396; SHIGARICIN.
DR PROSITE: PS02311; R1CN_2.
DR PROSITE: PS02311; R1CN_2.
KW Hydroxylase; Signal; Toxin.
FT SIGNAL 33
FT CHAIN 1 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN III.
SQ SEQUENCE 580 AA; 64421 MW; 940D10E01E7F5858 CRC64;

Query Match 60.3%; Score 856; DB 10; Length 580;
Best Local Similarity 62.1%; Pseq. No. 6,5e-64;
Matches 164; Conservative 33; Mismatches 65; Indels 2; Gaps 2;

Qy 1 DDTVCASBPYRIVGSGKRVDRDDPDHNGIOLMPSKSNNDPQWLTIRKGTIS 60
Db 317 NDDTCADPEPTVATSGNGLCVVRDGVKNNPNPIOLMPCQNSDVNOLTLRRDGAIS 376
Qy 61 NSCLITVGTAGVYVWIPDCNTAVRENTIWDNDGTTINPESNLVLAASGICGTLT 120
Db 377 NCKLTNGVSAGDYVWIDCTPTVAISIVQPMANGTIINPQALVLAASGNSPRTTLT 436
Qy 121 VGLDVTLAGQWLAGNDTAPREVTIYGFDDICNSGSGVWVETCSQKQKQKALYGD 180
Db 437 VADLTYSRQSLMANNTEPTVATSGNGLCVVRDGVKNNPNPIOLMPCQNSDVNOLTLRRDGAIS 495
Qy 181 GSIRPKQND-CLTSRGSADVTVINVASCGASGSGQWFTNBEALILTKKGPAMDVA 239
Db 496 GSIRPHODRCLSTIDNHSQSIIISCSFSBSQRMVFMNDOTLNLKNGLVMDVKG 555
Qy 240 ANPKRLRIIIPATGKPMQWMLPV 263
Db 556 SNPSLHQIILIPATGKPMQWMLPV 579

RESULT 10
Q9PV22 PRELIMINARY; PRT; 549 AA.

AC Q9PV22;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (RNA
N-glycosidase) (Fragment).
OS Cinnamomum camphora (Camphor tree)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Xie L., Liu W.-Y., Wang E.-D.;
RT Molecular cloning of cinnamomin A-, B-chain and the expression,
purification, characterization and mutagenesis of the A-chain.
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RL -1- CATALYTIC ACTIVITY: ENDORHYDOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL: A023548; A456397.2; -
DR Interpro: IPR000772; Ricin_B_lectin.
DR Pfam: PF00652; Ricin_B_lectin; 5.
DR PRINTS: PR00161; RIP; 1.
DR SMART: SM00458; R1CN_2.
DR PROSITE: PS02311; R1CN_2.
DR PROSITE: PS02311; R1CN_2.
KW Hydroxylase; Toxin.
FT NON-TER 1
FT SEQUENCE 549 AA; 60648 MW; 02607E607C044B0 CRC64;
Query Match 57.6%; Score 817.5; DB 10; Length 549;
Best Local Similarity 59.2%; Pseq. No. 1.1e-60;
Matches 177; Conservative 32; Mismatches 93; Indels 3; Gaps 2;

Qy 1 DDTVCASBPYRIVGSGKRVDRDDPDHNGIOLMPSKSNNDPQWLTIRKGTIS 60
Db 285 NDDTCADPEPTVATSGNGLCVVRDGVKNNPNPIOLMPCQNSDVNOLTLRRDGAIS 344
Qy 61 NSCLITVGTAGVYVWIPDCNTAVRENTIWDNDGTTINPESNLVLAASGICGTLT 120
Db 345 NCKLTNGVSAGDYVWIDCTPTVAISIVQPMANGTIINPQALVLAASGNSPRTTLT 404
Qy 121 VGLDVTLAGQWLAGNDTAPREVTIYGFDDICNSGSGVWVETCSQKQKQKALYGD 180
Db 405 VQNTIYASRQSLMANNTEPTVATSGNGLCVVRDGVKNNPNPIOLMPCQNSDVNOLTLRRDGAIS 463
Qy 181 GSIRPKQND-CLTSRGSADVTVINVASCGASGSGQWFTNBEALILTKKGPAMDVA 238
Db 465 GSIRPHODRCLSTIDNHSQSIIISCSFSBSQRMVFMNDOTLNLKNGLVMDVKG 523
Qy 239 ANPKRLRIIIPATGKPMQWMLPV 263
Db 524 SNPSLHQIILIPATGKPMQWMLPV 548

RESULT 11
Q94BM3 PRELIMINARY; PRT; 581 AA.
ID Q94BM3
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 22, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin I precursor
DE (EC 3.2.2.22) (RNA N-glycosidase)
OS Cinnamomum camphora (Camphor tree)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;

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DR PFAM: PF00161, RIP, 1.
DR PRINTS: PR00366, SHIGABICIN.
DR SMART: SM00459, RIGIN, 2.
DR PROSITE: PS00333, RIGIN_ELECTIN, 2.
DR PROSITE: PS00335, SHIGABICIN, 1.
DR PROSITE: PS00336, SHIGABICIN_2, 1.
KM Hydrolase, Poziti.
SQ NON TER.
SQ SEQUENCE 541 AA; 60281 NW; 2B7BCDEF1F2B9D3 CRC64;
Query Match 63.5%; SCORE 501.5; DB 10; Length 541;
Best local Similarity 63.3%; Freq. No. 8.6e+68;
Matches 165; Conservative 33; Mismatches 61; Indels 1;
Gaps 1

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QY	5	CSASFEYVAVRANRANVAVDDDFDNOIOIOMNKSINPNQIMTIKDDGTISNSGC	64
Db	283	CMPPPIYRVARSGNLCVDYDGRPFNNMNLDMCKSGVLAQMLTKLKDWTINSXGC	342
QY	65	LTYYVYAGVYVMIPODNTAVRALTWIDNGTINPSSVLVLAASGIGKFTITVOTL	124
Db	343	LTYYGAGLVADMDIAPRATITKRLTWMDNGTINPSSVLVLAASGIGKFTITVOTN	402
QY	125	DTLGGAGLVADMDIAPRATITKRLTWMDNGTINPSSVLVLAASGIGKFTITVOTSR	184
Db	403	IYVSGVLPITNNQIPVITIVLVSGLTQANSGVWIEDC-SSEKAGQMLVADGSR	
QY	185	PRONDOCLTSPGSPVATVIVYVCSGASGSGRWTFNFGALINLKKPMADVDAAPCL	244
Db	463	POONDNDLMSINRETFVYVILISGSPASGGRWTFNFGTILNLTSGVLVDRSPSL	521
QY	245	RRILTYPATKRNQMLVFE	264
Db	522	KQILTYPATKRNQMLVFE	541

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RESULT 7
ID Q41143      PRELIMINARY;      PRT: 263 AA.
AC Q41143
DT 01-NOV-1996 (TREMBLREL_01, Created)
DT 01-NOV-1996 (TREMBLREL_01, Last sequence update)
DT 01-MAR-2003 (TREMBLREL_23, Last annotation update)
DE Ricin B beta chain (Fragment) .
LN RICIN B BETA CHAIN.
OS Ricinus communis (Castor bean) .
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosoid I; Malpighiales; Euphorbiaceae; Ricinus.
OC NCBI_TaxId=3988;
LN (1)
RE SEQUENCE FROM N.A.
RT Latin S.F., Murray S.E., Halling A.C., Halling K.C., Thakaretna N.,
RT Leach G.L., Holscher J.L., Weaver R.F., Ricin E. a hybrid ricin-Ricinus
RT "C" gene from Ricinus communis.
RT Characterization of the ricin gene from the castor plant Ricinus communis."
RT Plant Mol Biol 19:287-296(1997).
RT EMBL: M17631; AAA63506.1; --
DR HSP; P02879; 2AA1.
DR Interpro: IRP000772; Ricin B lectin.
DR Interpro: IRP001400; Somatoctropin.
DR Pfam: PF00652; Ricin B lectin. 6.
DR SMART: SM00458; RICIN_2.
DR PROSITE: PS00321; RICIN B LECTIN; 2.
DR PROSITE: PS00338; SOMATOCTROPIN_2; 1.
FT NON TER
FT 1
SO SEQUENCE 263 AA; 29134 MW; AAB890FD1DD1E144 CRC64;

Query Match      60.8%; Score 864; DB 10; Length 263;
Best Local Similarity 60.9%; Freq. No. 5,1e-65;
Matches 159; Conservative 37; Mismatches 63; Indels 2; Gaps 2

5 CASABP7Y1YV9K9N9R9DD9F9Q9N9I9Q9E9K9S9N9P9Q9L9T9D9G9T9R9N9S9C 64

```

D5 CAGDDEPVTIVAGRGACVDRFGRHNGAGATQMPCKSRNDANQMLPLCKRNIJNSJNAC 63
QY 65 LITTTGTYAGVWVIMIPICNTLVREATIIMQIKONGTIIINRBNLVLASGATGTLTMYTL 124
D5 66 LITTTGTYAGVWVIMIPICNTLVREATIIMQIKONGTIIINRBNLVLASGATGTLTMYTL 124
D5 64 LITTTGTYAGVWVIMIPICNTLVREATIIMQIKONGTIIINRBNLVLASGATGTLTMYTL 123
QY 125 DTITAGGCMANQDPLREPLVITGGPDLCEMNGSVWTECCSSGCKNOCKNALYKXGGSIR 184
D5 124 IYASQGMPLFNPNQPFYITITVGLGMCICLQNSGSKWLEDC TSEKBEQWMLVLAQGSIR 182
QY 185 FKQNDQDCTSGSDSYSTVINIVSCSGASQSQRWFTYEGALINIKFKGPDVAQAPK X 243
D5 183 PQQNDQDCTITDANIKGTVYKILISGPIVSQSQRWFKQDGTILNGLVLDVSRDPS 242
QY 244 LRRILIVATKQNMQLPVF 264
D5 243 LKQILIVATKQNMQLPVF 263

	RESULT 8	
Q94BW4	PRELIMINARY:	EFT, 530 AA.
AJ064B4		
DJ064B4		
DT 01-DEC-2001 (TrEMBLrel_19)	(Created)	
DT 01-DEC-2001 (TrEMBLrel_19)	Last sequence update)	
DT 01-MAR-2003 (TrEMBLrel_23)	Last annotation update)	
DE type 2 ribosome-inactivating protein cinnamomii precursor		
DS R.3.0.2.122) Cinnamomi (Cinnamomum)		
OS Cinnamomi (Cinnamomum)		
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.		
OX NCBI_TaxID=33429;		
EN [1]		

RT	Molecular cloning of three type 2 RIP (ribosome-inactivating protein)	
RT	R gene encoding cinnamomoln proteins and study of their expression	
RT	patterns."	
RT	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.	
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE	
CC	SPECIFIC ADENOSINE ON THE 28S RRNA.	
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN	
DR	EMBL, AY039802; AKK82459.1	
DR	Interpro; IPR000572; Rctn_B_lectin.	
DR	Interpro; IPR000572; Rctn_B_lectin.	
DR	Pfam; PF000652; Rctn_B_lectin; 6.	
DR	Pfam; PF00161; Rctn_B_lectin; 1.	
DR	PRINTS; PR00386; SHSARACTIN.	
DR	SMART; SM00458; RCTN; 2.	
DR	PROSITE; PS00231; RCTN_B_LECTIN; 2.	
DR	HYDROLASE; Signal; 32xnm.	
FT	33 580 POTENTIAL	
FT	CHAIN TYPE 2 RIBOSOME-INACTIVATING PROTEIN	
FT	CINNAMOMIN II.	
SEQUENCE	580 AA; 64265 MW; 3784289ECDCRCHF CKG64;	
Query Match	60.8%; Score 863; DB 10; Length 590;	
Best Local Similarity	62.5%; Pred. No. 1.7E-64;	
Matches 165; Conservative 32; Mismatches 65; Indels 2; Gaps 2		
Qy	1	DVVTGSASEFTYRIVGRNGKRVVDVDDDFDQNOILMPFSKSNINPQNLTIKEDGTIRS 60
Db	317	NDPTCAPEETIRASGRGCLVDYDGRKNNGNPILPCKQNSVQMLTIRDRGTIRS 376
Qy	61	NSGCTTYGTYAGYVWIFDCNTAVREARTIQWIDNGTIIIPESNLVLAASGKIGKTLT 120
Db	377	NSGCTLTNGSGASGYWMLYDCEPFLYASWFWANGTIIINPQSLVLSASGSPRTILN 436
Qy	121	VQTLDTYLLQALNADIAPREVITVGFEDKLQMSNGSGSWETVCDSSQGNCKMALYD 180
Db	437	VQMTIKRQGLNGLNNEPSTVITVGFEDKQALQMGDMKMMVVECESSFEDCKMALYD 495
Qy	181	GIIRPKRQDQDTSVGRSGDSCGSGGQVQVTRTARITIKKXGANDVNO 239

[illegible]

RA	Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-Y., Kim J.-B.,
RA	Do M.-S., Song S.K.,
RT	"cDNA cloning and sequence analysis of the lectin genes of the Korean
RT	mistletoe (<i>Viscum album coloratum</i>)."
RL	1991. Cells 12:215-220(12001).
AP	SEQUENCE FROM N.A.
RA	Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-Y., Kim J.-B.,
RA	Do M.-S., Song S.K.,
EMBL	Submitted (May 2002) to the EMBL/GenBank/DBJ databases.
DR	InterPro: IPR000772; Rctn_B_lectin.
DR	Pfam: PF00652; Rctn_B_lectin; 5.
DR	SMART: SMD0453; Rctn_B_lectin; 1.
DR	RPS274; RS0021; Rctn_B_lectin; 2.
FT	NON TER
FT	NON TER
SO	SEQUENCE 266 AA; 29537 MW; 4A5147C37B9AC73 CRC64;
Qy	Query Match 69.9%; Score 992; DB 10; Length 266;
Bt	Best Local Similarity 69.2%; Pval: Med: No. e-le-76;
Mt	Matches 184; Conservative 31; Mismatches 47; Indels 4; Gaps 2
Dd	1 DDITCSAPPFRATIGNGKGRVDPPDHPHQGLOIPKSKNDPNCITIKGGCTRS 50
Dd	1 DVDTCSPPFVRFGRIEGLCDPDDPHGSILQMPCKSNQIQMTIARDCTTRS 60
Qy	61 NSSCLTGYGYPGVVYMPCONTNREATITQLWDGFIINPSNLVL--AASSGIKT 117
Dd	61 NSRCLTYGYMGSYIMLYCNCRNGDMTLQIRNGNGLLPSPSWITCFESGRSTGT 120
Qy	118 TLTVQVLTLYTAQGMLAGNDTPAREVTITYGFRLCHESNGSGSYWEFCDSQKQKAL 177
Dd	121 FPLDLISLSAQGMADANAFKSVITIVYGSCASAGSGAMFTTBETALINKKGADVD 179
Qy	178 YGDSGPDPNNQDCITSGGSDSYVINIVGSCASAGSGAMFTTBETALINKKGADVD 227
Dd	180 YGSGSIPEPYRDDCLTSQSDSRMYNVNFSCYSGSFPGRWFTFKGAILNKLRLLANDV 239
Qy	238 AQANKPKLFRIIIIVPATRGPNQMLPFV 263
Dd	240 AASSNSPLRFRIIIFSVTGAKPMQMLPFV 265
ID	QALL74 PRELIMINARY; PRF; 541 AA.
QC	QALL74
DT	01-NOV-1996 (TREMELZel_01_Created)
DT	01-NOV-1996 (TREMELZel_01_Last annotation update)
DT	01-MAR-2003 (TREMELZel_23_Last annotation update)
DR	Protein A chain (EC 3.2.2.22) (RNA-N-glycosidase)
DR	(Fragment.)
OC	Polysaccharide (Gaefer bean)
OC	Eubacteriales; Viridiales; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliopsida; eudicotyledons; Core eudicots; Rosidae;
OC	eucrobiales I; Malpighiales; Euphorbiaceae; Ricinus.
NCBI	NCBI TaxId=3987;
AN	[1]
AN	SEQUENCE FROM N.A.
EX	MEDLINE=9238577; PubMed=1633311;
EX	Kocherle L.M., Tregear U.C.H., Lord U.M.,
RL	Taxonomical Diagram Pub. 7:81-97(1992).
CC	-1- ARYLACTIC ACTIVITY. ENOCHORDYOSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC	SPECIFIC ADENOSINE ON THE 28S RNA.
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR	EMBL: S40366; AB22582.1; -.
DR	HSSP: P02879; IRB6.
DR	InterPro: IPR000772; Rctn_B_lectin.
DR	InterPro: IPR001574; RfP.
DR	InterPro: IPR001400; Semotocipin.
DR	Pfam: PF00652; Rctn_B_lectin; 6.

Matches 245; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
QY 1 DDTVCASEPTVRIYVGNKGVVVDVDDPHDNOIQIOWPSKSNNDPNQWTIKEDGTIRS 60
DB 269 DDTVCASEPTVRIYVGNKGVVVDVDDPHDNOIQIOWPSKSNNDPNQWTIKEDGTIRS 328
QY 61 NSGCLTYGTAGVYVMEFDNINAVKXATITWQIMDNGITINPSNVLAAASGIGKTT 120
DB 329 NSGCLTYGTAGVYVMEFDNINAVKXATITWQIMDNGITINPSNVLAAASGIGKTT 368
QY 121 VQTLDTYLGQGLAGNDTAPREVTIYGFRLQMSNGSVWETCVSGSQNQ-KMALYGD 180
DB 389 VQTLDTYLGQGLAGNDTAPREVTIYGFRLQMSNGSVWETCVSGSQNQ-KMALYGD 447
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCASGSGQRFVFNAGAILNLKGPAMDVAQA 240
DB 448 GSIRPKONODCLTSGRDSVSTVINIVSCASGSGQRFVFNAGAILNLKGLAMDVAQS 507
QY 241 NPKLRRIITTPATGKNQMWLPV 263
DB 508 NPKLRRIITTPATGKNQMWLPV 570

RESULT 2
Q8IKO2
ID Q8IKO2 PRELIMINARY; FRT; 263 AA.
AC Q8IKO2;
DT 01-OCT-2002 (Tremblrel. 22, Created).
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update).
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update).
DE Lectin Chain B isoform 2 (fragment).
OS Viscum album subsp. coloratum.
OC Burkariaceae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicot;
OC Spectralia; Viscaceae; Viscum.
OX NCBI_TaxID:159976;
RN [1]_TaxID:159976;
RP SEQUENCE FROM N.A.
RA MEDLINE-2156752; PubMed-11710524;
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-U., Kim J.-B.,
Do M.-S., Song S.K.;
RT "cDNA cloning and sequence analysis of the lectin genes of the Korean
mistlecote (Viscum album coloratum).";
RT M01. Cells 12:215-220(2001).
RN [1]_TaxID:159976;
RA SEQUENCE FROM N.A.
RA Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-U., Kim J.-B.,
Do M.-S., Song S.K.;
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF508918; AA04636.1; -;
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 5.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
FT NON_TER 1
FT NON_TER 263
SQ SEQUENCE 263 AA; 29150 MW; 8685BCE7C4CDD1P CRC64;

Query Match 78.3%; Score 1112.5; DB 10; Length 263;
Best Local Similarity 78.7%; Pred. No. 5,46-86;
Matches 207; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCASGSGQRFVFNAGAILNLKGPAMDVAQA 240
DB 180 GSIRPKONODCLTSGRDSVSTVINIVSCASGSGQRFVFNAGAILNLKGLAMDVAQS 239
QY 241 NPKLRRIITTPATGKNQMWLPV 263
DB 240 NPKLRRIITTPATGKNQMWLPV 262

RESULT 3
Q8W243
ID Q8W243 PRELIMINARY; FRT; 565 AA.
AC Q8W243;
DT 01-MAR-2002 (Tremblrel. 20, Created).
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update).
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update).
DE VCA precursor (EC 3.2.2.23) (RNA N-glycosidase).
OS Viscum album subsp. coloratum.
OC Burkariaceae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicot;
OC Spectralia; Viscaceae; Viscum.
OX NCBI_TaxID:159976;
RN [1]_TaxID:159976;
RP SEQUENCE FROM N.A.
RA Park W.-B., Lyu S.-I.;
RT "Cloning of Viscum album subsp. coloratum (Korean mistlecote).";
RT Biochem. Biophys. Res. Commun. 0:0(2002).
CC -I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DE EMBL; AF508918; AA04636.1; -;
DE InterPro; IPR000772; Ricin_B_lectin.
DE Pfam; PF00652; Ricin_B_lectin; 6.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00459; RICIN; 2.
DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
KV Hydrolyase; Signal; Toxin.
FT SIGNAL 1 22
FT CHAIN 23 273 VCA ALPHA CHAIN.
FT NON_TER 309 565
SQ SEQUENCE 565 AA; 62401 MW; 591E394D005F11 CRC64;

Query Match 77.4%; Score 1099.5; DB 10; Length 565;
Best Local Similarity 79.8%; Pred. No. 1,66-84;
Matches 210; Conservative 15; Mismatches 33; Indels 5; Gaps 2;

QY 1 DDTVCASEPTVRIYVGNKGVVVDVDDPHDNOIQIOWPSKSNNDPNQWTIKEDGTIRS 60
DB 307 DDTVCASEPTVRIYVGNKGVVVDVDDPHDNOIQIOWPSKSNNDPNQWTIKEDGTIRS 362
QY 61 NSGCLTYGTAGVYVMEFDNINAVKXATITWQIMDNGITINPSNVLAAASGIGKTT 120
DB 363 NSGCLTYGTAGVYVMEFDNINAVKXATITWQIMDNGITINPSNVLAAASGIGKTT 422
QY 121 VQTLDTYLGQGLAGNDTAPREVTIYGFRLQMSNGSVWETCVSGSQNQ-KMALYGD 180
DB 423 VQTLDTYLGQGLAGNDTAPREVTIYGFRLQMSNGSVWETCVSGSQNQ-KMALYGD 481
QY 181 GSIRPKONODCLTSGRDSVSTVINIVSCASGSGQRFVFNAGAILNLKGPAMDVAQA 240
DB 482 GSIRPKONODCLTSGRDSVSTVINIVSCASGSGQRFVFNAGAILNLKGLAMDVAQS 541
QY 241 NPKLRRIITTPATGKNQMWLPV 263
DB 542 NPKLRRIITTPATGKNQMWLPV 564

RESULT 4
Q8LKO1
ID Q8LKO1 PRELIMINARY; FRT; 263 AA.

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Page 1

GenDore version 5.1.6
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CM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 20.3487 seconds
(without alignments)
3347.915 Million cell updates/sec

Title: US-09-601-667C-10
Perfect score: 1420
Sequence: 1 DDVTCSSASEPTPIVGRNKN.....RRITIPATCKDNQMLPVF 264

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_wetphare:*
13: sp_unclassified:*
14: sp_virus:*
15: sp_bacteriap:*
16: sp_bacteriap:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1303.5	91.8	531	10 Q8RXH6	Q8RXH6 viscum albu
2	1112.5	78.3	263	10 Q8LXQ2	Q8LXQ2 viscum albu
3	1099.5	77.4	565	10 Q8W243	Q8W243 viscum albu
4	1078.5	76.0	263	10 Q8LXQ1	Q8LXQ1 viscum albu
5	992.5	69.9	286	10 Q8LXQ3	Q8LXQ3 viscum albu
6	904.5	63.5	541	10 Q41174	Q41174 ricinus com
7	883.5	60.8	263	10 Q41143	Q41143 ricinus com
8	863.5	60.3	580	10 Q44B84	Q44B84 cinnaomum
9	837.5	57.6	549	10 Q94BMS	Q94BMS cinnaomum
10	817.5	57.6	581	10 Q94BMS	Q94BMS cinnaomum
11	758.5	53.4	528	10 Q06076	Q06076 abrus prec
12	744.5	52.4	382	10 Q8SK43	Q8SK43 abrus prec
13	744.5	52.4	547	10 Q9W659	Q9W659 abrus prec
14	744.5	52.4	547	10 Q9W659	Q9W659 abrus prec
15	676.5	47.6	592	10 Q8W257	Q8W257 hirs holian
16	676.5	47.6	592	10 Q8W257	Q8W257 hirs holian

17	571	40.2	570	10 Q22415	Q22415 sambucus ni
18	560.5	39.5	564	10 Q94V22	Q94V22 sambucus ni
19	558.5	39.3	316	10 Q8G7R5	Q8G7R5 sambucus ni
20	557.5	39.3	316	10 Q93W11	Q93W11 sambucus ni
21	556.5	39.2	316	10 Q94554	Q94554 sambucus ni
22	539.5	38.0	563	10 Q04367	Q04367 sambucus ni
23	537	37.8	570	10 Q41358	Q41358 sambucus ni
24	520.5	37.4	320	10 Q8G132	Q8G132 sambucus ni
25	520.5	37.4	320	10 Q8G132	Q8G132 sambucus ni
26	528.5	37.2	563	10 Q94552	Q94552 sambucus ni
27	537	37.1	604	10 Q9W653	Q9W653 polygonatum
28	532	36.8	603	10 Q9W653	Q9W653 polygonatum
29	519.5	36.6	320	10 Q04366	Q04366 sambucus ni
30	509	35.8	565	10 Q04071	Q04071 sambucus ni
31	507	35.7	307	10 Q8G7R6	Q8G7R6 sambucus ni
32	506	35.6	566	10 Q04072	Q04072 sambucus ni
33	441	31.1	569	10 P93543	P93543 cucumis sat
34	182.5	13.9	293	10 Q9ELV9	Q9ELV9 sambucus ni
35	142	10.0	422	10 Q9EMV5	Q9EMV5 streptomyc
36	136	9.6	377	2 Q8RPU5	Q8RPU5 streptomyc
37	136	9.6	377	2 Q8RPU5	Q8RPU5 streptomyc
38	127.5	8.6	437	2 Q8G131	Q8G131 oestrivovis x
39	122.5	8.2	492	2 Q8G131	Q8G131 streptomyc
40	120.5	8.5	962	16 Q8K473	Q8K473 streptomyc
41	120.5	8.5	555	16 Q8K473	Q8K473 streptomyc
42	120	8.5	579	16 Q8K474	Q8K474 streptomyc
43	113.5	8.0	476	2 Q8W345	Q8W345 streptomyc
44	113.5	8.0	476	2 Q8W345	Q8W345 streptomyc
45	113.5	8.0	1545	16 Q9MD01	Q9MD01 streptomyc

ALIGNMENTS

RESULT 1

ID Q8RXH6 PRELIMINARY: PRT: 531 AA.
AC Q8RXH6;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Lectin chain A isoform 1 (EC 3.2.2.22) (RNA N-glycosidase)
DS (Fragment).
OS Viscum album (European mistletoe)
OC Euphorbiaceae
OC Sp. n. (Mistletoe)
OC Santalales Viscaceae Viscum.
CX NCBI_TaxID=9972;
XP SEQUENCE FROM N.A.
RA TISSUE=Leaf;
RC Paramasiyam M., Mitra V., Srinivasan A., Singh T.P.;
RT "Viscum album (Indian) mRNA for Mistletoe lectin chain A isoform 1 and
KT chain B.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SEQUENCE ALIGNED TO ENDOGLYCOSYLASES OF THE N-GLYCOSIDIC BOND AT ONE
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL: AY081149; AL87066.1; -!
DR InterPro: IPR001574; RLP.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00651; RLP; 1.
DR SMART: SM00458; Ricin_B_lectin; 2.
DR PROSITE: PS50231; Ricin_B_lectin; 2.
KM HYDROLASE; TOXIN.
FT CHAIN 1 243 LECTIN CHAIN A ISOFORM 1.
FT CHAIN 2 531 LECTIN CHAIN B ISOFORM 1.
SQ SEQUENCE 531 AA; 58802 NM; 162445BERF59422 CRC64;
Query Match 91.8%; Score 1303.5; DB 10; Length 531;
Best Local Similarity 93.2%; Pred. No. 9.9e-102;

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FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 545 AA; 60148 MM; 2DCSN/10CB95D9C CRC64;

Query Match 6.9%; Score 97.5; DB 1; Length 545;
Best Local Similarity 20.2%; Pred. No. 0.66; Indels 45; Gaps 8;
Matches 46; Conservative 40; Mismatches 97;

QY 22 VVVRDDPFDNDQNOIDLPSPKSNDDPNQIWKDGTIRSNKSLTYGYTA----- 72
DB 342 LPIIIRSLAMGDRLLTVLNKNT-----TVTRDIPVQWLGLETTCYTAEDLMGRTQ 395
QY 73 ----GYVWIFDCNTVRENTWQ---IMDNTILNRSNLYLAASGIGXTLTVQTL 124
DB 396 KISDHIKIILASHATNVRRLSLPQCSVYPTGLVFNPAAGNCLPAAS--NSSVAFQSC 452
QY 125 DYTLGGGMLAGNDTAPREVTIYGFRLCMESNGSVMETCDSSQAKGKALYQGLR 184
DB 453 NGETSQIWCYTPSGVIREFS--QTQCLADNLYLQACDSTDSDSQKWTYPTVTHLK 509
QY 185 PRONQDCLTSGRDSVSTVINIVSCSAGSGORWFTNEGAILNLKKG 232
DB 510 -NAKTDGCLTEGS-----VQWNSC-----LYERDQVFLPSG 541

Search completed: December 11, 2003, 14:09:07
Job time : 5.6201 secs

RC STRAIN-Bristol N2; PubMed=98192620; PMID=9525933;
RA Hagen F.K., Nehrkx X.;
RA "cDNA cloning and expression of a family of UDP-N-acetyl-D-
galactoseamine-polypyrrolidase-acylgalactosaminyltransferase sequence
RT from *Glycosyltransferases*.
RT J Biol. Chem. 273:8269-8277(1998).
RN [2].
RP SEQUENCE FROM N.A.
RX STRAIN-Bristol N2;
RX MEDLINE=94150719; PubMed=7906398;
RX Wilson R., Almsough R., Anderson K., Baynes C., Berts M.,
RA Bonfield U., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton W., Dear S., Du Z., Durbin R., Favellio A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Oler M.,
RA Jonsson L., Jones M., Karlsen U., Kristen T., Laister D.,
RA Darvell P., Lightning B., Lloyd I., Moore A., Saunders D., Shawken R.,
RA Stiles M., Gilmour N., Smith A., Smith M., Sonhammer R., Staden R.,
RA Shisler J., Murray-Wiegert J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstein L., Wilkinson-Sproat J.,
RA Wolldman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.*
RT elegans." Nature 368:32-38(1994).
RN [3].
RP REVISIONS:
RP Revisited R.;
RX MEDLINE=1007-2001 to the EMBL/Genbank/DDBB databases.
CC -! FUNCTION: THIS PROTEIN CATALYZES THE INITIAL REACTION IN O-LINKED
COLLAGENCARBIDE BIOSYNTHESIS, THE TRANSFER OF AN N-ACETYL-D-
GALACTOSAMINE RESIDUE TO A SERINE OR THREONINE RESIDUE ON THE
PROTEIN RECEPTOR.
CC -! CATALYTIC ACTIVITY: UDP-N-acetyl-D-galactosamine + polypeptide =
UDP + N-acetyl-D-galactosaminyl-polypeptide.
CC -! PATHWAY: Glycosylation.
CC -! SUBCELLULAR LOCATION: Type II membrane protein (potential).
CC -! SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
CC -! SIMILARITY: Contains 1 rich B-type beta-strand domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as they acknowledge it in any way modified and this statement is not removed. Usage by for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF031933; AACL3667.1; --
DR EMBL: AF031933.1; GI:242424.5; --
DR EMBL: AF031933.1; GI:242424.5; --
DR Wormpep: AK668.8; CE93669.
DR InterPro: IPRO00117; Glyco trans 2.
DR InterPro: IPRO00772; RICH_B lectin.
DR Pfam: PF00653; Glycos_transf_2.1.
DR Pfam: PF00652; RICH_B lectin; 2.
DR SMART: SMOU0458; RICHN_1.
DR ProSITE: PS00231; RICHN_B_LECTIN; 1.
KW Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
KW Glycoprotein; Lectin.
FT DOMAIN 1
FT TRANSMEM 14 34
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT POTENTIAL
FT LUMENAL (POTENTIAL)
FT CYTOPLASMIC (POTENTIAL)
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT POTENTIAL
FT LUMENAL (POTENTIAL)
FT RICHN_B_TYP_E LECTIN.
FT N-LINKED (GLYCAN...) (POTENTIAL)
FT CARBOHYD 239 239
FT CARBOHYD 612 AA; 68911 MW; 3031CEFS3JF9858 CRRQ64;
SQ SEQUENCE
Query Match 7.24; Score 102; DB 1; Length 612;
Query Local Similarity 26.44; E-value No 0.31;
Matches 32; Conservative 23; Mismatches 50; Indels 16; Gaps 6

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Oy 148 F8DGMKSNY-----GGSWVTECSDSDONKQKXALVGDSDS.FRKONQDQCLTNSRK-DPVSST 202
Db 492 FTEKCVDTYTKKKDQAPQIPQACGAGAGGQNDQ-WSLTSTKKEIR--SDCLSLSGSHVQIGS 547
Oy 203 VINITSSGASGSGORVET---NBQALNLTKKGPAMDVAQAMPKRIIRIITPATGPQM 259
Db 548 ELKERSVYSKINKRNVAVPDDQAGLTKLTKKACVQGLQAPRVTLDEC---GLSDNQM 603
Oy 260 N 260
Db 604 W 604

RESULT 15
AGAL ASPNG PRT, 545 AA.
P28351;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
548 FTEKCVDTYTKKKDQAPQIPQACGAGAGGQNDQ-WSLTSTKKEIR--SDCLSLSGSHVQIGS 547
A: alpha-galactosidase A precursor (EC 3.2.1.22) (Melibiose) .
DR AGLA
OC Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillius.
OC NCBI_Taxid=5061;
(1)
SEQUENCE FROM N.A., AND SEQUENCE OF 32-59.
RC STEINHAUS, J. & ROSELL, I.F. 1983. PubMed1320166;
RC van den Hondel C.A.M., J., Rosell I.F., van Zullen C.M., Punt P.J.,
RA van den Hondel C.A.M., J.,
RT Cloning and expression of a member of the Aspergillus niger gene
RL Mol. Gen. Genet. 233:404-410(1992).
-1- PUNCTON: REPRESENT A MINOR EXTRACELLULAR ALPHA-GALACTOSIDASE
ACTIVITY IN A NIGER.
-1- PHENOLACTIC ACTIVITY: WEIGHABLE + H(2)O = galactose + glucose.
-1- GROWTH ON GLYCOSYLATION.
-1- SIMILARITY: BELONGS TO FAMILY 27 OF GLYCOSYL HYDROLASES.
-1- SIMILARITY: CONTAINS 1 RICHIN B-TYPE LECTIN DOMAIN.
-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-9 IS THE INITIATOR.
CC CC
CC This SMS-S-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL collaborative
CC the European Bioinformatics Institute. There are no restrictions on
CC use by non-profit institutions as long as the source is acknowledged in no way
CC modified and this statement is included in the final usage by and for commercial
CC entities as well as in any agreement (see http://www.isb-stb.ch/announce
CC or email to lisb@isb-stb.ch).
CC -----
DR EMBL: X63348; CAA445950.1; --
DR P-R: S23582; S23582.
DR GlycoSiteDB: P28351; --
DR InterPro: IPR002241; Glyco_hydro.27.
DR InterPro: IPR000111; Glyco_hydro.GMD.
DR InterPro: IPR000772; RICHIN_1 Lectin.
DR Pfam: PF000682; RICHIN_B_Lectin; 3.
DR PRINTS: PR00740; GHYDRLASE27.
DR ProDom: PD002572; Glyco_hydro.GMD; 1.
DR SMART: SM00458; RICHIN_1.
DR PROSITE: PS00512; ALPHA-GALACTOSIDASE; 1.
DR PROSITE: PS02011; RICHIN_B_Lectin; 1.
Kv HydroLase; Glyco21; RICHIN_B_Lectin; Glycoprotein; Lectin.
FT SIGNAL 32
FT CHAIN 1 548
FT DISCIPLIN 548
FT ACT SITE 327
FT CARBOHYD 57 327
FT CARBOHYD 95 95
FT CARBOHYD 101 101
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).

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DR EMBL; M6451; AAC6524.1; -
 DR InterPro; IPR00193; Glyco_hydro_62.
 DR InterPro; IPR00772; Ricin_B_lectin.
 DR Pfam; PF03654; Glyco_hydro_62; 1.
 DR SMART; SM00324; Ricin_B_lectin; 3.
 DR PROSITE; PS0031; Ricin_B_lectin; 1.
 DR PROSITE; PS0031; Ricin_B_lectin; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Signal; Lactin.
 FT SIGNAL 1 37
 FT CHAIN 38 475
 FT DOMAIN 39 166
 SEQUENCE 475 AA; 50369 MW; C1C614E7B85AD CRC64;

Query Match: 7.9%; Score 112.5; DB 1; Length 475;
 Local Similarity 24.1%; Pred. No. 0.029; 104; Indels 25; Gaps 10;
 Matches 52; Conservative 35; Mismatches 104;

DR 6 SASPTVAVGNKGVYDDDFHGNQIQLPKSNNDPQWLTIRKDGTRNSG-SC 64
 DB 37 AAGSGALRAGASNEC-LDVAGSSODDALLADYDCWGT--HQWRTSTGTGRLTYGDK 93
 QY 65 LITVGYTA--GYVWIFDQNTAVRANTWQIMQNTIINRSENLV-AASGQ-KGTLT 120
 DB 94 LDVGHANVAGTRVQVWESGQNGNQ--RWVSDGVVGVESGLCLBAAGAPVNTAVQ 151
 QY 121 VQTDLYTLQGHLAGNDTARPT-----YGERDLCNESNGSVYETCP-SSQNSCK 174
 DB 152 LMTGSGNQWMTGTGTGTFPDTGTCALPSTVMSSTVGLAQKSGWALNDFTVTINR 211
 QY 175 WALYDGS-----IREKQNOCTLSGDSVS 201
 DB 212 HLYGTSVSGSVGWSVFSPTWMDVAGAGVANN 247

RESULT 13
 SPL RARA
 ID SPL RARA STANDARD; PRT; 525 AA.
 AC 005308;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serine protease I precursor (EC 3.4.21.-) (R1).
 OS Rarobacter faecitabidus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Rarobacteriaceae; Rarobacteraceae; Rarobacter.
 CX NCBI_TaxID=13243;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 212-222; 224-238 AND 240-244.
 RC STRAIN-TM-50;
 RX MEDLINE=3904226; PubMed=1339445;
 RA Shimoi H., Imura Y., Ohta T., Tadenuma M.;
 RT "Molecular structure of Rarobacter faecitabidus protease I. A yeast-
 lytic serine protease having mannose-binding activity.";
 RL J. Biochem. 110:608-613(1991).
 RL J. Biochem. 110:608-613(1991).
 CC -1- FUNCTION: MAJOR SERINE PROTEASE EXHIBITING LYTIC ACTIVITY TOWARD
 SPECIFICITY AND HAS A LECTIN-LIKE SPECIFICITY FOR R1.
 CC MANNOPROTEINS MAY BE THE NATIVE SUBSTRATE FOR R1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 52A.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.

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DR EMBL; D1073; A001585.1; -
 DR InterPro; IPR004236; AL protease.
 DR InterPro; IPR001316; Endopeptidase.
 DR InterPro; IPR00772; Ricin_B_lectin.
 DR InterPro; IPR001254; Ser. protease_TY.
 DR Pfam; PF02983; AL protease; 1.
 DR Pfam; PF02983; AL protease; 1.
 DR Pfam; PF02983; AL protease; 1.
 DR SMART; SM00458; Ricin_B_lectin; 3.
 DR PROSITE; PS0031; Trypsin_HIS; 1.
 DR PROSITE; PS0031; Trypsin_SER; 1.
 DR PROSITE; PS0031; Trypsin_SER; 1.
 DR PROSITE; PS0031; Trypsin_SER; 1.
 DR Xylan degradation; Hydrolase; Mannose-binding; Signal; Zymogen;
 FT SIGNAL 1 32
 FT PROPEP 33 211
 FT CHAIN 33 211
 FT DOMAIN 401 525
 SEQUENCE 525 AA; 55654 MW; DABCFD330EBB61 CRC64;

Query Match: 7.9%; Score 111; DB 1; Length 525;
 Local Similarity 31.1%; Pred. No. 0.044;
 Matches 33; Conservative 17; Mismatches 44; Indels 12; Gaps 5;

DR 2 DVTCASPTVAVGNKGVYDDDFHGNQIQLPKSNNDPQWLTIRKDGTRNSG-SC 64
 DB 399 DVTCASPTVAVGNKGVYDDDFHGNQIQLPKSNNDPQWLTIRKDGTRNSG-SC 64
 QY 62 GSGLT-TYVGYT-AGVWIFDQNTAVRANTWQIMQNTIINRSENLV-AASGQ-KGTLT 105
 DB 451 GKCLDARMVHTNQTETVALNKNCHGI--AQKFTLNAGDGLVANN 494

RESULT 14
 SPL RARA
 ID SPL RARA STANDARD; PRT; 612 AA.
 AC 034676; G09003;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Polypeptide N-acetylglucosaminyltransferase 3 (EC 2.4.1.41)
 DE (Protein-UDP N-acetylglucosaminyltransferase) (UDP-galactose 4-epimerase)
 DE N-acetylglucosaminyltransferase (GalNAc-T) (Epimerase 3).
 RA Shimoi H., Imura Y., Ohta T., Tadenuma M.;
 RT "Molecular structure of Rarobacter faecitabidus protease I. A yeast-
 lytic serine protease having mannose-binding activity.";
 RL J. Biochem. 110:608-613(1991).
 RL J. Biochem. 110:608-613(1991).
 CC -1- FUNCTION: MAJOR SERINE PROTEASE EXHIBITING LYTIC ACTIVITY TOWARD
 SPECIFICITY AND HAS A LECTIN-LIKE SPECIFICITY FOR R1.
 CC MANNOPROTEINS MAY BE THE NATIVE SUBSTRATE FOR R1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 52A.
 CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL: D23668; BAO4892.1; -

DR HSSP: P02879; 2NAI.

DR InterPro: IPR000772; Ricin_B_lectin.

DR Pfam: PF00652; Ricin_B_lectin_3.

DR PROSITE: PS50231; Ricin_B_lectin_1.

DR PROSITE: PS50231; Ricin_B_lectin_1.

KM Hydroxylase; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.

FT SIGNAL 1 36

FT CHAIN 37 548 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE.

FT DOMAIN 422 548 RICIN B-TYPE LECTIN.

SEQUENCE 548 AA; 58164 MW; BD5654315750596 CRC64;

Query Match

Best Local Similarity 31.3%; Pred. No. 0.026;

Matches 41; Conservative 18; Mismatches 52; Indels 20; Gaps 7;

QY 16 GRNGKRV-----DYRDDPHGNGIQLPSSKNDPQVLTIRKDTIRNSGCT--TT 67

DB 422 GTGALIGSTLCIDVPADPTDYNQV--ATCGAKAQQVTRGTGTVAKLCKLDVAR 479

QY 68 YGVYAGYVWTFDCK-TAVREATVQWNGT--INPSSNLYLAASGCT--KGTITLV 121

DB 480 SGTADGTAWITVTCNGTGAQKWT---YDAATKALNPQSGKCLDAQGAPLADQKVL 535

QY 122 QTLDTYLGQGW 132

DB 536 WTCNQTETAKRW 546

RESULT 11

ID E13B_OERXA STANDARD; PRT; 546 AA.

AC P22222;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase).

OS Oerskovia xanthineolytica.

OC Bacteria; Actinobacteriales; Actinobacteridae; Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1710;

RN [1]_taxid=1710;

RP SEQUENCE FROM N.A. AND SEQUENCE OF 37-63.

RX MEDLINE=91093212; PubMed=1985933;

RA Shen S.-H., Chretien P., Bastien L., Sliatay S.N.;

RT "Primary sequence of the glucanase gene from Oerskovia xanthineolytica. Expression and purification of the enzyme from Escherichia coli."

RT Escherichia coli."

RT J. Biol. Chem. 266:1058-1063(1991).

KL J.

CC -1- FUNCTION: LISTS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.

CC -1- INDICATED IN THE DEPENDS AGAINST FUNGAL PATHOGENS.

CC -1- XANTHINE ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages

CC -1- SUBCELLULAR LOCATION: Periplasmic.

CC -1- SIMILARITY: BELONGS TO FAMILY 64 OF GLUCOSYL HYDROLASES.

CC -1- SIMILARITY: CONTAINS 1 ricin B-type lectin domain.

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CC EMBL: M60826; AAA25520.1; -

DR PIR: A39094; A39094.

DR HSSP: P02879; 2NAI.

DR InterPro: IPR000772; Ricin_B_lectin.

DR Pfam: PF00652; Ricin_B_lectin_3.

DR SMART: SM00456; Ricin_1.

DR PROSITE: PS50231; Ricin_B_lectin_1.

KM Hydroxylase; Glycosidase; Signal; Periplasmic; Cell wall; Lectin.

FT SIGNAL 1 36

FT CHAIN 37 548 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE.

FT DOMAIN 422 548 RICIN B-TYPE LECTIN.

FT DOMAIN 37 430 POSSIBLE BETA-GLUCANASE ACTIVITY, BUT IS ESSENTIAL FOR THE BETA-GLUCANASE FUNCTION.

FT DOMAIN 472 548

SEQUENCE 548 AA; 58088 MW; 4125544A24C048D CRC64;

Query Match

Best Local Similarity 31.3%; Pred. No. 0.026;

Matches 41; Conservative 18; Mismatches 52; Indels 20; Gaps 7;

QY 16 GRNGKRV-----DYRDDPHGNGIQLPSSKNDPQVLTIRKDTIRNSGCT--TT 67

DB 422 GTGALIGSTLCIDVPADPTDYNQV--ATCGAKAQQVTRGTGTVAKLCKLDVAR 479

QY 68 YGVYAGYVWTFDCK-TAVREATVQWNGT--INPSSNLYLAASGCT--KGTITLV 121

DB 480 SGTADGTAWITVTCNGTGAQKWT---YDAATKALNPQSGKCLDAQGAPLADQKVL 535

QY 122 QTLDTYLGQGW 132

DB 536 WTCNQTETAKRW 546

RESULT 12

ID ABER_STRLI STANDARD; PRT; 475 AA.

AC ABER63

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 28-SEP-2003 (Rel. 41, Last annotation update)

DE Alpha-L-arabinofuranosidase precursor (EC 3.2.1.55) (Arabinosidase).

GN ABER.

OC Streptomyces lividans.

OC Bacteria; Actinobacteriales; Actinobacteridae; Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1916;

RN [1]_taxid=1916;

RP SEQUENCE FROM N.A.

RX MEDLINE=9148759; PubMed=9148759;

RA Vincent P., Shareck F., Dupont C., Morosoli R., Kluepfel D.;

RT "New alpha-L-arabinofuranosidase produced by Streptomyces lividans: cloning and DNA sequence of the abtB gene and characterization of the enzyme."

RT Biochem. J. 322:845-852(1997).

RT [2]

CC REVISIONS.

CC STRAIN=66 / 1326;

CC SHARECK F.; JUT-1998; to the EMBL/Genbank/DBI databases.

CC SUBMISSION HAS A SPECIFIC ARABINOFURANOSYL-DEBRANCHING ACTIVITY ON

CC -1- XYLAN FROM GRAMINEAE, ACTS SYNERGISTICALLY WITH THE XYLANASES AND

CC BINDS SPECIFICALLY TO XYLAN. FROM SMALL ARABINOXYLO-OLIGOSIDES,

CC IT LIBERATES ARABINOSE AND, AFTER PROLONGED INCUBATION, THE

CC PURIFIED ENZYME EXHIBITS SOME XYLANOXYLYTIC ACTIVITY AS WELL.

CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-arabinofuranoside residues in alpha-L-arabinosides.

CC -1- PATHWAY: Xylan degradation.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO FAMILY 62 OF GLUCOSYL HYDROLASES.

CC -1- SIMILARITY: CONTAINS 1 ricin B-type lectin domain.

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D6		507 LXEIILPFAKPKRQWITLFE 527	
RESULT 6			
IDC	Accession		
RC	AARC:AARCR	STANDARD;	PRT; 562 AA.
AC	P28590:		
DT	01-DEC-1992 (Rel. 24, Created)		
DT	01-DEC-1992 (Rel. 24, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Abirin - precursor [Contains: Abirin-A chain (tRNA N-glycosylase)]		
DS	(EC 3.2.2.22); Abirin-C chain).		
OS	Abirus prearcotus (Indian licorice) (Crab's eye).		
OC	Spermatophyta; Vitisidaceae; Stercobiya; Embryophyta; Tracheophyta;		
CC	Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
CC	Rubiales; Rubiaceae; Sapindales; Rubia; Abiria.		
CC	NCHI_TextID=5816;		
XN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISUSZ-Leaf;		
PX	MEDLINE:91268697; PubMed:2050149;		
RA	Wood K.A., Lord J.M., Wawrzyniak E.J., Piatek M.;		
RT	"Peptidobacterin: genomic cloning, characterization and the expression of		
RL	the A-chain in Escherichia coli."		
CL	Bur. J Biochem. 1987;213:1921-1931.		
CC	-1- This entry contains information for INHIBITING PROTEIN.		
CC	SYNTHESIS THROUGH THE CATALYTIC ACTIVATION OF 60S RIBOSOMAL		
CC	SUBUNIT BY REMOVING ARSENINE FROM POSITION 4,324 OF 28 S RRNA. THE		
CC	B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE		
CC	BINDING OF ABIRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one		
CC	specific adenosine on the 28S rRNA.		
CC	-1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.		
CC	-1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN		
CC	CONSISTS OF 1 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).		
CC	-1- FUNCTION: The protein is involved in the assembly of the RIBOSOME-		
CC	INHIBITING PROTEIN family type 2 RIP SUBUNIT.		
CC	-1- SIMILARITY: Contains 2 tRNA-B-type lectin domains.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see http://www.isdb-sib.ch/announce/)		
CC	-----		
DR	EMBL; X55667; CA93202.1; -;		
DR	PIR; S16022; S16022.		
DR	HSSP; P1140; IABR.		
DR	InterPro; IPRO00772; Ricin_B_lectin.		
DR	InterPro; IPRO01574; RIP.		
DR	Fam; PF00652; Ricin_B_lectin. 6.		
DR	Fams; PF00652; Ricin_B_lectin. 6.		
DR	PRINTS; PR00156; SHIDAICIN.		
DR	SMART; SM00458; RICIN_2.		
DR	PROSITE; PS50231; RICIN_B_Lectin; 2.		
DR	PROSITE; PS00275; SHIGA_Ricin_1.		
KM	Plant defense; Hydroxylase; Protein synthesis inhibitor; Toxin; Repeat;		
KV	Glycoprotein; Lectin; Signal; Pyrolysine carboxylic acid.		
FT	FT SIGNAL	1..34	
FT	FT CHAIN	35..285	
FT	PEPTIDE	286..295	
FT	CHAIN	296..562	
FT	CHAIN	307..314	
FT	DOMAIN	317..359	
FT	REPEAT	360..400	
FT	REPEAT	403..435	
FT	REPEAT	438..483	
FT	REPEAT	487..526	
FT	REPEAT	529..562	
FT	ACT_SITE	198..198	
FT	ACT_SITE	198	
FT	BY SIMILARITY.		

FT	DISULFID	281	303		INTERCHAIN (BY SIMILARITY),
FT	DISULFID	320	339		BY SIMILARITY,
FT	DISULFID	363	380		BY SIMILARITY,
FT	DISULFID	451	464		BY SIMILARITY,
FT	DISULFID	490	507		BY SIMILARITY,
FT	MOD_RES	35	35		HYDROLYSIS OF PEPTIDYLIC ACID (BY SIMILARITY).
FT	CARBOND	234	234		N-LINKED (GLNAC...) (POTENTIAL),
FT	CARBOND	395	395		N-LINKED (GLNAC...) (POTENTIAL),
FT	CARBOND	435	435		N-LINKED (GLNAC...) (POTENTIAL),
SO	SEQUENCE	562 AA;	62811 MW;	1PFOA607J7BA6278	CRC64.
Query Match					
		53.6%;	Score 761;	DB 1;	Length 562;
		Match Similarity	54.8%;	Pred. No. 1-5e-57;	
		Motif 143;	Conservative	42;	Miscellaneous 74;
					Indels 2;
					Gaps 2.
Dy	CSAS-REPTA;YVRNANQVDPDDPHGDCOIQAFSSSNPNQMNIKXDTIRNSGS	63			
Dy	303 CSAREPTAIRIGSDGMGVYDGDCHNONIIFAKCKDLSEHQLATIKSPITRISNGK	362			
Dy	CLTGYTGAGYVNVFDCCNNAREKTIWIMDNGITIPRSNLVLAAASGIGKITITLVTQT	123			
Dy	363 CLTBGAGSGYVIMDCTSAVAEKLVEWDNGITIPHSALVLVASBESSMGSLTVQTT	422			
Dy	124 DLTLGGMLAKNDPIPEBTIVYGFGRDLDMENSGSIWEIETCSSQDNCRKALVEDGI	183			
Dy	423 NETHLMQKSCNNHPVYSLSQSDLDNQMSQSVMLADDDNKRED-QMALYDSRI	481			
Dy	184 RPKMDQDCLTSRGDSVATYIVVSCGASSQGWYTFNSGAILLKAPMPADPAQMPK	243			
Dy	482 RSQMTGNCLTSSDHQSISTYLVASCNMASQRMTFYDGSTVYLLHDMMVDYKSDFS	541			
Dy	244 LRRITIVATEKPQNMPLVF	264			
Dy	542 LKEILLPHFGKPMQMLTLF	562			
RESULT 7					
ID	NIGB_SAMNI	STANDARD;	PERT:	563 AA.	
AC	P31183; P31184; P93542;				
DT	01-OCT-1993 (Rel. 27, Created)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Nigirin b precursor (Agglutinin 2) (SNV) [Comparative: Nigirin b chain				
OS	Sambucus nigra (European elder) (2); Nigirin b chain(1).				
OC	Buxaceae; Viridiales; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliopsida; eudicotyledons; Core eudicots;				
OC	Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.				
NC	NCBI_TaxId=4202;				
RN	SEQUENCE FROM N.A.				
RA	UNRESERVED; PUBMED:6647092;				
RA	VAN DAMME E.J., BARRE A.P., ROUGE P., VAN LEUVEN F., PENNAE W.J.;				
RT	"Characterization and molecular cloning of sambucus nigra agglutinin V				
RT	nigirin b, a GALNAc-specific type-2 ribosome-inactivating protein				
RT	from the bark of elderberry (Sambucus nigra)." ;				
RL	Eur. J. Biochem. 237:505-513 (1996).				
RZ	[2]				
RZ	SEQUENCE OF 26-49 AND 296-321.				
RC	TISSUE-Bark;				
RC	MEDLINE=94003077; PubMed=8400135;				
RA	Girdes S., Clottes J., Gerezes J.M., Rojo M.A., Iglesias R.,				
RA	"Isolation and partial characterization of nigrin b, a non-toxic				
RT	novel type 2 ribosome-inactivating protein from the bark of Sambucus				
RT	nigra L."				
PL	Plant Mol. Biol. 22:1181-1186 (1999).				
CC	-1- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN				
CC	PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN				
CC	SYNTHESIS. THIS A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN				

Db	306	CMQEPFVTRVAKMGADVYGGSEFPDQNLGMPECKSTDMQWLTLDSTSTISNGKC	365
Qy	65	LTETYSAYGVYVIMTPOCNATREARLITKQINDGNTIIPNSNVLTASSCKIKETLTLYQL	124
Db	366	LITSSSPQGVIVYVNSTATVAGRAWQIDNRITINPSSGLVLAATISNGSKFLTYQEN	422
Qy	125	DYLTQQGMYLAKMGDVAPEPVITVYFEDLTCKMSNGSVWVETDSSQGNQGMALYVDDGSR	184
Db	426	TVASQGLTINQTPPTVITVYVSKQGLDQNSGVFWGWDG-TSEKAMQALVAYDSR	484
Qy	185	PKQNDQCLTSGRSPGTVYVIVYVSGASQSGSRVFWGWDG-TSEKAMQALVAYDSR	244
Db	485	POQNDQCLTAKIAIKIYVIVYVLTSGPSSQGRWFWGWDGTLINLVGLVLDVSRDEL	544
Qy	245	RRIITVYPAIKENQMLPVV 264	
	545	KQIVAPRHNINQIMLVP 564	

RESULT 5

ABRB ABRPR	STANDARD:	PRT:	527 AA.
ID ABRB ABRPR			

AC Q06077, p81374;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-2003 (Rel. 41, Last annotation update)
 DE *Arabidopsis thaliana* (strain At1g19900) cDNA
 FC 3.2.1.921 Arabidopsis thaliana
 DE *Arabidopsis thaliana* (indian isolate) (Crab's eye).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
 OC Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosales;
 OC eucosids I; Fanales; Fabaceae; Papilionoideae; Abrus.
 NCBI_TaxID:3516; OX

RP SEQUENCE FROM N. A.
EX MEDLINE=91133798; PubMed=842113;
RT Pang C.-H., Lee W.-C., Lee T.-C., Lin J.-Y.;
RT "Primary structure of three distinct isoforms determined by cDNA
RT sequencing. Conservation and significance.";
RL J. Mol. Biol. 129:263-267 (1993) .
RN [2]
RN SEQUENCE OF 260-527.

RX MEDLINE:8507330; PubMed:753422.
 RA Kimura M, Sumizawa T, Funatsu G;
 RT "The complete amino acid sequences of the B-chains of abrin-A and
 RT abrin-B, toxic proteins from the seeds of *Abus precatorius*.";
 RL Biochem. Biotechnol. Blochem. 57:166-169(1993).
 RL 1-
 CC SYNTHESIS THROUGH THE CATALYTIC ACTIVATION OF 60S RIBOSOMAL
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA
 CC ABRIN-A IS MORE TOXIC THAN RICIN.

CC - FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
CC FLOURISHES THE BINDING OF AARIN TO THE CELL MEMBRANE THAT
CC
CC - CATALYTIC ACTIVITY: hydrolysis of the N-glycosidic bond a
CC
CC - specific domains on the 281 TRPA
CC
CC - SUBUNIT: DISTURBE LINKED DIMER OF A AND B CHAINS
CC
CC - DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC - SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOM
CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIT SUSCEPTIBILITY
CC - SIMILARITY: Contains 2 ricin B-type lectin domains.

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[illegible]

	59 %	Score 765	DB 1	Length 527
Best Local Similarity	55.2%	Pred. No. 6	46-58	
Matches 144	Conservative 41	Mismatches 74	Indels 2	Gaps 2
QY	CSAS	SEPTAYVIGNMGREVDVDDPFDNQOLQWMSKSNNDPNOQMTIKRGTIRSNDS	63	
DB	CSAS	REPTAYVIGNMGREVDVDDPFDNQOLQWMSKSNNDPNOQMTIKRGTIRSNDS	132	
QY	64	CLFTGYTGYVYVILFDQNTVAEATLWQIMQNGITINRSNLVYLAASGKIGTTLTVOT	127	
DB	328	CLFTGYTGYVYVILFDQNTVAEATLWQIMQNGITINRSNLVYLAASGKIGTTLTVOT	387	
QY	124	LDYTGQGLVANDTTPAEPTVYGRPLCSNDSGSAVWTFCSGSRQKQKXWALVGGSTI	188	
DB	388	NETLIRMGRRDNTTPEVTSIGYSDLCMQKQCSNVMLACDNNKXQ-QWALVYGGSTI	444	
QY	184	RPYQMGQCLTSGSDSVTYINIVCSGASGSGRMYWTBZAILNKKGPAWDVQAKNR	243	
DB	447	RSYQNTNCLTCSKHQSGSPVYALACNSMGASQEWLFRDQSTIVNLHDQWMDVRESDS	506	
QY	244	LRRLIIVPNTKSNQMLPEPV	264	

FT	A-chains."	298	FT	CONFLICT	298	FT	N -> Y (IN REF. 4)
FT	J. Biol. Chem. 266:6848-6852(1991).	297	FT	CONFLICT	427	FT	M -> L (IN REF. 4)
RN	(4)	467	FT	CONFLICT	467	FT	T -> P (IN REF. 4)
RN	SEQUENCE OF 262-528.	483	FT	CONFLICT	483	FT	V -> L (IN REF. 4)
RX	EMBL:2231165; PubMed:150674; RIN J.-Y.;	1	FT	STRAND	1	FT	
RX	EMBL:2231165; PubMed:150674; RIN J.-Y.;	5	FT	STRAND	5	FT	
RT	"The complete primary structure of abrin-a B chain."	15	FT	HELIIX	14	FT	
RT	FEB5 Lett. 309:115-116(1992).	8	FT	HELIIX	15	FT	
RN	[5]	1	FT	STRAND	1	FT	
RP	X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).	PT	STRAND	PT	STRAND	PT	
RX	MEDLINE:5533188; PubMed:7608960;	PT	STRAND	PT	STRAND	PT	
RA	Taylor T.H., Lu T.-H., Liaw Y.-C., Chen Y.-Y.;	PT	STRAND	PT	STRAND	PT	
RA	"Crystal structure of abrin-a at 2.14 A.";	PT	HELIIX	PT	HELIIX	PT	
RL	J. Mol. Biol. 250:354-367(1995).	PT	STRAND	PT	STRAND	PT	
RL	"FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN	PT	STRAND	PT	STRAND	PT	
CC	SUMMING BY REMOVING ADJACENT PROPOSITION 4,324 OF 285 RNAM.	PT	STRAND	PT	STRAND	PT	
CC	ABRIN-A IS MORE TOXIC THAN RICTIN	PT	STRAND	PT	STRAND	PT	
CC	-1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT	PT	TURN	PT	TURN	PT	
CC	FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT	PT	HELIIX	PT	HELIIX	PT	
CC	PRECEDES ENDOCYTOSIS.	PT	TURN	PT	TURN	PT	
CC	-1- CATALYTIC ACTIVITY: Endopolyolysis of the N-glycosidic bond at one	PT	TURN	PT	TURN	PT	
CC	-1- Specific adenosine on the 285 rRNA.	PT	STRAND	PT	STRAND	PT	
CC	-1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.	PT	TURN	PT	TURN	PT	
CC	-1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN	PT	HELIIX	PT	HELIIX	PT	
CC	CONTAINS ONE 1-HOMOLOGOUS SUBDOMAIN (ALPHA, BETA, GAMMA).	PT	TURN	PT	TURN	PT	
CC	-1- SIMILARITY: THE B CHAIN IS A MEMBER OF THE RIBOSOME-	PT	STRAND	PT	STRAND	PT	
CC	-1- INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.	PT	TURN	PT	TURN	PT	
CC	-1- SIMILARITY: Contains 2 ricin B-type lectin domains.	PT	HELIIX	PT	HELIIX	PT	
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration	PT	STRAND	PT	STRAND	PT	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation on	PT	TURN	PT	TURN	PT	
CC	the European Bioinformatics Institute. There are no restrictions on its	PT	STRAND	PT	STRAND	PT	
CC	use by non-profit institutions as long as its content is in no way	PT	HELIIX	PT	HELIIX	PT	
CC	modified and this statement is not removed. Usage by and for commercial	PT	TURN	PT	TURN	PT	
CC	entities requires a license agreement (See http://www.ksb-stb.ch/announce/	PT	HELIIX	PT	HELIIX	PT	
CC	or send an email to license@ksb-stb.ch).	PT	TURN	PT	TURN	PT	
DR	EMBL: M98144; AAA32674.1; ALT INIT.	PT	TURN	PT	TURN	PT	
DR	EMBL: X54872; -; NOT_ANNOTATED_CDS.	PT	STRAND	PT	STRAND	PT	
DR	PIR: S32429; TZLSA.	PT	TURN	PT	TURN	PT	
DR	InterPro: IPR000772; Ricin_B_lectin.	PT	STRAND	PT	STRAND	PT	
DR	InterPro: IPR001574; RIP.	PT	STRAND	PT	STRAND	PT	
DR	Pfam: PF00652; Ricin_B_lectin; 6.	PT	STRAND	PT	STRAND	PT	
DR	Pfam: PF00161; RIP.1.	PT	STRAND	PT	STRAND	PT	
DR	STRINGS: PF00286; STRINGS:CM.	PT	STRAND	PT	STRAND	PT	
DR	SMART: S00028; SMART:CM.	PT	STRAND	PT	STRAND	PT	
DR	PROSITE: PS00275; SHIKG_RICIN; 1.	PT	TURN	PT	TURN	PT	
KW	Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;	PT	HELIIX	PT	HELIIX	PT	
KW	Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.	PT	STRAND	PT	STRAND	PT	
FT	CHAIN	251	FT	HELIIX	311	FT	
FT	PEPTIDE	252	FT	TURN	315	FT	
FT	CHAIN	262	FT	TURN	319	FT	
FT	DOMAIN	273	FT	TURN	322	FT	
FT	DOMAIN	273	FT	TURN	322	FT	
FT	REPEAT	283	FT	TURN	326	FT	
FT	REPEAT	326	FT	TURN	327	FT	
FT	REPEAT	359	FT	TURN	337	FT	
FT	REPEAT	401	FT	STRAND	340	FT	
FT	REPEAT	414	FT	STRAND	340	FT	
FT	REPEAT	453	FT	TURN	346	FT	
FT	REPEAT	495	FT	HELIIX	351	FT	
FT	ACG SITE	154	FT	STRAND	355	FT	
FT	DISULFID	247	FT	STRAND	357	FT	

FT	VAR	1	231	231	N -> S OR T.
FT	VARIANT	231	231		NCI -> KGP.
FT	VARIANT	231	233		GLAM -> SLAM.
FT	VARIANT	232	225		
SC	SEQUENCE	264 AA:	28981 NM:	7DD0CG32CCCFE5N4	CMCC4:
Query Match			98.84:	Score 1405:	DB 1:
Similarity			98.24:	Ident 106:	3e-113
Matches	262:	Conservative	0:	Mismatches	2:
				Indels	0:
				Gaps	0
DB	1	DDVTSASAEFTVRLVIGNEMGVEDDDDFDGNQIOLMPSKSNDDPNOLATLKDKGTIRS	60		
DB	1	DDVTSASAEFTVRLVIGNEMGVEDDDDFDGNQIOLMPSKSNDDPNOLATLKDKGTIRS	60		
QY	61	NSSCLTGYGTAGVYVAFIDGNVRENTVWIMDNNGTINPSSNVLANSGLIKGTLT	120		
QY	61	NSSCLTGYGTAGVYVAFIDGNVRENTVWIMDNNGTINPSSNVLANSGLIKGTLT	120		
DB	6	VSCVLTATGGWALANDPAPETVYSPRLCMSSNGSVYVETCMSSQKQGMALYGD	180		
DB	121	VQVLTATGGWALANDPAPETVYSPRLCMSSNGSVYVETCMSSQKQGMALYGD	180		
DB	121	VQVLTATGGWALANDPAPETVYSPRLCMSSNGSVYVETCMSSQKQGMALYGD	180		
QY	181	GSTRPNQMOQCLTSGSDSVTVYNIVCSGASGSGWFFNBEGLINLKKGPANVDA	240		
DB	181	GSTRPNQMOQCLTSGSDSVTVYNIVCSGASGSGWFFNBEGLINLKNGLANDVDA	240		
QY	241	NPKRRIITVIRATGKNQVWVLP 264			
DB	241	NPKRRIITVIRATGKNQVWVLP 264			
RESULT 2					
ID	RICI RICCO	STANDARD:	PRT:	576 AA.	
AC	P02870:	P02880:			
DT	21-JUL-1986	(Rel. 01, Created)			
DT	13-AUG-1987	(Rel. 05, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DR	Ricin precursor	(contains: Ricin A chain (rRNA N-glycosidase)			
DS	Ric 3.12.2.22)	(Enzyme: Ricin A chain (rRNA N-glycosidase)			
OC	Fukuyama; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eucosids I; Malpighiales; Euphorbiaceae; Ricinus.				
OK	NCBI_Taxid:3389;				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=86067214; PubMed=2899712;				
RX	Halling R.C., Halling A.C., Mutzay B.E., Latin B.F., Houston L.L.,				
KA	Weaver R.F.,				
RT	Communis", cloning and characterization of a ricin gene from Ricinus				
RU	Nucleic Acids Res. 13:8019-8033 (1985).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=92163016; PubMed=3171405;				
RA	Tregerer J.W., Roberts L.M.,				
RT	The lectin gene family of Ricinus communis: cloning of a functional				
RU	ricin gene and three lectin pseudogenes.",				
RL	Plant Mol. Biol. 18:515-525 (1992).				
RP	SEQUENCE OF 12-576 FROM N.A.				
RP	MEDLINE=85178479; PubMed=3383723;				
RA	Lamb A., Roberts L.M., Lord J.M.,				
RT	"Nucleotide sequence of cloned cDNA coding for preprolectin.",				
RL	Eur. J. Biochem. 148:265-270 (1985).				
RN	[4]				
RP	SEQUENCE OF 36-302.				
RA	Yoshitake S., Funatsu G., Funatsu M.,				
RT	Isolation and sequences of peptide peptides, and the complete				
RU	sequences of the chain 27-127.				
RL	J. Biol. Chem. 267:12679-1274 (1992).				
RN	[5]				
RP	SEQUENCE OF 315-576.				

RA Funatsu G., Kimura M., Funatsu M.;
RA "Primary structure of Ala chain of ricin D.";
RL Agric. Biol. Chem. 43:2221-2224(1978).
RL
RL CHROMOPHORE-LINKAGE STATES AND PARTIAL SEQUENCE.
RX MEDLINE=90144223; PubMed=11668517;
RX Kimura Y., Kusudo H., Tada M., Takagi S., Funatsu G.;
RT "Structural analysis of sugar chains from ricin A-chain variant.";
RT Agric. Biol. Chem. 54:157-162(1990).
RN [7].
RN REVIEW.
RP MEDLINE=2148122; Pubmed=11595634;
RX Olmes S., Kozlov J.V.;
RX "Ricin.";
RL "Ricin.";
RL "Ricin.";
RL "Ricin.";
RX MEDLINE=917223-1728(2001).
RX
RX X-RAY CRYSTALLOGRAPHY (2, 8 ANGSTROMS).
RP MEDLINE=87165993; PubMed=5583297;
RP Montfort W., Villafranca J.E., Monzingo A.F., Ernst S.R., Katzin B.,
RA Ralubner E., Xiong N.H., Hamlin R., Roberts J.D.;
RT "The three-dimensional structure of ricin at 2.8 Å.";
RT J. Biol. Chem. 263:5398-5405(1987).
RN [9].
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=9155700; PubMed=1891881;
RX Katzin B.J., Collins F.J., Roberts J.D.;
RT "Structure of ricin A-chain at 2.5 Å.";
RT Proteins 10:251-259(1991).
RN [10].
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
RX MEDLINE=91551005; PubMed=1891882;
RX Ralubner E., Roberts J.D.;
RT "Structure of ricin B-chain at 2.5-Å resolution.";
RT Proteins 10:260-269(1991).
RN [11].
RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=95082010; PubMed=79901330;
RX Weston S.A., Tucker A.D., Thatcher D.R., DePryshire D.J.,
PA Paspartic R.;
RT "X-ray structure of recombinant ricin A-chain at 1.8-Å resolution.";
RT J. Mol. Biol. 244:410-422(1994).
RN [12].
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
RX MEDLINE=95174222; PubMed=7870513;
RX Day F.J., Ernst S.R., Frankel A.B., Monzingo A.F., Pascal J.M.,
RA Molina-Serrano M.C., Roberts J.D.;
RT "Structure and activity of an active site substitution of ricin A chain.";
RT Biochemistry 35:11098-11103(1996).
RN [13].
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=97240820; PubMed=9068200;
RX Yan X., Hollis T., Svahn M., Day P., Monzingo A.F., Milne G.W.,
RA Robertus J.D.;
RT "Structure-based identification of a ricin inhibitor.";
RT J. Mol. Biol. 266:1043-1049(1997).
RN [14].
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
RX MEDLINE=93165623; PubMed=1287657;
RX Kin Y., Robertus J.D.;
RT "Analysis of several key active site residues of ricin A chain by mutagenesis and x-ray crystallography.";
RN [15].
RN FUNCTION: Ricin is highly toxic to animal cells and to a less extent to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic effect that removes a specific adenine base involved in the binding of elongation factors. The modified ribosomes are unable to support protein synthesis. The A chain can inactivate a few thousand ribosomes per minute. This inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal

Thu Dec 11 16:03:46 2003

us-09-601-667c-10.rsp

Page 1

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18. Search time 4.61677 Seconds
(without alignments)
2736.539 Million cell updates/sec

Title: US-09-601-667c-10

Perfect score: 1420
Sequence: 1 DVTCSASEPTVATVGRNKM.....RRIIVPATKPKQWMLPVF 264

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt_41.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1405	98.9	264	1	MLB_VISAL
2	899.5	63.3	576	1	RIC1_RICCO
3	775	54.6	528	1	ABRA_ABRBR
4	770.5	54.3	564	1	AGGL_RICCO
5	765	52.7	527	1	ABRA_ABRBR
6	763	52.2	563	1	ABRA_ABRBR
7	528.5	37.2	563	1	ABRA_ABRBR
8	125.5	8.8	477	1	ABRA_ABRBR
9	115.5	8.1	475	1	ABRA_ABRBR
10	114	8.0	548	1	ABRA_ABRBR
11	114	8.0	548	1	ABRA_ABRBR
12	112.5	7.9	475	1	ABRA_ABRBR
13	111	7.8	475	1	ABRA_ABRBR
14	111	7.8	475	1	ABRA_ABRBR
15	111	7.8	475	1	ABRA_ABRBR
16	111	7.8	475	1	ABRA_ABRBR
17	111	7.8	475	1	ABRA_ABRBR
18	111	7.8	475	1	ABRA_ABRBR
19	111	7.8	475	1	ABRA_ABRBR
20	111	7.8	475	1	ABRA_ABRBR
21	111	7.8	475	1	ABRA_ABRBR
22	111	7.8	475	1	ABRA_ABRBR
23	111	7.8	475	1	ABRA_ABRBR
24	111	7.8	475	1	ABRA_ABRBR
25	111	7.8	475	1	ABRA_ABRBR
26	111	7.8	475	1	ABRA_ABRBR
27	111	7.8	475	1	ABRA_ABRBR
28	111	7.8	475	1	ABRA_ABRBR
29	111	7.8	475	1	ABRA_ABRBR
30	111	7.8	475	1	ABRA_ABRBR
31	111	7.8	475	1	ABRA_ABRBR
32	111	7.8	475	1	ABRA_ABRBR
33	111	7.8	475	1	ABRA_ABRBR

ALIGNMENTS

Result ID	Score	Match	Length	DB ID	Description
1	1405	98.9	264	1	MLB_VISAL
2	899.5	63.3	576	1	RIC1_RICCO
3	775	54.6	528	1	ABRA_ABRBR
4	770.5	54.3	564	1	AGGL_RICCO
5	765	52.7	527	1	ABRA_ABRBR
6	763	52.2	563	1	ABRA_ABRBR
7	528.5	37.2	563	1	ABRA_ABRBR
8	125.5	8.8	477	1	ABRA_ABRBR
9	115.5	8.1	475	1	ABRA_ABRBR
10	114	8.0	548	1	ABRA_ABRBR
11	114	8.0	548	1	ABRA_ABRBR
12	112.5	7.9	475	1	ABRA_ABRBR
13	111	7.8	475	1	ABRA_ABRBR
14	111	7.8	475	1	ABRA_ABRBR
15	111	7.8	475	1	ABRA_ABRBR
16	111	7.8	475	1	ABRA_ABRBR
17	111	7.8	475	1	ABRA_ABRBR
18	111	7.8	475	1	ABRA_ABRBR
19	111	7.8	475	1	ABRA_ABRBR
20	111	7.8	475	1	ABRA_ABRBR
21	111	7.8	475	1	ABRA_ABRBR
22	111	7.8	475	1	ABRA_ABRBR
23	111	7.8	475	1	ABRA_ABRBR
24	111	7.8	475	1	ABRA_ABRBR
25	111	7.8	475	1	ABRA_ABRBR
26	111	7.8	475	1	ABRA_ABRBR
27	111	7.8	475	1	ABRA_ABRBR
28	111	7.8	475	1	ABRA_ABRBR
29	111	7.8	475	1	ABRA_ABRBR
30	111	7.8	475	1	ABRA_ABRBR
31	111	7.8	475	1	ABRA_ABRBR
32	111	7.8	475	1	ABRA_ABRBR
33	111	7.8	475	1	ABRA_ABRBR

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Db	309	GEKDLAAGTGNSSKXQLYSQWGGNKK--NRHNSDSVVGVSGLLNNVGNITNGIL	366
Qy	119	LTVGLDLYTLGGC	132
		: : :	
Db	367	IQLYTCSNSNQKX	390

RESULT 14
T35697

arabinofuranosylase - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:date: 05-Nov-1999 #sequence, revision 05-Nov-1999 #text, change 03-Dec-1999
 C:Accession: J35697
 R:Wu, P. Y., Harris, D., Perchall, J., Barrell, B. G., Rajadream, M. A.
 Submitted to the EMBL Data Library, January 1998
 A:Reference number: J21546
 A:Accession: J35697
 A:Status: preliminary / translated from GB/EMBL/DDbJ
 A:Molecule type: translated from GB/EMBL/DDbJ
 A:Residues: 1-475 c-mur
 A:Cross-references: EMBL:AL021411; FIDN:CA16189.1; GSPDS:GN00070; SCoEDB:SC7H1.02
 A:Experimental source: strain A3(2)
 C:Genetics:
 C:Name: abD3; SCoEDB:SC7H1.02

Query Match	8.1%;	Score 115.5;	DB 2;	Length 475;
Best Local Similarity	24.1%;	Pred. No. 0.052;		
Matches 52;	Conservative 35;	Mismatches 104;	Indels 25;	Gaps 10;

Qy 6 SASEPTTIVIGRNGMRVDVRDDDFHONQIQMPKSNNDNQMTIKDGTISNG-SC 64
:
Db 37 AAGSGALRGAGSNC-IDVLGSSQDDCDAALLDYCWGGT--NQQWSTSDTGRLTYGDKC 93

```

QY      65 LTTTGYTA--GYVMIPEDCNTAVREALIWTQIDNGTILINRSNLVL--ASSSG-IGKTITLT 1200
      |  :  |  |  |  |  |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      94 LDVFGHATAPGTITVQIINSCSGGANQC--WRVNSDGIIVGVESGLCLEAAGAGLTAVAQ 1511

```

```

QY      121 VQGLIDYTLGGGWLGNADIPAREY-----IYFRDLQMESNGSGSWVEED-SSQKNGK 174
          :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      152 LMTGNGGGNGKWTGLTGTPPTDGTALPSTYRWSSGIVLAQPKSGWALADFTVTHNGR 211

```

```
QY      175 MALYGDS-----IRKXNQDQCTSGRSDVS 201
          :|||         |           :|:::
Db      212 HLVTGSTSGSSYGSMVFSPTTWSDMASAGQNAM 247
```

RESULT 15
710004

glican endo-1,3-beta-glucosidase (EC 3.2.1.1-) precursor - Oerskovia xanthinolytica
 G:Species: Oerskovia xanthinolytica
 G:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 22-Oct-1999
 R:Shen S.H., Chretien, P., Bastien, L., Sillaty, S.N.
 J. Biol. Chem. 265, 1058-1063, 1991
 A:File: Primary sequence of the glucanase gene from Oerskovia xanthinolytica. Express
 A:Accession: M3094; MD5:51093212; PMID:1985933
 A:Accession: M3094
 A:Accession: M3094
 A:Accession: M3094
 A:Molecule type: cDNA
 A:Residues: 1-548 <SRE>
 A:Cross-references: GB:M60826; GB:M89734; NID:G150444; PID:AA25520.1; PID:G150445
 A:Keywords: glycosidase; hydrolytic

Query Match	8.0%;	Score 114;	DB 2;	length 548;
Best Local Similarity	31.3%;	Pred. No. 0.084;		
Matches. 41;	Conservative 18;	Mismatches 52;	Indels 20;	Gaps 7

```

QY      16 GRNCRV-----DYRDDFDHGNGQIQLPMSKNNENQWLTKIKGTIRKNGSGL--TT 67
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      422 GTGALRIGSTLCDVPWADPTDINQVL--ATCSGNAAQWTRGTGTVALTKGCLDVAR 477

```

```
QY      68  XGYAGVYMI FDCN-TAVREATIQIDUNST--INPRSNLYLAASGI---KGTITLV 122
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
```

Db	480	SGRDSTAVWLYICNGTQAKWT	----	YDAKRLARPGSGCIDAAGAFIRGQGVQL	533
Q7	122	QTLDYTLRGW			132
Db	536	WTCNQTENAKM			546

Search completed: December 11, 2003, 13:55:45
Job time : 9.20622 secs

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	Matches	116:	Conservative	33:	Mismatches	96:	Indels	12:	Gaps	6:
Qy	5	CSASPTFAIVQNGKRVADVRDDPFHQNGQIQAMPSKSNDDNDQWLTIKEDGRTISNGAGC								
Db	316	CSVETVETRIISGMDGLCVDRVKGHYIDGAPQALRP--CGNECNDLQTRRDYGTIFMGIC								
Qy	65	LTFTGYAGVYVIMPDQCNAMREATTIQMDNNGTIIIPRSNLVLAASSAQITLLTYOVL								
Db	374	L-----YASSSVIMDQCNVPEAPKAAVVSIDITFTPHSGVLTLPQAMGALSTLENN								
Qy	125	DYTGSGMAGNLTAPATRYATVYGRDLCHENQGS--VHTFTCTVATVQADMLVKGSS								
Db	429	IHAAQGMVTVG-DVETLVETVIGKMKCLPENEENRTVYMLDCTVLRNQ--EMHLYDQQT								
Qy	133	IPKQNDQCCTSGRSYVSIVINVSQSGASQGMFTNEALILMLKKSGPMDVADQAP								
Db	487	IVVSNNSLCVTSSEHBSIDLVTILCKEG--SGNQGMVFNTNGTISNPNAKLMDVAGREV								
Qy	243	KLRRIIIVPATGRKNQML								
Db	546	SLKRLIIVPATGRKNQMI								

RESULT 11
JC7535

chitinase [EC 3.2.1.14] 35 - Streptococcus thermophilus
C|Species: Streptococcus thermophilus
C|Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #ext_change 30-Jun-2001
C|Accession: JCT535
R|Synonyms: H.; Okamoto, T.; Hatano, N.; Miyamoto, K.; Watanabe, T.; Mitsutomi, M.; Inami,
Biosci., Biotechnol., Biochem., 64, 2445-2453, 2000
A|Molecule family: 19 chitinases from Streptococcus thermophilus OJC-520 | Molecular cloning
A|Reference number: JCT535; PMID:21036907; PMID:1193414
A|Accession: JCT535
A|Molecule type: DNA
A|Residues: 1-377 <TS>
A|Cross-references: DDBJ:A016842
A|Experimental source: strain OJC-520
C|Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin degradation.
I|Saccharide-binding domain that is important for the efficient hydrolysis of insoluble c
C|Genetics:
A|Gene: chl35
K|Keywords: glycosidase; hydrolase

Query Match	9.6%;	Score 136;	DB 2;	Length 377;
Best Local Similarity	20.8%;	Prod No 0	00074.	

Matches 60; Conservative 33; Mismatches 108; Indels 88; Gaps 9,

Qy	7	EEEPRTVIGSNGMYVYVRDDPHDNOQIUMSXSNSNDPQMTIKDGTISNSGCT	66
Dp	33	AQAATSLTGIDKCLDPAHNSNSNGPVQVYCNCGN--AQQVYVTSIHALGACD	90
Qy	67	TGVTIA--GYVVIPECNIVAEVITMOIMDNSTIPSSNIVLAAS--SGIKPTLTQ	122
Dp	91	VDSSTADGATVOLDCTGGANOK--VYVTAADIVNPADKCLDPTRNSNSNGPVQI	148
Dy	123	TLDTYVIGQGMIA--GNDTAPREVTI-----XGPRLCHESNSGSAVW	162
Dy	149	ITCTGSGNCFMHPAATGGSGSTPSTSGPVSBAQNOQNPNNFTYQGLVQALSGFGR	208
Qy	163	ETCSGSGRNO-----	181
Dp	209	NGSDTITKQEAALFLANVHETSGQGYVVELTANFTYCMQSGSYCGRPALVYGRG	268
Qy	182	STRPKNODCTSGSGDSVTVIVYSGASG---SGPWFVFNCAI	226
Dp	269	PIQLSNV-----YVYKAAGALITVDLLNMPVLENDPAI	302

RESULT 12

US0569
endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - *Streptomyces lividans*
N/Alternate names: xylanase A

C:Species: Streptomyces lividans
C:Date: 10-Mar-1993 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1993
C:Accession: J05089, F50238
P:Subunit: 107, 75-82, 1091, 1298
P:Author: Iguchi, M., Morosoli, R., Kluepfel, D.
A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A:Reference number: J05089; PMID:92077439; PMID:1743521
A:Accession: J05089
A:Molecule type: DNA
A:Residues: 1-477 <SMA>
A:Accession: GEM64551
A:Residues: 1-50238
A:Molecule type: protein
A:Residues: 43-92 <SMA>
A:Gene: xlnA
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
C:Pathway: xylan degradation
C:Keywords: extracellular protein; glycosylase; hydrolase; polysaccharide degradation
F:1-41/Domain: signal sequence #status predicted <SIG>
F:42-477/Product: endo-1,4-beta-xylanase A #status experimental <EMT>
F:159-277/Domain: Streptomyces endo-1,4-beta-xylanase A homology <SMY>
F:159-277/Active site: Glu #status predicted

Query Match	Score	DB	Length
8.8%;	125.5;	DB 1;	477;

Best Local Similarity 45.9%; Freq. NO. 0.00/6;
Matches 40; Conservative 20; Mismatches 61; Indels 13; Gaps 6;

7 ASEP-----TVRIIVGRNGMRYDVRRDDFDHGNQIQLPSPSKNNDPNQLTWIKEDGTIRSN 61

Db 346 SSEPADGGQIKGVG-SGRCLDVPDASTSGTQLQINDCHSGT--NQWATDAGELRVY 402

62 G-SCLTGYGAYGVYMFDCNTAVREATIOWIDNGTIINPESNLVLA--SSGIKGT 118

Db 403 GDKCDAGTSGNSKVQIYSCMGEDNOK--WRLNSDGSIVGVOSGLCTDAVNGTANGTTL 460

119 LTVQTLDYTLGQGN 132

461 IOLYTCNSNGSNOW 474

RESULT 13
T34603

Xylanase A - *Streptomyces coelicolor* (fragment)

```

C/Species: scyrtomyces coriolicolor
C/Date: 05-Nov-1999 #sequence 05-Nov-1999 #text_change 28-Jul-2000
C/Accession: m1000

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C/Accession: 134603
R/Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, January 1998
A/Reference number: Z21548

A/Accession: T34603
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 1-383 <MTR>

A/Cross-references: EMBL:AL021529; PIDN:CAA16468.1; GSPDB:GN00070; SCOPEDB:SC10M
A/Experimental source: strain A3(2)

C/Genetics:
A:Gene: X1NA: SC0EDB:SC10A5.36C

C/Superfamily: Streptomyces endo-1,4-beta-xylanase A; Streptomyces endo-1,4-beta-xylanase F-1-247/DomAin: Streptomycetes endo-1,4-beta-xylanase A homology (SV)

Onerv March 8 68: Score 133 E. DP 3. Length 383.

Match	10	20	30	40	50	60	70	80	90	100
Local Similarity	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03
Best Local Similarity	29.9%	Pred. No.	0.01							

matchnes	40;	conservative	19;	mismatches	62;	indels	13;	gaps	6
----------	-----	--------------	-----	------------	-----	--------	-----	------	---

7 ASBP-----LWLVGRNGRNVDPDRDDFDHGNQIQLPSPKSNNDPNQJWTTIKRDPGIRSN 61

Db 252 SSEPADGGQIKVG-SGRCLDVPDASISDGTQLQLTWCHSGT--NQMAATDAGEIRVY 308

62 G-SCITTYGYTAGVYMI FPDNTAVREALTIWQIWDNGTII INPRSNVLAA--SSGJKGTT 118

RESULT 8

S16022
 abrin-c precursor - Indian licorice
 N/Contamin: RNA N-glycosidase (EC 3.2.2.22)
 C/Species: Abrus precatorius (Indian licorice)
 C/Date: 19-Mar-1997 #sequence, revision 19-Mar-1997 #text, change 20-Aug-1999
 C/Accession: S16022
 R/Wood K.M., J.M.; Nairn, R.J., Pickett, M.
 Eur. J. Biochem. 1997; 243:732-737.
 A/Title: Peptide mapping, characterization and the expression of the A-chain
 A/Reference number: S16022; MIMD:91266957; PMID:2050149
 A/Accession: S16022
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-562 <W00>
 A/Cross-references: EMBL:X55667; NID:916084; PIRN:CA39202.1; PDB:16085
 C/Comment: The A chain, which inhibits protein synthesis by inactivating
 C/Superfamily: rRNA N-glycosidase homology
 C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglyutamic acid
 F/1-285/Product: abrin-c chain A #status predicted <ACH>
 F/1-285/Domain: RNA N-glycosidase homology <RNG>
 F/1-285/62/Product: abrin-c chain B #status predicted <BCH>
 F/1-359/359-400,403-441,448-483,487-526,529-562/Region: 40-residue repeats
 F/135/Modified site: pyroglutamic carboxylic acid (Glu) (in mature form) #status predicted
 F/135/147/223/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F/135/287/395,416/Binding site: substrate predicted (Asp) (covalent) #status predicted
 F/135/303/320-339,363-380,451-464,490-507/disulfide bonds: #status predicted
 F/322,346/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F/534,555/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 53.6%; Score 761; DB 2; Length 562;
 Best Local Similarity 54.8%; Pred. No. 3, 5e-56;
 Matches 143; Conservative 42; Mismatches 74; Indels 2; Gaps 2;

QY	5	CSAS-EPPTVIVNGKRVDPDHPDNOQLMPSKNNNDQTLTKYDPTISNGS	63
DB	303	CSRVETPLVIGRQKCVDDYDGNHGRILAMKCKRLRNGQTLTKSPKTIISNGK	362
QY	64	CLTIVYAGVYVIMPCVTAVENTIMQWNGTILNFRSNVLAASGIGTTLTVQT	123
DB	363	CLTIVYAGVYVIMPCVTAVENTIMQWNGTILNFRSNVLAASGIGTTLTVQT	422
QY	124	LDYTLQGLAANDAPREVITTFGRDLCESNGSVYFCTSSGKQKALYKDSI	183
DB	423	NEVLMQKRTNNISPFYTSISGIDLCQKSNVMAADCKNKKEQ-QALYIDSI	481
QY	184	RPKQNDCLTSGNDSTVIVNIVSGASGQSFVTFEGATILNKKGPADVPAQMPK	243
DB	482	RSVQNTNCLTSGNDSTVIVNIVSGASGQSFVTFEGATILNKKGPADVPAQMPK	541
QY	244	LRRIIVPATGRNOMLPEV	264
DB	542	LRRIIVPATGRNOMLPEV	562

RESULT 9

S32431
 abrin-d precursor - Indian licorice (fragment)
 N/Contamin: RNA N-glycosidase (EC 3.2.2.22)
 C/Species: Abrus precatorius (Indian licorice)
 C/Date: 30-Sep-1993 #sequence, revision 01-Aug-1997 #text, change 01-Aug-1997
 C/Accession: S32431; S34408
 R/Hung, C.; Lee, M.; Lee, T.; Lin, T.
 Eur. J. Biochem. 1993; 205:167-193.
 A/Title: Primary structure of three distinct isoforms determined by cDNA sequencing.
 A/Reference number: S32429; MIMD:9132798; PMID:8421113
 A/Accession: S32431
 A/Molecule type: RNA
 A/Residues: 1-528 <R00>

A/Cross-references: GB:M99346
 R/Hung, C.; Lee, M.; Lee, T.; Lin, T.
 submitted to the EMBL data library, March 1993
 A/Reference number: S34408
 A/Accession: S34408
 A/Molecule type: RNA
 A/Residues: 1-169, 'C', 171-320, 'I', 322-528 <R02>

A/Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating
 C/Superfamily: rRNA N-glycosidase homology
 C/Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin;
 F/1-251/Product: abrin-d chain A #status predicted <ACH>
 F/7-246/Domain: RNA N-glycosidase homology <RNG>
 F/7-246/528/Product: abrin-d chain B #status predicted <BCH>
 F/1283-325,328-366,369-407,414-445,453-492,495-528/Region: 40-residue repeats
 F/1283/Modified site: pyroglutamic carboxylic acid (Glu) #status predicted
 F/1283/113/155,156/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F/1283/269/386-405,329-346,417-430,456-473/disulfide bonds: #status predicted
 F/1283/312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F/500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 53.5%; Score 760; DB 2; Length 528;
 Best Local Similarity 54.8%; Pred. No. 3, 5e-56;
 Matches 143; Conservative 43; Mismatches 73; Indels 2; Gaps 2;

QY	5	CSAS-EPPTVIVNGKRVDPDHPDNOQLMPSKNNNDQTLTKYDPTISNGS	63
DB	269	CSRVETPLVIGRQKCVDDYDGNHGRILAMKCKRLRNGQTLTKSPKTIISNGK	328
QY	64	CLTIVYAGVYVIMPCVTAVENTIMQWNGTILNFRSNVLAASGIGTTLTVQT	123
DB	329	CLTIVYAGVYVIMPCVTAVENTIMQWNGTILNFRSNVLAASGIGTTLTVQT	368
QY	124	LDYTLQGLAANDAPREVITTFGRDLCESNGSVYFCTSSGKQKALYKDSI	183
DB	389	NEVLMQKRTNNISPFYTSISGIDLCQKSNVMAADCKNKKEQ-QALYIDSI	447
QY	184	RPKQNDCLTSGNDSTVIVNIVSGASGQSFVTFEGATILNKKGPADVPAQMPK	243
DB	448	RSVQNTNCLTSGNDSTVIVNIVSGASGQSFVTFEGATILNKKGPADVPAQMPK	507
QY	244	LRRIIVPATGRNOMLPEV	264
DB	508	LRRIIVPATGRNOMLPEV	528

RESULT 10

S62627
 agglutinin I precursor - European elder
 C/Species: Sambucus nigra (European elder)
 C/Date: 24-Aug-1996 #sequence, revision 13-Mar-1997 #text, change 20-Aug-1999
 C/Accession: S62627; S62619
 R/Ryan, P.; Barré, A.; Rouge, P.; van Leeuwen, F.; Peumans, W.J.
 Eur. J. Biochem. 1996; 235:128-137.
 A/Title: The N-glycanase-binding lectin from elderberry (Sambucus nigra)
 A/Accession: S62627
 A/Status: preliminary
 A/Molecule type: RNA
 A/Residues: 1-570 <VNA>
 A/Cross-references: EMBL:U27122; NID:9114772; PIRN:AAQ9158.1; PDB:9114773
 A/Accession: S62619
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 25-319-353
 A/Superfamily: rRNA N-glycosidase homology
 F/1-7-283/Domain: RNA N-glycosidase homology <RNG>

Query Match 37.8%; Score 537; DB 2; Length 570;
 Best Local Similarity 45.6%; Pred. No. 2, 3e-37;

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	Matches	145; Conservative	42; Mismatches	72; Indels	2; Gaps	2
QY	5	CSAS-EPTVATVIGSAGARVDDDDFDGNOQTLMESKNNIDPQATWIKETGTRRNS	63			
Db	269	CSASREPTVATVIGSDGACDVYNGSHNGNRILIMKCRILBERMQLMLESIRIRNSK	328			
QY	64	CLTTTGYGAYTVNIEDCNATVAEATIMQIMDNGSTINRSNTVLAASIGITGLTVO	123			
Db	329	CLTTTGYGASSTVNIHDCSNAEATITWNGSTINRSNTVLAASISMGITGLTVO	388			
QY	124	LDVTLTGASMLANQTPAEFVATVIGPDICAESNGSWFVCSGKXQKQAKALVGGSI	183			
Db	389	NETLRAQMTANTSTSPVTSIGTSVDCIAQKQSGSNVLAACDSNKKQ-CNALTLTGSI	444			
QY	184	RFXKQVQDCLTSGDSDSVTVNIVSCGASGASQQRVTEAGALINLKSGPMDVQAANK	243			
Db	448	RSQVNTNCLCTKPHKRGSGTILLMGCSNGMASQRFKNDGSIVSLYDMVMDVKGSDPS	507			
QY	244	LRRIITVATGSPQNMALPVF	264			
Db	508	LKQITLWATVIGSPQNMALVTLTF	528			

Qy	125	DTYLGQGLMAGNDPTAPREVTVIGRDLCEWESNGSVWETCTSSGKQKQKALVGGDSIR	184
Ds	426	IVASQGLPENNTPQFPVTVITGVGLVNGCLQANSGKWLSEDC-TSEAEQDQALVADSSIR	484
Qy	185	PKQNDQCLISGSGDSVSTVINTVSCGASGQNPPTNEGATLITLKGPADVDAQNSK	245
Ds	485	FGQNDQCLITDQAKIGCVITLGLSGLSSQGNFPRKQDITLVNGLVLDPRSDSL	544
Qy	245	RLIIVYPAKCGNQMLPVY	264
Ds	545	KQIVHPFGQNLQIMLEPL	564

RESULT 7

532430

abrin-b precursor - Indian licorice (fragment)

N:Contains: rRNA N-glycosylase (EC 3.2.2.22)

C:Species: Abrus precatorius (Indian licorice)

C>Date: 30-Sep-1993 #sequence_rev:ston 01-Aug-1997 #text_change 20-Aug-1999

R:Accession: S32430, C:Cl1932

R:Length: 541, 228, 263, 263, 1993

R:Author: Saito, T.C., Lin, J.Y.

```

RESULT 6
R1CSAD
agglutinin precursor - castor bean
N:Contains: rRNA-N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
R:Accession: A24261; A24210
J:Title: Chem 260, 15682-15686, 1965
A:Reference number: A24261; MIM:60059449; PMID:2395130
R:Accession: A24261
A:Reference number: A24261
R:Accession: A24261
A:Cross-references: GB:M12089; NID:9169700; PDB:AAA3869; PDB:9169701
R:Atx1, T.; Yoshiocka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A:Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin
A:Reference number: A24210
A:Accession: A24210
A:Molecule type: Protein
A:Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-563
C:Comment: This protein has strong agglutinating activity and weak glycosylating activity compared
C:Keywords: duplication; glycoprotein; N-glycosidase; hydrolase; lectin; RNA binding; seed
P:1-250:Domain: signal sequence; signal peptide; predicted <ACH>
P:125-281:Domain: rRNA-N-glycosidase homology <RMS>
P:303-564:Product: agglutinin chain B #status experimental <ECH>
P:319-351, 365-402, 405-443, 450-485, 489-528, 533-564:Region: 40-seconds repeats
P:323-259:Binding site: carbohydrate (Aam) (covalent) #status predicted
P:104-147, 231-233:Binding site: substrate (TYR, TYR, GLU, Asn) #status predicted
F:200, 203/Active site: Glu, Arg #status predicted
F:282-306, 322-341, 365-382, 453-466, 492-509/Disulfide bonds: #status predicted
F:334, 337, 348/Binding site: N-acetylgalactosamine (ASP, Glu, Asn) #status predicted
F:337, 437/Binding site: carboxypeptide (Asn) (covalent) #status experimental
F:356, 557/Binding site: N-acetyl-galactosamine (ASP, Asn) #status predicted

Query Match 54.3%; Score 770.5; DB 1; Length 564;
Matches 144; Conservative 41; Protein 577; Indels 1; Gaps 1;

QY 5 CASPEPTVIRYRKARVDVDDPHNGKGLQMPSEKSNDDNOLMTIRPGRGISNSGC 64
DB 306 CMPEPTVIRYVRNGLCVDVYGEPEFNGPQLMPCKSNDDNOLMTLKXSTISNGKC 365
QY 65 LTYGVGVGVVMTFCNTATREATITQMTWNGTINRNSNVLVAASQIGITLVQTL 124
DB 366 LITSNSPQVVTVNSCTATVATRNQQLWDRITLIRNNGSVLVAASNSGKTLTVQTN 425

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[illegible]

	A: Molecule type: protein	C: Superfamily: richin, rRNA	N: Glycosidase homology	P: 65,76,116	B: Binding site: carbohydrate (asn) (covalent)	# status experimental
Query Match	98.24;	Score 1394.5;	DB 2;	Length 265;		
Best Local Similarity	98.94;	Field, No. 66-110;				
Matches 262;	Conservative 0;	Mismatches 2;	Indels 1;	Gaps 1		
Dy	1	DVTGSGSEPTTITVYGNKQKQVWTRDDHDCNQIQMFSKSNPNQMTTETGGTGRS	60			
Dy	1	DVTGSGSEPTTITVYGNKQKQVWTRDDHDCNQIQMFSKSNPNQMTTETGGTGRS	60			
Dy	61	NSGCTTGYTGAGYVYVDDCNARVAREATIMQINDGNTIMPESMLVLAASGSKGTLT	120			
Dy	61	NSGCTTGYTGAGYVYVDDCNARVAREATIMQINDGNTIMPESMLVLAASGSKGTLT	120			
Dy	121	VQTLDTYLGQGLVAGNDTAPPEVYTYGFRDLQESNSGSSVWATDSSGQDNQKALVYED	180			
Dy	121	VQTLDTYLGQGLVAGNDTAPPEVYTYGFRDLQESNSGSSVWATDSSGQDNQKALVYED	180			
Dy	181	GSIRPNQPOGCTSGSDVSTVYINVYSCGASGSGQWFTNEGALINLQGLAVDVQA	240			
Dy	181	GSIRPNQPOGCTSGSDVSTVYINVYSCGASGSGQWFTNEGALINLQGLAVDVQA	240			
Dy	241	NPTLRRLITVYATKGNQWV-LVPE 264				
Dy	241	NPTLRRLITVYATKGNQWV-LVPE 265				

RESULT 3

Ricin D precursor - cactor bean
N.Contains: rRNA N-glycosidase (EC 3.2.3.22)
C.Species: Ricinus communis (cayston bean)
C.Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #next change 16-Jul-1999
CAccession: A24041; S20513; A24614; A08742; M2410; A0374; S1203 L.L.; Weaver R.F.
R.Rating: Grade B; Hm1; Hm2; Hm3; Hm4; Hm5; Hm6; Hm7; Hm8 E.E.; Uddén, B.J.; Houston, L.L.
Article: genomic cloning and characterization of a ricin gene from Ricinus communis.
A.Reference number: J24041; PMID:86067214; PMID:2999772

A.Accession: A24041
AMolecule type: DNA
A.Residues: 1-576 <HAL>
A.Cross-references: GB:X03179; MID:g21082; PIDN:CMA26939.1; PID:g21083
P.Reviewer: W.M.; Roberts,L.M.
Plant Mol Biol.: 10, 315-323, 1992
A.Creation date: 19930109
A.Update sequence numbers:
A.Sequence numbers: S20513; MID:s2163016; PMID:1371405
A.Accession: S20513
AMolecule type: DNA
A.Residues: 1-576 <TRB>

A.Protein: F.I.; Robertes, L.M.; Lord, J.M.
Eur. J. Biochem. 148, 265-270, 1995
Article: Nucleotide sequence of cDNA coding for preproprotein.

A.Accession: A24614
AMolecule type: mRNA
A.Residues: 12-75/'D'/,77-550/'R'./,552-576 <LMB>
A.Cross-references: GB:X02388; MID:g21077; PIDN:CMA26230.1; PID:g21078
J.Yoshitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
Article: Isolation and sequences of peptic peptides, and the complete sequence of the chymotrypsinogen-like protein.

A.Accession: A03372
AMolecule type: protein
A.Residues: 36-97/'O'./,99-109/'S'./,111-269/'D'./,272-283/'L'./,285-288,290-302 <YOS>
A.Note: This paper cites the others in the series providing experimental details for the
R.Aoki, T.; Funatsu, G.
FEBS Lett. 191, 120-124, 1995
Article: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A:Reference number: A24010
A:Accession number: A24010
A:Molecule type: protein
A:Residues: 315-383, PS, 386-576 <RB>
R:Emanuel, G.; Kimura, M.J. J Biol Chem 1971, 246, 979
R:Giblin, D.L. J Biol Chem 1971, 246, 979
A:Title: Primary structure of Ala chain of ricin D.
A:Reference number: A03374
A:Accession number: A03374
A:Molecule type: protein
A:Residues: 315-353, N, 337-342, NH, 345-362, 364-383, PS, 386-576, T, 401, D, 403, E,
S27, E, 539-564, W, 566, H, 567-570, LK, 573-574, F, <RU>
A:Note: this paper, 'W', of the same author, summarizes the experimental details for the deter-
mination of the primary structure of ricin B-chain.
R:Ready, M.P.; Kim, Y.; Robertus, J.D.
Proteins 10, 270-278, 1991
A:Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of
action.
A:Reference number: A48237, PMID:91352006, PMID:1081863
A:Accession number: A48237
A:Keywords: amonoxian, active site
R:Hutcheon, R. Biochemistry 1990, 29, 1890

A; References:

[illegible]

Thu Dec 11 16:09:46 2003

US-09-601-667c-10.rpr

Page 1

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 8.2622 Seconds

Title: US-09-601-667C-10

Perfect score: 1420

Sequence: 1 DVTCSASEPTVIVRNGM.....SRITVPAKGNKQMLPVF 264

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616662 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Display first 45 summaries

Database: PIR 76:*

1: P112:*

2: P112:*

3: P113:*

4: P114:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1405	98.9	264	2 PD0019	miscletoe lectin I
2	1394.5	98.2	265	2 JMO090	lectin-I B chain -
3	899.5	63.3	376	1 R1230	ricin D precursor
4	894.5	63.3	376	1 R1230	ricin D precursor
5	775	54.6	528	1 T215A	abrin-a precursor
6	770.5	54.3	564	1 R1230	abrin-a precursor
7	765	53.9	527	2 S1243G	abrin-b precursor
8	761	53.6	562	2 S1243G	abrin-b precursor
9	760	53.5	528	2 S1243G	abrin-d precursor
10	537	37.8	570	2 S1243G	agglutinin I precur
11	136	9.6	377	2 JCT555	endo-1,4-beta-xyla
12	125.5	8.8	477	1 US0589	xylosylase A - strep
13	122.5	8.6	382	2 T34603	arabinosyltransfera
14	119.5	8.0	548	2 A33064	probable hydrolase
15	113	8.0	464	2 T33943	probable hydrolase
16	111	7.8	525	2 A45033	actinobivirin precur
17	106	7.5	160	2 JCT622	polypeptide N-acet
18	102	7.2	563	2 A88515	probable polypepti
19	102	7.2	612	2 T42233	hypothetical prote
20	102	7.2	612	2 T42233	hypothetical prote
21	101	7.1	386	2 AE1936	probable lipoprote
22	98.5	7.0	1067	2 T28665	alpha-galactosidas
23	98.5	6.9	452	2 T33988	probable hydrolase
24	98.5	6.9	452	2 T33988	probable hydrolase
25	98.5	6.9	452	2 T33988	probable hydrolase
26	94.5	6.7	962	2 AD0835	large repetitive p
27	93.5	6.5	875	2 AD0835	lora toxin compone
28	93	6.5	875	2 AD0835	polymorphic membra
29	93	6.5	1723	2 H86557	

30	93	6.5	1723	2 E72067	polymorphic membra
31	93	6.5	1723	2 E72067	polymorphic membra
32	92	6.5	895	1 IUX1CP	EP-cadherin precur
33	90.5	6.4	908	2 AE2254	hypothetical prote
34	90.5	6.4	1008	2 T32986	hypothetical prote
35	90.5	6.4	1711	2 AB1283	peptidoglycan link
36	88.5	6.3	471	2 A41478	cytochrome vha pre
37	88.5	6.3	624	2 T42247	polypeptide N-acet
38	88.5	6.3	624	2 T42247	polypeptide N-acet
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42	88	6.2	1704	2 A55426	glutathione R (BC 3
43	88	6.2	3083	2 AH2493	hypothetical prote
44	86.5	6.1	1032	2 T42257	beta-1,3 exoglucan
45	86.5	6.1	1231	1 A48450	endo-1,4-beta-xyla

ALIGNMENTS

RESULT 1

PD0019

miscletoe lectin I B chain - Viscum album (fragment)

C/Species: Viscum album

C/Date: 03-Jul-1998 #sequence.revision 10-Jul-1998 #extl.Change 07-May-1999

C/Accession: PD0019

C/Accession: S.1.242568141 R.1.242568141 A.1.242568141 S.1.242568141

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Thu Dec 11 16:10:07 2003

us-09-601-667c-9.ra1

Db 224 AKQAVYVWVDFKSGVPIDC-----VGFQSHNSGNPYNRRTLLQAPAL-GVDV 276
Qy 120 TVGTLDTYTLGGGMLAGNDTAPRE-----VTTCGRPD-----LC 152
Db 277 EYTELDI-----ENAPDQTVASVIRDCIADVRCGTGITWGVDRSDSWMSYQNPIL 326
Qy 153 MESN-----GGSVWV-----BT 164
Db 327 FNNKSKKQAYATLALNBSDDGGGSRPVSPPFGSSGQJNGVANSKCIQVKNRT 386
Qy 165 CDSSQ-----KNGKQVALYGDGSIKPKQNDQCLAGDSVGVIVIVSCGASGS 215
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RESULT 15
US-09-468-812-5
; Sequence 5, Application US/09468812
; Patent No. 5935836
; GENERAL INFORMATION:
; APPLICANT: Vehmaamp, Jari
; APPLICANT: M nyl, Atja
; APPLICANT: Fagerstr m, Richard
; APPLICANT: Lantto, Raija
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pekko
; APPLICANT: Kuitinen, Raija
; APPLICANT: Kuitinen, Raija
; TITLE OF INVENTION: Xylanadure Xylanase Sequences and Methods
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER: IBM PC compatible
; MEDIUM TYPE: 3.5 disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,812
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332,412
; FILING DATE: 01-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/282,001
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Larry B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 1050.0340002
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear

MOLECULE TYPE: peptide
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: AM50
US-08-468-812-5
Query Match 8.6%; Score 122.5; Db 2; Length 480;
Best Local Similarity 32.4%; Pred.No.0.00029;
Matches 33; Conservative 16; Mismatches 48; Indels 5; Gaps 3;
Qy 22 VPRGDDPHFGNQIQUMSKSNNDPQMLTKNDGTSRSG-CLTTCGTACTYTMFD 80
Db 379 IDVPKNTADGTQVLYDCHSGS--NQWTYTSSEPRIFPKKCLDAGSSNNAVQIYS 436
Qy 81 CMTAVREATIWMQNDGIIINFRSNVYLAASSGKGTLLTVO 122
Db 437 CWGANQK--NELRADGTIVGVQSLCLDAVGGGTGNGTLLQ 476

Search completed: December 11, 2003, 14:11:35
Job time : 10.1403 secs

Thu Dec 11 16:10:07 2003

us-09-601-667c-9.rat

Page 7

APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Regalaky, Lawrence B.
REGISTRATION NUMBER: 35,086
ADDRESS: 1050.0340003
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-770-621-4

Query Match 8.8%; Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00019;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

23 DYRDDDFHNGNOIOLMPS--KSNNDPNOQMTIKEDGTR--SNGLTLYGV-----70
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224 AKQAYNNVNVDPKSRNPVPLD-----VGRQSHNSGNPVPVPTLQAPALGVVV 276
120 TVQTLIVYTLQGLAGNDTPPE-----VTIYGRD-----LC 152
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327 FDNNGKCAIYAVIDALNNGSDGGSANPVPSPGSSQIRGVASRCIDVPRKNT 366
165 CDSGQ-----KNGKMLYGDGSIKPRKQDGLTSRPSDVSQVYINIVSGASGS 215
387 ADGTQVQVLDCHGSGNQ--CWYTSGRFRIRG--KILDAQGSNGAVQVQTSWQA--N 442
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US-09-770-621-7
Sequence 7, Application US/09/770621
Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Regalaky, Lawrence B.
REGISTRATION NUMBER: 35,086
ADDRESS: 1050.0340003
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENEOME:
CHROMOSOME/SEGMENT: AM50
US-09-770-621-7

Query Match 8.8%; Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.00019;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

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71 --TAGYVWI-----FDCTAVRBAITWQINDGTTINPESNLVLAASGIGKTTL 119

443 GRWVFNBGAILNLTQGLAMD--VQANFRRLRIITFRATKPKNQW 488

Thu Dec 11 16:10:07 2003

us-09-601-667c-9.ra1

Page 6

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 1056
REFERENCE/DOCKET NUMBER: 1050, 0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
FAX: 202-371-2640
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-590-563-4

Query Match 8.8%; Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred No 0.0019;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

DB 23 DVARDPDDGNGQIQMPG---KSNNDPQQLMTIKEDGTR---SNQSCLTYYGY--- 70
168 DVNNAEFDGNSGRCDNLTQRTGND---WIEVAFRTAQDPSAKLCYNDVNIEMNNA 223
QY 71 --TAGYTYNI-----FDGNTAVREATTQIMDNGTINPRSNLYLAASGIXKTTL 119
DB 224 AKTQAVYNNVADPKRGVPIIDC-----VQSHFNSGNTVNFRTTLQDPAL-GDVV 276
QY 120 TVQCLDYLGGCMLANDTAPR-----VITVGFPD-----LC 152
DB 277 EYVELDI-----ENAPQYAVIRDLAVDRCTGTTVGVYRDSMSRYONPL 326
QY 153 MSNN-----GGSVWV-----ET 164
DB 327 FDNNGKKAQYAVYALNAGSDGGGSPVSPPGGSGQIRGVASRCIDVPNGNT 386
QY 165 CDSGQ-----INQKMAIYDGSIRPKQNDQCLTSGRDSYATVINIVSCGASGS 215
DB 387 ADGTQVQLDCHGSSND-QWTTTSSGEFRIFGN-KCLDAGSSNGAVQIYSCMGQA-N 442
QY 216 QRMVFTNBAIILNKTGLAND-VYQANPKLRIIIPATGKNQW 260
DB 443 QKWEIRADGTIVGVSGCLDAVGGGTGNGTILQIYSCMGANNQW 488

RESULT 12
US-08-590-563-7
Sequence 7; Application US/08590563
GENERAL INFORMATION:
APPLICANT: M RYJ, Arija
APPLICANT: Wegman, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: KESKINEN, KESKINEN, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050, 0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
FAX: 202-371-2640
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STANDARDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-08-590-563-7

Query Match 8.8%; Score 124.5; DB 4; Length 492;
Best Local Similarity 20.8%; Pred No 0.0019;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

DB 23 DVARDPDDGNGQIQMPG---KSNNDPQQLMTIKEDGTR---SNQSCLTYYGY--- 70
168 DVNNAEFDGNSGRCDNLTQRTGND---WIEVAFRTAQDPSAKLCYNDVNIEMNNA 223
QY 71 --TAGYTYNI-----FDGNTAVREATTQIMDNGTINPRSNLYLAASGIXKTTL 119
DB 224 AKTQAVYNNVADPKRGVPIIDC-----VQSHFNSGNTVNFRTTLQDPAL-GDVV 276
QY 120 TVQCLDYLGGCMLANDTAPR-----VITVGFPD-----LC 152
DB 277 EYVELDI-----ENAPQYAVIRDLAVDRCTGTTVGVYRDSMSRYONPL 326
QY 153 MSNN-----GGSVWV-----ET 164
DB 327 FDNNGKKAQYAVYALNAGSDGGGSPVSPPGGSGQIRGVASRCIDVPNGNT 386
QY 165 CDSGQ-----INQKMAIYDGSIRPKQNDQCLTSGRDSYATVINIVSCGASGS 215
DB 387 ADGTQVQLDCHGSSND-QWTTTSSGEFRIFGN-KCLDAGSSNGAVQIYSCMGQA-N 442
QY 216 QRMVFTNBAIILNKTGLAND-VYQANPKLRIIIPATGKNQW 260
DB 443 QKWEIRADGTIVGVSGCLDAVGGGTGNGTILQIYSCMGANNQW 488

RESULT 13
US-09-770-621-4
Sequence 4; Application US/09770621
GENERAL INFORMATION:
APPLICANT: M RYJ, Arija
APPLICANT: Wegman, Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija

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Page 5

QY 71 --TAGYYWMI-----FCQNTAVREATIQWINDGTINPRSLVLAASGKGTTL 119
DB 224 AKTQAVYVWVDFKRGVPIDC-----VQFSHNSGNPNYENREFTLLQCFPAL-GUDV 276
QY 120 TVQTLDTLTLGQWMLAGNDTAPRE-----VTYGFPRD-----LC 152
DB 277 EYVLELDI-----ENAPROTASVIRDOCLAVDRCTGIVWAVGRSDPSMSRYONPUL 326
QY 153 MESN-----GGSVWV-----ET 164
DB 327 PUNGNKQKQAVYAVDMLNBSDDGGSPNPVSPPGSGSGQIRGVASNRCDIVPQNT 386
QY 165 CDSQ-----KNOGKVALYGDGSIRKPNODCLTSGRDSVSTYINIVSCGASGS 215
DB 387 ADGTQVQVLYDCHGSSNQ-QWYTSSEGRIFPN-KCLDAGSSNGAVQVYSCWGA-N 442
QY 216 QRWFTNREGALNMTGLAND-VQANPKLRRIIYFANGKPNQW 260
DB 443 QWELRADDTIVQVSGELCLDVGGGTNGTIRLOLYSCWGNQW 488

RESULT 10

US-08-468-812-7
Sequence 7, Application US/08468812
Patent No. 5935836
GENERAL INFORMATION:
APPLICANT: Wehmanper, Jari
APPLICANT: Miettinen, Risto
APPLICANT: Fagerström, Richard
APPLICANT: Lantto, Raimo
APPLICANT: Palomäki, Marja
APPLICANT: Shominen, Pirkko
APPLICANT: Lantinen, Taina
APPLICANT: Kari, Paula
TITLE OF INVENTION: Of Use
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08468812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
TELECOMMUNICATION INFORMATION:
FAX NUMBER: 202-371-5260
TELEPHONE: 202-371-5260
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STANDARDNESS: not relevant

TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50

US-08-468-812-7

Query Match
Query Length: 492
Query Local: 23, 88, 167, 10019, 105, 133, 17,
Matches: 167, 10019, 105, 133, 17,
Score: 124.5, DB 2, Length 492,
Matches: 167, 10019, 105, 133, 17,

QY 23 DVRODFFHGNQOLMPS---KSNVDPNOLMTREKDTIR---SWSCLTYYGY---- 70
DB 168 DVVKEAFEDNSGRCDSMLRTGND---MIEVAFTRAGDPSAKLCYNVINENMA 223
QY 71 --TAGYYWMI-----FCQNTAVREATIQWINDGTINPRSLVLAASGKGTTL 119
DB 224 AKTQAVYVWVDFKRGVPIDC-----VQFSHNSGNPNYENREFTLLQCFPAL-GUDV 276
QY 120 TVQTLDTLTLGQWMLAGNDTAPRE-----VTYGFPRD-----LC 152
DB 277 EYVLELDI-----ENAPROTASVIRDOCLAVDRCTGIVWAVGRSDPSMSRYONPUL 326
QY 153 MESN-----GGSVWV-----ET 164
DB 327 PUNGNKQKQAVYAVDMLNBSDDGGSPNPVSPPGSGSGQIRGVASNRCDIVPQNT 386
QY 165 CDSQ-----KNOGKVALYGDGSIRKPNODCLTSGRDSVSTYINIVSCGASGS 215
DB 387 ADGTQVQVLYDCHGSSNQ-QWYTSSEGRIFPN-KCLDAGSSNGAVQVYSCWGA-N 442
QY 216 QRWFTNREGALNMTGLAND-VQANPKLRRIIYFANGKPNQW 260
DB 443 QWELRADDTIVQVSGELCLDVGGGTNGTIRLOLYSCWGNQW 488

RESULT 11

US-08-550-563-4
Sequence 4, Application US/08590563
Patent No. 6306114
GENERAL INFORMATION:
APPLICANT: Miettinen, Risto
APPLICANT: Fagerström, Richard
APPLICANT: Lantto, Raimo
APPLICANT: Palomäki, Marja
APPLICANT: Shominen, Pirkko
APPLICANT: Lantinen, Taina
APPLICANT: Kari, Paula
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P. L. C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08550563
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 536

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Page 4

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/ APPLICANT: Halkier, Torben
/ TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
/ FILE REFERENCE: 4693.204-05
/ CURRENT APPLICATION NUMBER: US/09/159,106
/ EARLIER FILING DATE: 1996-08-23
/ EARLIER FILING DATE: 1996-12-04
/ EARLIER APPLICATION NUMBER: 0885/96
/ EARLIER FILING DATE: 1996-08-23
/ EARLIER APPLICATION NUMBER: PCT/DK97/00160
/ EARLIER FILING DATE: 1997-04-14
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 15
/ TYPE: PART
/ ORGANISM: Oerskovia xanthineolytica
US-09-159-106-15

Query Match
Best Local Similarity 36.3%; Score 136; DB 3; Length 132;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;
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Oy 18 NNNRVVDDDDPHDNGOIQLPKSKNDPQQLMTIKDQTRNSGCLTYY--GYTAGY 75
Db 14 NNNRVVDDDDPHDNGOIQLPKSKNDPQQLMTIKDQTRNSGCLTYY--GYTAGY 71
Oy 76 VNIIDNTAVREATTIOWI--DNGT--IIPRSNLYLAASGI--KQTLTVQTLDTYL 128
Db 72 VQVWTCN-----GTQAKAYADGSKALNPSGLDIDATGAPLRDQRLQVWTCNGIT 126
Oy 129 GCGW 132
Db 127 AQGW 130

RESULT 8
US-09-159-106-11
/ Sequence 11; Application US/09159106
/ Patent No. 6246103
/ GENERAL INFORMATION:
/ APPLICANT: Petter, Pan
/ APPLICANT: Dieters, Ivan
/ APPLICANT: Halkier, Torben
/ APPLICANT: Hedegard, Lisbeth
/ TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
/ FILE REFERENCE: 4693.204-05
/ CURRENT APPLICATION NUMBER: US/09/159,106
/ EARLIER FILING DATE: 1996-08-23
/ EARLIER FILING DATE: 1996-12-04
/ EARLIER APPLICATION NUMBER: 0885/96
/ EARLIER FILING DATE: 1996-08-23
/ EARLIER APPLICATION NUMBER: PCT/DK97/00160
/ EARLIER FILING DATE: 1997-04-14
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 11
/ LENGTH: 135
/ TYPE: PART
/ ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11
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Query Match
Best Local Similarity 36.3%; Score 136; DB 3; Length 132;
Matches 45; Conservative 11; Mismatches 52; Indels 16; Gaps 6;
Oy 18 NNNRVVDDDDPHDNGOIQLPKSKNDPQQLMTIKDQTRNSGCLTYY--GYTAGY 75
Db 317 NNNRVVDDDDPHDNGOIQLPKSKNDPQQLMTIKDQTRNSGCLTYY--GYTAGY 374
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Oy 76 VNIIDNTAVREATTIOWI--DNGT--IIPRSNLYLAASGI--KQTLTVQTLDTYL 128
Db 375 VQVWTCN-----GTQAKAYADGSKALNPSGLDIDATGAPLRDQRLQVWTCNGIT 429
Oy 129 GCGW 132
Db 430 AQGW 433
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RESULT 9
US-08-468-812-4
/ Sequence 4; Application US/08468812
/ Patent No. 5935836
/ GENERAL INFORMATION:
/ APPLICANT: Vehmeyer, Tati
/ APPLICANT: M ntyl, Rita
/ APPLICANT: Fagerstr m, Richard
/ APPLICANT: Lantto, Ralf
/ APPLICANT: Raitanen, Maria
/ APPLICANT: Soderstrom, Peter
/ APPLICANT: Lantto, Tati
/ APPLICANT: Kristo, Paula
/ TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods
/ NUMBER OF SEQUENCES: 25
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
/ STREET: 1100 New York Ave., N.W.
/ CITY: Washington
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/468,812
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: A13
/ PRIOR APPLICATION NUMBER: US 08/332,412
/ FILING DATE: 31-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/282,001
/ FILING DATE: 29-JUL-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bysastry, Larry B.
/ REGISTRATION NUMBER: 35,086
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2640
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 492 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-468-812-4
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Query Match
Best Local Similarity 20.8%; Score 124.5; DB 2; Length 492;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;
Oy 23 DVPDDPHDNGOIQLPKSKNDPQQLMTIKDQTRNSGCLTYY--GYTAGY 70
Db 168 DVPDDPHDNGOIQLPKSKNDPQQLMTIKDQTRNSGCLTYY--GYTAGY 223
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Page 3

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Qy 5 CSASEPTVATVGRNKRVDVDDPHDGNQIQWFSKSNNDPNQMLTKEDGTISNSGC 64
Db 282 QNDPEPTVATVGRNKRVDVDDPHDGNQIQWFSKSNNDPNQMLTKEDGTISNSGC 341
Qy 65 LTTVGTAGVYVIMFDCTAVRENTIQTINDGTIINPSRLVLAASGKGTLLVQTL 124
Db 342 LTTKSSEPRQGVVYVNSCTATVQATVQIWDNRITIIIPSGVLVLAATSGKGTLLVQTN 401
Qy 125 DYTLCQGLAGNDTPAREVTITVGRNLCNESNGSVWETCDSSQKQKALYGDGSR 184
Db 402 IVASQGLPTNNQPEVTITVGLYQWCLQNSGKWLSDC-TSEKADQOMALYADGSR 460
Qy 185 PRONODCITSGRDSVTVINIVSGSGASQGRWFTNEGALINLTGLAMVDQANPEL 244
Db 461 PQGNRNCITTDNIKQIVYKILSCGPASQGRWFTNEGALINLTGLVLDVRSRPSL 520
Qy 245 RRIIYPATGRNQMMLPVF 264
Db 521 KQIIYVPHGNQIMLWLPF 540
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RESULT 5

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US-08-485-286-77
Sequence 77, Application us/08485286
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: MALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESS: 233 N. ZION ST.
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/778761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: HORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 382728
TELECOMMUNICATION INFORMATION:
TELEPHONE (317) 337-4846
FAX (317) 337-4846
INFORMATION SOURCE: SEQ ID NO: 77
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-77
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Query Match 54.3%; Score 777.5; DB 1; Length 540;
Best Local Similarity 55.8%; Pred. No. 48-72;
Matches 145; Conservative 41; Mismatches 73; Indels 1; Gaps 1;

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Qy 5 CSASEPTVATVGRNKRVDVDDPHDGNQIQWFSKSNNDPNQMLTKEDGTISNSGC 64
Db 282 QNDPEPTVATVGRNKRVDVDDPHDGNQIQWFSKSNNDPNQMLTKEDGTISNSGC 341
Qy 65 LTTVGTAGVYVIMFDCTAVRENTIQTINDGTIINPSRLVLAASGKGTLLVQTL 124
Db 342 LTTKSSEPRQGVVYVNSCTATVQATVQIWDNRITIIIPSGVLVLAATSGKGTLLVQTN 401
Qy 125 DYTLCQGLAGNDTPAREVTITVGRNLCNESNGSVWETCDSSQKQKALYGDGSR 184
Db 402 IVASQGLPTNNQPEVTITVGLYQWCLQNSGKWLSDC-TSEKADQOMALYADGSR 460
Qy 185 PRONODCITSGRDSVTVINIVSGSGASQGRWFTNEGALINLTGLAMVDQANPEL 244
Db 461 PQGNRNCITTDNIKQIVYKILSCGPASQGRWFTNEGALINLTGLVLDVRSRPSL 520
Qy 245 RRIIYPATGRNQMMLPVF 264
Db 521 KQIIYVPHGNQIMLWLPF 540
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RESULT 6

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US-09-512-342-14
Sequence 14, Application us/09512342
Patent No. 6388068
GENERAL INFORMATION:
APPLICANT: SATOH, SHINBU
APPLICANT: NAKUDA, SHINBU
TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT
TITLE OF INVENTION: INTERCELLULAR FLUID
FILE REFERENCE: 2001/0356142
CURRENT APPLICATION NUMBER: US/09/512,342
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 14
LENGTH: 293
TYPE: PRT
ORGANISM: Cucumis sativus
US-09-512-342-14
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Query Match 13.1%; Score 185; DB 4; Length 293;
Best Local Similarity 27.5%; Pred. No. 4,8e-11;
Matches 67; Conservative 36; Mismatches 101; Indels 40; Gaps 11;

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Qy 14 TVGNKGRVDRDPPHDMQQLW-----PSK-----SNPNQMLTKEDGTI-- 59
Db 41 LVGDGDLQENSP-----WYKAGINPRLSPDCKKQKQTLVVDGTHFM 89
Qy 60 SNGSCLT---YGTAGVYVIMFDCTAVRENTIQTINDGTIINPSRLVLAASGK 116
Db 90 NKRCLAAVEFYGIN--KAYVSECKVSDNKRKQTKQNDGTIALVDSRWVLGDLY-- 145
Qy 117 TTLVQTLDTYLCQGLAGNDTPAREVTITVGRNLCNESNGSVWETCDSSQK 174
Db 146 --VTLGSKTIFPQSHVETESLNSMNTIEMVNLCLQSTDSSSHGALGCDNRKY 202
Qy 175 NALYGDGSRPRONODCITSGRDSVTVINIVSGSGASQGRWFTNEGALINLT 233
Db 203 WALYADGTRQVHNKNCILNSDQGFGRFY--VVSKECKEPQGRMSLDADVTD 260
Qy 234 ANDV 237
Db 261 VLDV 264
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RESULT 7

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US-09-159-106-15
Sequence 15, Application us/09159106
Patent No. 6284509
GENERAL INFORMATION:
APPLICANT: Ferrer, Pau
APPLICANT: Diers, Ivan
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Page 2

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RESULT 2
US-08-776-059-33
; Sequence 33, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
; APPLICANT: LENTZEN, Hans
; APPLICANT: ECK, Jürgen
; APPLICANT: HILGERT, Holger
; APPLICANT: ZINKE, Axel
; TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
; FILE REFERENCE: 674503-2003
; CURRENT APPLICATION NUMBER: US/08/776,059B
; EARLIER FILING DATE: 1999-06-19
; EARLIER APPLICATION NUMBER: PCT/EP96/02273
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 9510949.8
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 33
; TYPE: PRT
; ORGANISM: Viscum album
US-08-776-059-33
Query Match 93.7%; Score 1327.5; DB 3; Length 264;
Best Local Similarity 95.1%; Pred. No. 1.2e-129;
Matches 250; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

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QY 1 DDTGASAEPTVAVGNKRVYRDDDFHGNQIQALPSSKNDPNQNTIKDGTIR 60
DB 2 DDTGASAEPTVAVGNKRVYRDDDFHGNQIQALPSSKNDPNQNTIKDGTIR 61
QY 61 NSGLTGYGTAGVYVWIFPCNTAVREATTIWIQNGTIIINPRSNVLAASSGIGKTT 120
DB 62 NSGLTGYGTAGVYVWIFPCNTAVREATTIWIQNGTIIINPRSNVLAASSGIGKTT 121
QY 121 VQILDYTLQGMALAGNDTAPREVITYVGFEDLCWESNGSGSWVETCSQKQKALYGD 180
DB 122 VQILDYTLQGMALAGNDTAPREVITYVGFEDLCWESNGSGSWVETCSQKQKALYGD 180
QY 181 GSIRPKNDQCLTSGDSVSTVNTVSCASAGSGQWVFTNEGALINLYGLAMDVQA 240
DB 181 GSIRPKNDQCLTSGDSVSTVNTVSCASAGSGQWVFTNEGALINLYGLAMDVQA 240
QY 241 NPKLRRIIIVPATGKPKQWMLPV 263
DB 241 NPKLRRIIIVPATGKPKQWMLPV 263

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RESULT 3
US-08-776-059-35
; Sequence 35, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
; APPLICANT: LENTZEN, Hans
; APPLICANT: ECK, Jürgen
; APPLICANT: HILGERT, Holger
; APPLICANT: ZINKE, Axel
; TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
; FILE REFERENCE: 674503-2003
; CURRENT APPLICATION NUMBER: US/08/776,059B
; EARLIER FILING DATE: 1999-06-19
; EARLIER APPLICATION NUMBER: PCT/EP96/02273
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 9510949.8
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 35
; LENGTH: 564
; TYPE: PRT
; ORGANISM: Viscum album

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US-08-776-059-35
Query Match 93.7%; Score 1327.5; DB 3; Length 564;
Best Local Similarity 95.1%; Pred. No. 3.8e-129;
Matches 250; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

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QY 1 DDTGASAEPTVAVGNKRVYRDDDFHGNQIQALPSSKNDPNQNTIKDGTIR 60
DB 302 DDTGASAEPTVAVGNKRVYRDDDFHGNQIQALPSSKNDPNQNTIKDGTIR 361
QY 61 NSGLTGYGTAGVYVWIFPCNTAVREATTIWIQNGTIIINPRSNVLAASSGIGKTT 120
DB 362 NSGLTGYGTAGVYVWIFPCNTAVREATTIWIQNGTIIINPRSNVLAASSGIGKTT 121
QY 121 VQILDYTLQGMALAGNDTAPREVITYVGFEDLCWESNGSGSWVETCSQKQKALYGD 180
DB 422 VQILDYTLQGMALAGNDTAPREVITYVGFEDLCWESNGSGSWVETCSQKQKALYGD 480
QY 181 GSIRPKNDQCLTSGDSVSTVNTVSCASAGSGQWVFTNEGALINLYGLAMDVQA 240
DB 481 GSIRPKNDQCLTSGDSVSTVNTVSCASAGSGQWVFTNEGALINLYGLAMDVQA 540
QY 241 NPKLRRIIIVPATGKPKQWMLPV 263
DB 541 NPKLRRIIIVPATGKPKQWMLPV 563

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RESULT 4
US-08-378-761A-77
; Sequence 77, Application US/08378761A
; Patent No. 6635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSER: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/378,761A
; APPLICATION NUMBER: 26-728-195
; FILING DATE: 26-728-195
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 382728
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; STRATEGY: repeat
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-77
Query Match 54.9%; Score 1277.5; DB 1; Length 540;
Best Local Similarity 55.8%; Pred. No. 4e-72;
Matches 145; Conservative 41; Mismatches 73; Indels 1; Gaps 1;

Thu Dec 11 16:10:07 2003

us-09-601-667c-9.ra1

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 9.14026 Seconds
(without alignments)
1222.073 Million cell updates/sec

Title: US-09-601-667C-9

RefSeq score: 1417

Sequence: 1 DVTVCASSEPVTAVIGNCHN.....RRIIIVPACPKQNMWLPV 264

Scoring table: BLOSUM62

Gapcp 10.0 / Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 2: /sgn2_6/prodata/1/1aa/5B_COMB.pep.*
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- 5: /sgn2_6/prodata/1/1aa/PCPUS_COMB.pep.*
- 6: /sgn2_6/prodata/1/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1377.3	93.7	264	3	US-08-776-059-43 Sequence 33, App1
3	1377.3	93.7	264	3	US-08-776-059-43 Sequence 35, App1
4	1377.3	93.7	264	3	US-08-776-059-43 Sequence 77, App1
5	1377.3	93.7	264	3	US-08-776-059-43 Sequence 15, App1
6	1377.3	93.7	264	3	US-08-776-059-43 Sequence 17, App1
7	1377.3	93.7	264	3	US-08-776-059-43 Sequence 19, App1
8	1377.3	93.7	264	3	US-08-776-059-43 Sequence 11, App1
9	1377.3	93.7	264	3	US-08-776-059-43 Sequence 11, App1
10	1377.3	93.7	264	3	US-08-776-059-43 Sequence 11, App1
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30	87.5	6.2	553	1	US-08-565-386-6 Sequence 10, App1
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33	86.5	6.1	420	2	US-08-282-197C-63 Sequence 4740, App1
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36	86.5	6.1	420	2	US-08-282-197C-63 Sequence 10, App1
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ALIGNMENTS

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Thu Dec 11 16:10:07 2003

us-09-601-667c-9.rapb

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
EXPIRATION DATE: 09/30/2003
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2640
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20010024815A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: AM50
US-09-770-621-7

Query Match 8.8%; Score 124.5; DB 9; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.0005;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

QY 23 DYRDDPHDGNQIQLPSP--KSNNDPQNLWTIKRQGTIR---SNSCLTYGY----- 70
DB 168 DVNBEAFEDNSGRCDLORFAND---WIEVAFRTAQDPSAKLCINDYINENRMA 223
QY 71 --TQGYVMT-----PCRTAVRENTIQIWMQGTIINRSMVLAASSGKGTLL 119
DB 224 AKQAVNVNVRDFKSGVPIDC-----VGQSHFNSGNPNYVNFRTLLQFPAL-GVDV 276
QY 120 TVQILDYTLGGWLAGNDIAPRE-----VTYGFPRD-----LC 152
DB 277 EYVELDI-----ENAPQVYASVIRDCIAYVRCGTIGTWGVDSDSRSYONPL 326
QY 153 MBSN-----GQYVW-----ET 164
DB 327 FDNNSNKKQAYVALDLNBSDDGGSPNSPVSPFGSSQCLRYASNRCIDYVKNMT 386
QY 165 CDSGQ-----KQCKALYVGGISIRPKQNDQCLTSRDSVSTVINYVSGSGASGS 215
DB 387 ADGTQVQYLDCHSGSNQ--QWYVSSGSEFRIFGN--KCLDAGSSNNAVQVYISCGWGA-N 442
QY 216 QRWVFNKGAIIINLKTGLAND-VQAQNFKLRIIITPATKPKQW 260
DB 443 QKWEIPLADGTIVGVSGCLDAVAGGTGNGCTRLQLYSCWGNQW 488

RESULT 15
US-10-286-993-4
SEQUENCE 4 Application US/10286993
GENERAL INFORMATION NO US20030148453A1
APPLICANT: Mantyla, Arja
APPLICANT: Palcheim, Marja
APPLICANT: Lantto, Ralja

APPLICANT: Fagerstrom, Richard
APPLICANT: Lantto, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Vehmaampere, Jari
TITLE OF INVENTION: Production and Secretion of Proteins in Filamentous
TITLE OF INVENTION: Fungi
FILE REFERENCE: 1716.034004
CURRENT APPLICATION NUMBER: US/10/286,993
PRIOR APPLICATION NUMBER: 08/102,804
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/Fin97/00037
PRIOR FILING DATE: 1997-01-24
PRIOR APPLICATION NUMBER: US 08/590,563
PRIOR FILING DATE: 1996-01-26
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 492
ORGANISM: Actinomyces flexuosa
US-10-286-993-4

Query Match 8.8%; Score 124.5; DB 12; Length 492;
Best Local Similarity 20.8%; Pred. No. 0.0005;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

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QY 71 --TQGYVMT-----PCRTAVRENTIQIWMQGTIINRSMVLAASSGKGTLL 119
DB 224 AKQAVNVNVRDFKSGVPIDC-----VGQSHFNSGNPNYVNFRTLLQFPAL-GVDV 276
QY 120 TVQILDYTLGGWLAGNDIAPRE-----VTYGFPRD-----LC 152
DB 277 EYVELDI-----ENAPQVYASVIRDCIAYVRCGTIGTWGVDSDSRSYONPL 326
QY 153 MBSN-----GQYVW-----ET 164
DB 327 FDNNSNKKQAYVALDLNBSDDGGSPNSPVSPFGSSQCLRYASNRCIDYVKNMT 386
QY 165 CDSGQ-----KQCKALYVGGISIRPKQNDQCLTSRDSVSTVINYVSGSGASGS 215
DB 387 ADGTQVQYLDCHSGSNQ--QWYVSSGSEFRIFGN--KCLDAGSSNNAVQVYISCGWGA-N 442
QY 216 QRWVFNKGAIIINLKTGLAND-VQAQNFKLRIIITPATKPKQW 260
DB 443 QKWEIPLADGTIVGVSGCLDAVAGGTGNGCTRLQLYSCWGNQW 488

Search completed: December 11, 2003, 14:48:50
Job time: 18.0129 secs

Thu Dec 11 16:10:07 2003

us-09-601-667c-9.rapb

Page 5

APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIMA, TADASHI
APPLICANT: SHIMA, TADASHI
APPLICANT: HATTORI, HISASHI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-282
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQUENCE ID NO: 12246
LENGTH: 647
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-10246

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Best Local Similarity 26.3%; Score 126; DB 15; Length 647;
Matches 45; Conservative 20; Mismatches 60; Indels 46; Gaps 8;

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QY 67 TGYTAGVYVWIPDQCNVAREACTNQMNTINPMSNVLAASGKLTITVQTLDTV 126
DB 578 SASPADAKITQYDGN-----CTAAQKNSYV-----ASTGVVWTAAXKLDTV 620
QY 127 TVGGWLAGNDTAPREVTVYGRDLCHBSNGSVMVETCDSSGQKQKAL 177
DB 621 T-----GNSSA-----NQAHAQIMSC-TGAAQ-KWKL 646

RESULT 13

US-09-770-621-4
Sequence 4; Application US/09770621
Patent No. US20010024815A1

GENERAL INFORMATION:

APPLICANT: M nyl, Arja
APPLICANT: Vehmanner, Jari
APPLICANT: Pegerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lantinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Sequencer Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,621
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/590,563
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION: INFORMATION:
ATMOSPHERIC/ASTROPHYSICAL INFORMATION:
B
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050,0340003
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPES: amino acid
MOLSCULE TYPE: linear
US-09-770-621-4

Query Match

Best Local Similarity 20.8%; Score 124.5; DB 9; Length 492;
Matches 72; Conservative 36; Mismatches 105; Indels 133; Gaps 17;

QY 23 DVADDPFDNDNOIQMPKSNNDPNQMTIKEDTIRKNSGCT--T 70
DB 168 DVNAPFEDNSGRCDNSLQRTGND--MVEAFRTAKQSPAKLCYNDIMENNA 223
QY 71 --TACVYVMT-----PCTAVNENTWQWNGTIIINRNLVLAASGIGTTL 119
DB 224 AKQAVVWVRDPRKSGVPLD-----VQPSHPNSGVPNNRRTTLQPKAL-SDV 276
QY 120 TVQTLDTVLAGGMLAGNDTAPREVTVYGRDLCHBSNGSVMVETCDSSGQKQKAL 177
DB 277 EYTBELDI-----ENAAQTVASVIRDLAVDRCGTITVWGVSDSDWSRYQPL 326
QY 153 MESN-----GSSVWV-----ET 164
DB 327 FDNNAKQAVYVALDNESSDGGSPNPVSPPGSSGQKQKAVASRCLDIPNGVT 386
QY 165 CDSGQ-----KQCVKALYGGASIRKXNDQDGLNSGRSVYIYISGSGSOS 215
DB 387 ADGTQVQLYCHSSGND-QWYTSSEGRFLPQN-KILNAGSSNGAVQVYISCMGA-N 442
QY 216 QRWVFPNEGALINKETGLAND-VQANPKRRIIIPATGRPNQW 260
DB 443 QKVELRADGTIVYQSLCLDAVAGGTGNGTDLVYSCWGGNNQW 488

RESULT 14

US-09-770-621-7
Sequence 7; Application US/09770621
Patent No. US20010024815A1

GENERAL INFORMATION:

APPLICANT: M nyl, Arja
APPLICANT: Vehmanner, Jari
APPLICANT: Pegerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Palohelmo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lantinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

Thu Dec 11 16:10:07 2003

us-09-601-667c-9.rapb

Page 4

LENGTH: 536
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-8170

Query Match 9.5%; Score 134; DB 15; Length 536;
Best Local Similarity 30.1%; Pred. No. 6e-05; 59; Indels 16; Gaps 6;

Matches 40; Conservative 18; Mismatches 59; Indels 16; Gaps 6;

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QY 69 GTTAGVYVWIPDCTAVR--EATITWQIMDNGTINRSNVLAASSGIGTITLTG 125
DB 466 GTTAGVYVWIPDCTAVR--EATITWQIMDNGTINRSNVLAASSGIGTITLTG 125
QY 123 TLDYTLGGGMLAG 135
DB 524 TLDYTLGGGMLAG 135

RESULT 9

US-10-137-077-18
Sequence 18, Application US/10137077
Publication No. US20030092109A1

GENERAL INFORMATION:
APPLICANT: Goldstein, Irwin J.

APPLICANT: Wainer, Harry C.

APPLICANT: Kruger, Robert P.

FILE REFERENCE: US-07124
CURRENT FILING DATE: 2002-05-02
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 60/288,596
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/354,322
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 41
TYPE: PRT
ORGANISM: Rickettsia communis
US-10-137-077-18

Query Match 9.4%; Score 133; DB 15; Length 41;
Best Local Similarity 56.1%; Pred. No. 2.3e-06;
Matches 23; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

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RESULT 10

US-09-973-457-5
Sequence 5, Application US/09973457
Patent No. US2002016476A1

GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana

TITLE OF INVENTION: 47174, A NOVEL HUMAN GLYCOSYLTRANSFERASE
FILE REFERENCE: 1048-099001 US/09/973,457
CURRENT APPLICATION NUMBER: US/09/973,457
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,849
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 135
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus sequence
US-09-973-457-5

Query Match 9.0%; Score 127; DB 10; Length 135;
Best Local Similarity 25.0%; Pred. No. 4.8e-05;
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;

QY 14 IYGNMNR-IVPDDPHDQIOQMPKSNNDPQMLMTI--KDDGTRNSG-CLFTT 67
DB 7 IYGNMNR-IVPDDPHDQIOQMPKSNNDPQMLMTI--KDDGTRNSG-CLFTT 67
QY 68 GTTAGVYVWIPDCTAVR--EATITWQIMDNGTINRSNVLAASSGIGTITLTG 125
DB 65 GTTAGVYVWIPDCTAVR--EATITWQIMDNGTINRSNVLAASSGIGTITLTG 125
QY 126 GTTAGVYVWIPDCTAVR--EATITWQIMDNGTINRSNVLAASSGIGTITLTG 125
DB 107 GTTAGVYVWIPDCTAVR--EATITWQIMDNGTINRSNVLAASSGIGTITLTG 125

RESULT 11

US-10-074-527-6
Sequence 6, Application US/10074527
Publication No. US2002014242A1

GENERAL INFORMATION:
APPLICANT: Olander, Peter J.

APPLICANT: Meyers, Rachel E.

APPLICANT: Smith, Kristine A.

TITLE OF INVENTION: 33945, A Human Glycosyltransferase and
FILE REFERENCE: MF2001-0181RCP1M1
CURRENT APPLICATION NUMBER: US/10/074,527
CURRENT FILING DATE: 2002-02-12
PRIOR FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 60/469202
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 135
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus
US-10-074-527-6

Query Match 9.0%; Score 127; DB 14; Length 135;
Best Local Similarity 25.7%; Pred. No. 4.8e-05;
Matches 44; Conservative 20; Mismatches 53; Indels 54; Gaps 9;

QY 14 IYGNMNR-IVPDDPHDQIOQMPKSNNDPQMLMTI--KDDGTRNSG-CLFTT 67
DB 7 IYGNMNR-IVPDDPHDQIOQMPKSNNDPQMLMTI--KDDGTRNSG-CLFTT 67
QY 68 GTTAGVYVWIPDCTAVR--EATITWQIMDNGTINRSNVLAASSGIGTITLTG 125
DB 65 GTTAGVYVWIPDCTAVR--EATITWQIMDNGTINRSNVLAASSGIGTITLTG 125
QY 126 GTTAGVYVWIPDCTAVR--EATITWQIMDNGTINRSNVLAASSGIGTITLTG 125
DB 107 GTTAGVYVWIPDCTAVR--EATITWQIMDNGTINRSNVLAASSGIGTITLTG 125

RESULT 12

US-10-156-761-10246
Sequence 10246, Application US/10156761
Publication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO
APPLICANT: ISHITAMA, JUN

Qy 121 VQTLDTYLGQGMAGNDTAPREVTIYGFROLCNESNGSSVWETCDSQKQKQKALYGD 180
 Db 121 VQTLDTYLGQGMAGNDTAPREVTIYGFROLCNESNGSSVWETCDSQKQKQKALYGD 179
 Qy 181 GSIRPKQNDQCLTSGSDSVSTVINIVSCGASGSGQWFTNEGALIMLKTGLANDVQA 240
 Db 180 GSIRPKQNDQCLTSGSDSVSTVINIVSCGASGSGQWFTNEGALIMLKTGLANDVQA 239
 Qy 241 NPKLRRIIYPATGKQNMPLFV 263
 Db 240 NPKLRRIIYPATGKQNMPLFV 262

RESULT 2
 US-09-347-064-4
 / Sequence 4, Application US/09347064A
 / Patent No. US20020045208A1
 / GENE: RIBOSOME INACTIVATING PROTEIN
 / APPLICANT: Schmitt, James
 / APPLICANT: Schmitt, James
 / TITLE OF INVENTION: Recombinant Fusion Proteins Based on
 / TITLE OF INVENTION: Ribosome-Inactivating Proteins of the misticloe Vascum
 / TITLE OF INVENTION: album
 / FILE REFERENCE: 09282-5
 / CURRENT APPLICATION NUMBER: US/09/347,064A
 / CURRENT FILING DATE: 1999-07-02 / PCT/EP98/00009
 / EARLIER APPLICATION NUMBER: PCT/EP98/00009
 / EARLIER FILING DATE: 1998-01-02 / E297 10 0012.0
 / EARLIER FILING DATE: 1997-01-02
 / NUMBER OF SEQ ID NOS: 18
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 4
 / LENGTH: 267
 / TYPE: PRT
 / ORGANISM: Vascum album
 / US-09-347-064-4

Query Match 83.7%; Score 1327.5; DB 9; Length 267;
 Best Local Similarity 95.1%; Freq. No. 38-127;
 Matches 250; Conservative 2; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 DDTVCASEPTVIVGNMGWCVDRDDPRDQNOIQLPKSKNDPNQIWTIRKDTGTS 60
 Db 1 DDTVCASEPTVIVGNMGWCVDRDDPRDQNOIQLPKSKNDPNQIWTIRKDTGTS 60
 Qy 61 NQSCLTYYGTAGVYVIMPCNTVVEATVIMQNGFTIINFRSNVYLAASGIGTIT 120
 Db 61 NQSCLTYYGTAGVYVIMPCNTVVEATVIMQNGFTIINFRSNVYLAASGIGTIT 120
 Qy 121 VQTLDTYLGQGMAGNDTAPREVTIYGFROLCNESNGSSVWETCDSQKQKQKALYGD 180
 Db 121 VQTLDTYLGQGMAGNDTAPREVTIYGFROLCNESNGSSVWETCDSQKQKQKALYGD 179
 Qy 181 GSIRPKQNDQCLTSGSDSVSTVINIVSCGASGSGQWFTNEGALIMLKTGLANDVQA 240
 Db 180 GSIRPKQNDQCLTSGSDSVSTVINIVSCGASGSGQWFTNEGALIMLKTGLANDVQA 239
 Qy 241 NPKLRRIIYPATGKQNMPLFV 263
 Db 240 NPKLRRIIYPATGKQNMPLFV 262

RESULT 3
 US-10-083-336A-1
 / Sequence 1, Application US/1008336A
 / Publication No. US2003018165A1
 / GENERAL INFORMATION:
 / APPLICANT: Olson, Mark A
 / APPLICANT: Willard, Charles B
 / APPLICANT: Byrne, Michael P
 / APPLICANT: Mannemacher, Robert W

Qy 5 CSASEPTVIVGNMGWCVDRDDPRDQNOIQLPKSKNDPNQIWTIRKDTGTSNSC 64
 Db 318 CNDPEPTVIVGNMGWCVDRDDPRDQNOIQLPKSKNDPNQIWTIRKDTGTSNSC 377
 Qy 65 LITTYGQGMAGNDTAPREVTIYGFROLCNESNGSSVWETCDSQKQKQKALYGD 124
 Db 378 LITTYGQGMAGNDTAPREVTIYGFROLCNESNGSSVWETCDSQKQKQKALYGD 437
 Qy 125 DYTLCQGMAGNDTAPREVTIYGFROLCNESNGSSVWETCDSQKQKQKALYGD 184
 Db 438 IYAVSQGMAGNDTAPREVTIYGFROLCNESNGSSVWETCDSQKQKQKALYGD 496
 Qy 185 PKQNDQCLTSGSDSVSTVINIVSCGASGSGQWFTNEGALIMLKTGLANDVQA 244
 Db 497 PKQNDQCLTSGSDSVSTVINIVSCGASGSGQWFTNEGALIMLKTGLANDVQA 556
 Qy 245 PRRIIYPATGKQNMPLFV 264
 Db 557 KQIILYPLHSDPNQIWTIRKDTGTSNSC 576

Query Match 64.0%; Score 907.5; DB 12; Length 576;
 Best Local Similarity 63.8%; Freq. No. 6-78-84;
 Matches 166; Conservative 33; Mismatches 60; Indels 1; Gaps 1;
 US-10-083-336A-1
 / Sequence 1, Application US/10074527
 / Patent No. US20030092109A1
 / GENE: RIBOSOME INACTIVATING PROTEIN
 / APPLICANT: Mannemacher, Robert W
 / APPLICANT: Mannemacher, Robert W
 / TITLE OF INVENTION: Isolation, Characterization, Cloning and Use of a Mushroom Lectin
 / FILE REFERENCE: US-071124
 / CURRENT APPLICATION NUMBER: US/10/137,077
 / CURRENT FILING DATE: 2002-05-03
 / EARLIER APPLICATION NUMBER: 60/288,596
 / EARLIER FILING DATE: 2001-05-03
 / EARLIER FILING DATE: 2000-05-02
 / NUMBER OF SEQ ID NOS: 12
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 17
 / LENGTH: 44
 / TYPE: PRT
 / ORGANISM: Ricinus communis
 / US-10-137-077-17

Query Match 13.3%; Score 186; DB 15; Length 44;
 Best Local Similarity 77.3%; Freq. No. 9-86-12;
 Matches 34; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 Qy 12 VYIVGNMGWCVDRDDPRDQNOIQLPKSKNDPNQIWTIRKDTGTSNSC 64
 Db 1 VYIVGNMGWCVDRDDPRDQNOIQLPKSKNDPNQIWTIRKDTGTSNSC 44

RESULT 5
 US-10-074-527-5
 / Sequence 5, Application US/10074527

Thu Dec 11 16:10:07 2003

us-09-601-667c-9 .rapb

Page 1

GenCafe version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 14:01:14 : Search time 17.0129 Seconds
(without alignments)

2866.029 Million cell updates/sec

Title: US-09-601-667C-9
Sequence: 1 DVTGCSAEPYRIVGRNM.....RRIITPYNKNGMPLVF 264
Perfect score: 1417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 18593659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgm2_6/ptcdat/1/pubpa/US07_PUBCOMB.pep.*
2: /cgm2_6/ptcdat/1/pubpa/PTC_NEW_PUB.pep.*
3: /cgm2_6/ptcdat/1/pubpa/US06_NEW_PUB.pep.*
4: /cgm2_6/ptcdat/1/pubpa/US06_PUBCOMB.pep.*
5: /cgm2_6/ptcdat/1/pubpa/US07_NEW_PUB.pep.*
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11: /cgm2_6/ptcdat/1/pubpa/US09_NEW_PUB.pep.*
12: /cgm2_6/ptcdat/1/pubpa/US10_PUBCOMB.pep.*
13: /cgm2_6/ptcdat/1/pubpa/US10_PUBCOMB.pep.*
14: /cgm2_6/ptcdat/1/pubpa/US10_PUBCOMB.pep.*
15: /cgm2_6/ptcdat/1/pubpa/US10_PUBCOMB.pep.*
16: /cgm2_6/ptcdat/1/pubpa/US10_NEW_PUB.pep.*
17: /cgm2_6/ptcdat/1/pubpa/US60_NEW_PUB.pep.*
18: /cgm2_6/ptcdat/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the best hit being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1327.5	93.7	263	9 US-09-347-064-10	Sequence 10, Appl
2	1307.5	93.7	263	9 US-09-347-064-10	Sequence 1, Appl
3	1307.5	93.7	263	9 US-09-347-064-10	Sequence 4, Appl
4	1307.5	93.7	263	9 US-09-347-064-10	Sequence 17, Appl
5	1307.5	93.7	263	9 US-09-347-064-10	Sequence 12, Appl
6	1307.5	93.7	263	9 US-09-347-064-10	Sequence 19, Appl
7	1307.5	93.7	263	9 US-09-347-064-10	Sequence 16, Appl
8	1307.5	93.7	263	9 US-09-347-064-10	Sequence 13, Appl
9	1307.5	93.7	263	9 US-09-347-064-10	Sequence 14, Appl
10	1307.5	93.7	263	9 US-09-347-064-10	Sequence 15, Appl
11	1307.5	93.7	263	9 US-09-347-064-10	Sequence 18, Appl
12	1307.5	93.7	263	9 US-09-347-064-10	Sequence 11, Appl
13	1307.5	93.7	263	9 US-09-347-064-10	Sequence 10, Appl
14	1307.5	93.7	263	9 US-09-347-064-10	Sequence 17, Appl
15	1307.5	93.7	263	9 US-09-347-064-10	Sequence 12, Appl

16	122.5	8.6	480	9 US-09-770-621-5	Sequence 5, Appl
17	122.5	8.6	491	9 US-09-770-621-8	Sequence 8, Appl
18	111	7.8	625	15 US-10-156-761-15008	Sequence 15008, A
19	109	7.7	41	15 US-10-137-077-20	Sequence 20, Appl
20	107	7.6	612	14 US-10-001-851-25	Sequence 25, Appl
21	104	7.3	45	15 US-10-137-077-19	Sequence 19, Appl
22	104	7.3	45	15 US-10-137-077-19	Sequence 16, Appl
23	95	6.7	295	9 US-09-841-132-395	Sequence 13, Appl
24	94	6.6	1723	9 US-09-841-132-395	Sequence 13, Appl
25	94	6.6	1723	9 US-09-841-132-395	Sequence 13, Appl
26	92	6.5	2771	10 US-09-808-602-82	Sequence 82, Appl
27	92	6.5	2771	10 US-09-808-602-82	Sequence 82, Appl
28	90.5	6.4	340	15 US-10-128-714-8037	Sequence 8037, Ap
29	89	6.3	770	9 US-09-815-654-31	Sequence 31, Appl
30	88	6.2	1032	11 US-09-733-643-16	Sequence 16, Appl
31	88	6.2	1032	11 US-09-733-643-16	Sequence 16, Appl
32	87.5	6.2	826	10 US-09-858-528-10	Sequence 10, Appl
33	87.5	6.2	826	10 US-09-858-528-10	Sequence 10, Appl
34	87	6.1	1704	12 US-10-229-062-12	Sequence 12, Appl
35	86.5	6.1	181	12 US-10-229-062-12	Sequence 12, Appl
36	86.5	6.1	181	12 US-10-229-062-12	Sequence 12, Appl
37	84.5	6.0	239	10 US-09-910-071-15	Sequence 15, Appl
38	84	5.9	247	11 US-09-880-748-2127	Sequence 2127, Ap
39	83.5	5.9	788	11 US-09-733-643-14	Sequence 14, Appl
40	83	5.9	247	11 US-09-880-748-1885	Sequence 1885, Ap
41	82.5	5.8	2353	10 US-09-797-862-33	Sequence 33, Appl
42	82.5	5.8	955	15 US-10-156-761-15004	Sequence 15004, A
43	82.5	5.8	1732	12 US-10-229-066-11	Sequence 11, Appl
44	82.5	5.8	3571	10 US-10-229-066-11	Sequence 11, Appl
45	82.5	5.8	3571	10 US-10-229-066-11	Sequence 2, Appl

ALIGNMENTS

RESULT 1	US-09-347-064-10	
Sequence 10, Application US/09347064A		
Reference No. US20020045208A1		
GenBank accession: US09347064A		
APPLICANT: Schindler, Rino		
APPLICANT: Schindler, Rino		
TITLE OF INVENTION: Ribosome Inactivating Proteins Based on		
TITLE OF INVENTION: Ribosome Inactivating Proteins Based on		
FILE REFERENCE: 09282-5		
CURRENT FILING DATE: 1999-07-02		
EARLIER FILING DATE: 1998-01-02		
EARLIER APPLICATION NUMBER: EP 97 10 0012.0		
NUMBER OF SEQ IDS: 137		
SOFTWARE: PatentIn Ver. 2.1		
SEQ ID NO 10		
LENGTH: 263		
TYPE: PRT		
ORGANISM: Viscum album		
US-09-347-064-10		
Query Match	93.7%: Score 1327.5; DB 9: Length 263;	
Best Local Similarity	95.1%: Pred. No. 2.9e-127;	
Matches 250; Conservative	2; Mismatches 10; Indels 1; Gaps 1;	
Cy	1 DVTGCSAEPYRIVGRNMVDDDDHNOGIDLPSSNPNQATTCDDTTS 60	
Db	1 DVTGCSAEPYRIVGRNMVDDDDHNOGIDLPSSNPNQATTCDDTTS 60	
Cy	61 NSGCLITVGTAGVYVMTFCQNTAVRATIQINDGTTINPSNVLAASGKICETIT 120	
Db	61 NSGCLITVGTAGVYVMTFCQNTAVRATIQINDGTTINPSNVLAASGKICETIT 120	

CC Fibroses. Non-cytotoxic forms of (1) activate T-cell and
 CC lymphokine-activated macrophages, so stimulate immunity. (1) and its
 CC fragments are used to treat cancer growth (particularly
 CC cancers) and if they lack cytotoxicity to normal cells.
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains. In many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin I protein variant.
 SQ Sequence 532 AA.

Query Match 94.1%; Score 133.5; DB 20; Length 532;
 Best Local Similarity 95.4%; Pred. No. 119e-123;
 Matches 251; Conservative 9; Indels 1; Gaps 1;

QY 1 DDVTCASAPPTVAIVGNKGVVDDPFDHGNQIQAMPKSNNDPNOIWTIKEDGTIS 60
 DB 269 DDVTCASAPPTVAIVGNKGVVDDPFDHGNQIQAMPKSNNDPNOIWTIKEDGTIS 328
 QY 61 NSCCTTGTGTAGTVMIPCNVAVEATINQIMNGTINRNSNLVLAASGKGTIT 120
 DB 329 NSCCTTGTGTAGTVMIPCNVAVEATINQIMNGTINRNSNLVLAASGKGTIT 388
 QY 121 VQTLDTYTLGGWLAGNDTAPREVTYGFRLQMSNGSVMWETCDSSQNGKALYXD 180
 DB 389 VQTLDTYTLGGWLAGNDTAPREVTYGFRLQMSNGSVMWETCDSSQNGKALYXD 447
 QY 181 GSIRKPNODQCLTGRDSVSTVINIVSCGASGSGRWFTNKGALINLKTGLAMDVQA 240
 DB 448 GSIRKPNODQCLTGRDSVSTVINIVSCGASGSGRWFTNKGALINLKTGLAMDVQA 507
 QY 241 NPKLRITITVPATKXKQNMWLPV 263
 DB 508 NPKLRITITVPATKXKQNMWLPV 530

RESULT 15
 AAM64662
 ID AAM64662 standard; Protein; 263 AA.
 AC AAM64662;
 XX 23-OCT-1998 (first entry)
 XX Mistletoe rMB variant protein.
 DE Lectin B-chain; mistletoe; rMB; fusion protein; effector; cytotoxic;
 KW intracellular; processing module; protease recombination; targeting module;
 KW internalisation; treatment; disorder; cell proliferation; activation;
 KW autoimmune disease; allergy; tumour; ricin; translocation.
 OS Viscum album.
 XX Key
 FT Location/Qualifiers
 FT Protein 1..263
 FT /note= "partial protein"
 PV MO9829540-A2.
 XX 09-JUL-1998.
 XX 02-JAN-1998; 98MO-EP00009.
 PF 02-JAN-1997; 97EP-0100012.
 PR (BRAI-) BRAIN BIOTECHNOLOGY RES & INFORMATION NE.
 EA Eck J, Schmidt A, Zinke H;
 XX WPI, 1998-386122/33.
 DR N-PSDB; AAV51344.

XX Nucleic acid encoding fusion protein containing mistletoe lectin A
 FT chain - useful for treatment of proliferative and autoimmune
 PT diseases, allergies and tumours
 XX Disclosure; Fig 11b', 115pp; German.
 CC This sequence represents a variant mistletoe lectin B-chain rMB. This
 CC sequence can be used in the construction of a fusion protein which
 CC comprises an effector module that is cytotoxic intracellularly, a
 CC processing module covalently bonded to the effector module and
 CC containing a protease recognition sequence, and a targeting module
 CC covalently bonded to the processing module, able to bind specifically to
 CC the surface of a cell so as to mediate internalisation of the fusion
 CC protein. Such a fusion protein can be used for treating disorders
 CC involving proliferation and/or elevated activation of cells, especially
 CC e.g. by intracellular, and especially by intravenous injection.
 CC at 1 mg to 500 mg g/kg/day for a period of 1 to 30 days.
 CC Fusion proteins can develop toxic activity in a wide range of tissue
 CC cells. The processing module prevents extracellular dissociation and
 CC fusion proteins based on mistletoe lectin A-chain are far more active
 CC than those based on ricin and do have the associated problems of
 CC non-specific toxicity. The protein may be expressed in a non-glycosylated
 CC form that does not bind to sugar receptors in the liver, and which has a
 CC long half-life in the blood. Where the mistletoe lectin B-chain is used,
 CC it actively assists in translocation of the ML A-chain from the
 CC endoplasmic reticulum to the cytoplasm.

Sequence 263 AA;
 SQ

Query Match 93.7%; Score 137.5; DB 19; Length 263;
 Best Local Similarity 95.1%; Pred. No. 2.8e-123;
 Matches 250; Conservative 10; Indels 1; Gaps 1;

QY 1 DDVTCASAPPTVAIVGNKGVVDDPFDHGNQIQAMPKSNNDPNOIWTIKEDGTIS 60
 DB 1 DDVTCASAPPTVAIVGNKGVVDDPFDHGNQIQAMPKSNNDPNOIWTIKEDGTIS 60
 QY 61 NSCCTTGTGTAGTVMIPCNVAVEATINQIMNGTINRNSNLVLAASGKGTIT 120
 DB 61 NSCCTTGTGTAGTVMIPCNVAVEATINQIMNGTINRNSNLVLAASGKGTIT 120
 QY 121 VQTLDTYTLGGWLAGNDTAPREVTYGFRLQMSNGSVMWETCDSSQNGKALYXD 180
 DB 121 VQTLDTYTLGGWLAGNDTAPREVTYGFRLQMSNGSVMWETCDSSQNGKALYXD 179
 QY 181 GSIRKPNODQCLTGRDSVSTVINIVSCGASGSGRWFTNKGALINLKTGLAMDVQA 240
 DB 180 GSIRKPNODQCLTGRDSVSTVINIVSCGASGSGRWFTNKGALINLKTGLAMDVQA 239
 QY 241 NPKLRITITVPATKXKQNMWLPV 263
 DB 240 NPKLRITITVPATKXKQNMWLPV 262

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 Job time : 27.0864 secs

XX Sequence 264 AA;
 SQ Query Match 94.1%; Score 1333.5; DB 20; Length 264;
 Best Local Similarity 95.4%; Pred. No. 7.1e-124;
 Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DPTVCSAEPFVRIYGRNKMVDEDDPHDQIQIAMPKSNNDPQNLTKKDGRTIS 60
 DB 1 DPTVCSAEPFVRIYGRNKMVDEDDPHDQIQIAMPKSNNDPQNLTKKDGRTIS 60
 QY 61 NGSCLTGYAGYVYVIFDCNTAVREATTWQIDNGTINPRSNLYLAASGIGKTTLT 120
 DB 61 NGSCLTGYAGYVYVIFDCNTAVREATTWQIDNGTINPRSNLYLAASGIGKTTLT 120
 QY 121 VQTLDTYLGQCMALANDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKALYED 180
 DB 121 VQTLDTYLGQCMALANDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKALYED 180
 QY 121 VQTLDTYLGQCMALANDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKALYED 179
 DB 121 VQTLDTYLGQCMALANDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKALYED 179
 QY 181 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGQWFTNKGALINLTGLANDVQA 240
 DB 181 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGQWFTNKGALINLTGLANDVQA 240
 QY 241 NPKLRRIIYFATGKPNQMLPV 263
 DB 241 NPKLRRIIYFATGKPNQMLPV 263
 QY 240 NPKLRRIIYFATGKPNQMLPV 262
 DB 240 NPKLRRIIYFATGKPNQMLPV 262

RESULT 13
 AA25979 standard, Protein, 531 AA.
 ID AAZ5979
 XX AAZ5979;
 AC AAZ5979;
 DT 18-OCT-1999 (first entry)
 XX
 DE Mistletoe lectin I protein fragment.
 XX
 KM Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KW ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;
 KM lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin I.
 OS
 XX Viscum album.
 XX
 FN DE19804210-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 PI Morris P, Stiefel T, Voelter W, Welters P;
 XX
 DR WPI; 1999-44535/38.
 XX
 DR N-PSDB; AAZ09103.
 XX
 PT Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 PI Claim 7; Fig 1b; 78pp; German.
 XX

CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a mistletoe lectin I protein fragment.
 XX

XX Sequence 531 AA;
 SQ Query Match 94.1%; Score 1333.5; DB 20; Length 531;
 Best Local Similarity 95.4%; Pred. No. 7.1e-123;
 Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 DPTVCSAEPFVRIYGRNKMVDEDDPHDQIQIAMPKSNNDPQNLTKKDGRTIS 60
 DB 1 DPTVCSAEPFVRIYGRNKMVDEDDPHDQIQIAMPKSNNDPQNLTKKDGRTIS 60
 QY 269 DPTVCSAEPFVRIYGRNKMVDEDDPHDQIQIAMPKSNNDPQNLTKKDGRTIS 328
 DB 269 DPTVCSAEPFVRIYGRNKMVDEDDPHDQIQIAMPKSNNDPQNLTKKDGRTIS 328
 QY 61 NGSCLTGYAGYVYVIFDCNTAVREATTWQIDNGTINPRSNLYLAASGIGKTTLT 120
 DB 61 NGSCLTGYAGYVYVIFDCNTAVREATTWQIDNGTINPRSNLYLAASGIGKTTLT 120
 QY 329 NGSCLTGYAGYVYVIFDCNTAVREATTWQIDNGTINPRSNLYLAASGIGKTTLT 388
 DB 329 NGSCLTGYAGYVYVIFDCNTAVREATTWQIDNGTINPRSNLYLAASGIGKTTLT 388
 QY 121 VQTLDTYLGQCMALANDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKALYED 180
 DB 121 VQTLDTYLGQCMALANDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKALYED 180
 QY 399 VQTLDTYLGQCMALANDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKALYED 447
 DB 399 VQTLDTYLGQCMALANDTAPREVTIYGFADLCMSNGSQQWVETCDSSQKQKALYED 447
 QY 181 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGQWFTNKGALINLTGLANDVQA 240
 DB 181 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGQWFTNKGALINLTGLANDVQA 240
 QY 448 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGQWFTNKGALINLTGLANDVQA 507
 DB 448 GSIRPKONDOCLTSGRDSVSTVINIVSCGASGQWFTNKGALINLTGLANDVQA 507
 QY 241 NPKLRRIIYFATGKPNQMLPV 263
 DB 241 NPKLRRIIYFATGKPNQMLPV 263
 QY 508 NPKLRRIIYFATGKPNQMLPV 530
 DB 508 NPKLRRIIYFATGKPNQMLPV 530

RESULT 14
 AA25982 standard, Protein, 532 AA.
 ID AAZ5982
 XX AAZ5982;
 AC AAZ5982;
 DT 18-OCT-1999 (first entry)
 XX
 DE Mistletoe lectin I (variant) protein fragment.
 XX
 KM Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KW ribozyme 268 subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin I.
 OS
 XX Viscum album.
 XX
 FN DE19804210-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 03-FEB-1998; 98DE-1004210.
 XX
 XX 03-FEB-1998; 98DE-1004210.
 XX
 PA (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 XX
 PI Morris P, Stiefel T, Voelter W, Welters P;
 XX
 DR WPI; 1999-44535/38.
 XX
 DR N-PSDB; AAZ09106.
 XX
 PT Preparation of mistletoe lectins in heterologous systems,
 PT particularly for use as anticancer agents and immunostimulants
 XX
 PI Disclosure; Fig 4b; 78pp; German.
 XX

QY 61 NSGCLATGTYGAGTAAVAFPCNTAVAREATTWQIMNGTIIINPRSNLYLAASSGIGKTTLT 120
 DB 61 NSGCLATGTYGAGTAAVAFPCNTAVAREATTWQIMNGTIIINPRSNLYLAASSGIGKTTLT 120
 QY 121 VQTLDPYTLGGGMLAGNDTAPREVTIYGPRDLCEMSNGSVWVETCSSQNGKALYGD 180
 DB 121 VQTLDPYTLGGGMLAGNDTAPREVTIYGPRDLCEMSNGSVWVETCSSQNGKALYGD 180
 QY 181 GSIRKQNDQCLTSGSDSVSTVINIVSCSGASGSGRWFTNEGALINLKTGLANDVAQA 240
 DB 181 GSIRKQNDQCLTSGSDSVSTVINIVSCSGASGSGRWFTNEGALINLKTGLANDVAQA 240
 QY 241 NPKLRITIIYPATGKRNQMLTPV 264
 DB 241 NPKLRITIIYPATGKRNQMLTPV 264

RESULT 11

AAV25985 ID AAV25985 standard; Protein; 263 AA.

AAV25985; AC

18-OCT-1999 (first entry) DX

Mistletoe lectin B protein fragment. DE

Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity; KM

lymphokine-producing macrophage; T-cell activation; immune response; KM

cancer; cytotoxicity; antigen; isoform; lectin B. XX

Viscum album. OS

DE19804210-A1. XX

12-AUG-1999. PD

03-FEB-1998; 98DB-1004210. PF

03-FEB-1998; 98DB-1004210. PR

(BIOS-) BIOSYN ARZNEIMITTEL GMBH. XX

Morris P, Stiefel T, Voelter W, Welters P; PI

WPI; 1999-44535/38. XX

N-PSDB; AA209109. DR

Preparation of mistletoe lectins in heterologous systems, PT

particularly for use as anticancer agents and immunostimulants PS

Claim 9; Fig 7B; 78pp; German. XX

This invention describes a novel mistletoe lectin (I) and its fragments CC

which have antitumor and immunostimulatory activity. The A-chain (MIA) CC

of the mistletoe lectin binds to, and inactivates, the 28S subunit of CC

ribosomes. Non-cytotoxic forms of (I) activate T-cell and CC

lymphokine-producing macrophages, so stimulate immunity. (I) and its CC

fragments are used to treat uncontrolled cell growth (particularly CC

immune response, particularly T-cell activation, and increase production of the CC

(tumour-associated, bacterial or viral). The method antigen production of CC

mistletoe lectin, and its individual chains, in many different CC

and on a large scale, at any time of the year. Recombinant products are CC

free from toxins present in natural mistletoe extracts. This sequence CC

Matches 251; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
 QY 1 DDTVCSASEPTVRAIVGNKQGVVDHDDPFDGNOIQAFPSKSNPNQNLTKRDTGIS 60
 DB 1 DDTVCSASEPTVRAIVGNKQGVVDHDDPFDGNOIQAFPSKSNPNQNLTKRDTGIS 60
 QY 61 NSGCLATGTYGAGTAAVAFPCNTAVAREATTWQIMNGTIIINPRSNLYLAASSGIGKTTLT 120
 DB 61 NSGCLATGTYGAGTAAVAFPCNTAVAREATTWQIMNGTIIINPRSNLYLAASSGIGKTTLT 120
 QY 121 VQTLDPYTLGGGMLAGNDTAPREVTIYGPRDLCEMSNGSVWVETCSSQNGKALYGD 180
 DB 121 VQTLDPYTLGGGMLAGNDTAPREVTIYGPRDLCEMSNGSVWVETCSSQNGKALYGD 180
 QY 181 GSIRKQNDQCLTSGSDSVSTVINIVSCSGASGSGRWFTNEGALINLKTGLANDVAQA 240
 DB 181 GSIRKQNDQCLTSGSDSVSTVINIVSCSGASGSGRWFTNEGALINLKTGLANDVAQA 240
 QY 241 NPKLRITIIYPATGKRNQMLTPV 263
 DB 241 NPKLRITIIYPATGKRNQMLTPV 263

RESULT 12

AAV25991 ID AAV25991 standard; Protein; 264 AA.

AAV25991; AC

18-OCT-1999 (first entry) DX

Mistletoe lectin B variant protein fragment. DE

Mistletoe; lectin; antitumor; immunostimulant; A-chain; MIA; immunity; KM

lymphokine-producing macrophage; T-cell activation; immune response; KM

cancer; cytotoxicity; antigen; isoform; lectin B. XX

Viscum album. OS

DE19804210-A1. XX

12-AUG-1999. PD

03-FEB-1998; 98DB-1004210. PF

03-FEB-1998; 98DB-1004210. PR

(BIOS-) BIOSYN ARZNEIMITTEL GMBH. XX

Morris P, Stiefel T, Voelter W, Welters P; PI

WPI; 1999-44535/38. XX

N-PSDB; AA209115. DR

Preparation of mistletoe lectins in heterologous systems, PT

particularly for use as anticancer agents and immunostimulants PS

Disclosure; Fig 1B; 78pp; German. XX

This invention describes a novel mistletoe lectin (I) and its fragments CC

which have antitumor and immunostimulatory activity. The A-chain (MIA) CC

of the mistletoe lectin binds to, and inactivates, the 28S subunit of CC

ribosomes. Non-cytotoxic forms of (I) activate T-cell and CC

lymphokine-producing macrophages, so stimulate immunity. (I) and its CC

fragments are used to treat uncontrolled cell growth (particularly CC

immune response, particularly T-cell activation, and increase production of the CC

(tumour-associated, bacterial or viral). The method antigen production of CC

Db 181 GSIRPKNOQDCLTSGRDSVSTVINIVSCGASGSRWFTNEGAILNKLSIMVDVAQA 240
 Qy 241 NPKLRILITPARKKRNQWMLPWF 264
 Db 241 NPKLRILITPARKKRNQWMLPWF 264

RESULT 9

AAV25987
 ID AAV25987 standard; Protein; 264 AA.

XX AAV25987;
 XX 18-OCT-1999 (first entry)
 XX Mistletoe lectin B2 protein fragment.
 KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B2.

XX Viscum album.
 OS DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 PA Morris P, Stiefel T, Voelter W, Welters P;
 DR WPI; 1999-44535/38.
 XX N-PSDB; A8209117.
 PT Preparation of mistletoe lectins in heterologous systems.
 PT particularly for use as anticancer agents and immunostimulants
 XX Claim 9; Fig 9b; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 CC lymphokine-producing macrophages, so stimulate immunity. (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response (particularly to a co-administered antigen production of
 CC tumour-associated bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a mistletoe lectin B2 protein.

SQ Sequence 264 AA;

Query Match 97.3%; Score 1379; DB 20; Length 264;
 Best Local Similarity 97.7%; Pred. No. 2, 2e-128;
 Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DDVTCASAPFTVIRVGRKRVADDDPHDQNGIOLTFPSKSNDDPQWLTKRDKTIRIS 60
 Db 61 NSQCLTGYGAGVYVWIPQCVYVETATWQINQNGTIIINPNSNDVLAASSGKGTITL 120
 Db 61 NSQCLTGYGAGVYVWIPQCVYVETATWQINQNGTIIINPNSNDVLAASSGKGTITL 120

Qy 121 VQTLDTYLLGGWGLAGNDTPAPREVTITGFRDLCEMSNGSVVETCDSSQKQKMAKYCD 180
 Db 121 VQTLDTYLLGGWGLAGNDTPAPREVTITGFRDLCEMSNGSVVETCDSSQKQKMAKYCD 180
 Qy 181 GSIRPKNOQDCLTSGRDSVSTVINIVSCGASGSRWFTNEGAILNKLSIMVDVAQA 240
 Db 181 GSIRPKNOQDCLTSGRDSVSTVINIVSCGASGSRWFTNEGAILNKLSIMVDVAQA 240
 Qy 241 NPKLRILITPARKKRNQWMLPWF 264
 Db 241 NPKLRILITPARKKRNQWMLPWF 264

RESULT 10

AAV25993
 ID AAV25993 standard; Protein; 265 AA.

XX AAV25993;
 XX 18-OCT-1999 (first entry)
 XX Mistletoe lectin B2 variant protein fragment.
 KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MIA; immunity;
 KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
 KW lymphokine-producing macrophage; uncontrolled cell growth; treatment;
 KW cancer; cytotoxicity; antigen; isoform; lectin B2.

XX Viscum album.
 OS DE19804210-A1.
 XX 12-AUG-1999.
 XX 03-FEB-1998; 98DE-1004210.
 XX 03-FEB-1998; 98DE-1004210.
 XX (BIOS-) BIOSYN ARZNEIMITTEL GMBH.
 PA Morris P, Stiefel T, Voelter W, Welters P;
 DR WPI; 1999-44535/38.
 XX N-PSDB; A8209117.
 PT Preparation of mistletoe lectins in heterologous systems.
 PT particularly for use as anticancer agents and immunostimulants
 XX Disclosure; Fig 15b; 78pp; German.

XX This invention describes a novel mistletoe lectin (I) and its fragments
 CC which have antitumour and immunostimulatory activity. The A-chain (MA)
 CC of the mistletoe lectin binds to, and inactivates, the 28S subunit of
 CC ribosomes. Non-cytotoxic forms of (I) activate T-cell and (I) and its
 CC fragments are used to treat uncontrolled cell growth (particularly
 CC cancer) and if they lack cytotoxicity, to increase the strength of the
 CC immune response, particularly to a co-administered antigen
 CC (tumour-associated, bacterial or viral). The method allows production of
 CC mistletoe lectin, and its individual chains, in many different isoforms
 CC and on a large scale, at any time of the year. Recombinant products are
 CC free from toxins present in natural mistletoe extracts. This sequence
 CC represents a fragment of a variant mistletoe lectin B2 protein.

SQ Sequence 265 AA;

Query Match 97.3%; Score 1379; DB 20; Length 265;
 Best Local Similarity 97.7%; Pred. No. 2, 2e-128;
 Matches 258; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DDVTCASAPFTVIRVGRKRVADDDPHDQNGIOLTFPSKSNDDPQWLTKRDKTIRIS 60
 Db 1 DDVTCASAPFTVIRVGRKRVADDDPHDQNGIOLTFPSKSNDDPQWLTKRDKTIRIS 60

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ID AAY25990 standard; Protein: 264 AA.
AC AAY25990;
XX
XX
XX 18-OCT-1999 (first entry)
DT
DE Mistletoe lectin B5 protein fragment.
DE
XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.
XX
XX Viscum album.
XX DE19804210-AL.
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welters P.
XX WPI: 1999-44535/38.
XX N-PSDB; AA209114.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 9; Fig 12b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MHA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a mistletoe lectin B5 protein.
XX
XX Sequence 264 AA;
SQ
Query Match 98.6%; Score 1397; DB 20; Length 264;
Best Local Similarity 98.5%; Pred. No. 3,66-130;
Matches 260; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 DDTGSASEPTVRIYRNGKRVVDDDFPDGNOIQLPKSNNDPNQMTTKEDGTIRS 60
DB 1 DDTGSASEPTVRIYRNGKRVVDDDFPDGNOIQLPKSNNDPNQMTTKEDGTIRS 60
OY 61 NSGCLTYGTAGVYVMIPDNTAVREATINQINDGIIIPRSNLVLAASGKIGTTLT 120
DB 61 NSGCLTYGTAGVYVMIPDNTAVREATINQINDGIIIPRSNLVLAASGKIGTTLT 120
OY 121 VQTLDTLQGLAGNDTAPREVITIGFRDLCKSSGSGVWVETDSSQKQKALYED 180
DB 121 VQTLDTLQGLAGNDTAPREVITIGFRDLCKSSGSGVWVETDSSQKQKALYED 180
OY 181 GSIRKQNDQCLTSRDSVSIVIVISGASGSGRWFTNMGALINLAKSLANDVAQA 240
DB 181 GSIRKQNDQCLTSRDSVSIVIVISGASGSGRWFTNMGALINLAKSLANDVAQA 240
OY 241 NPLMRRIIYPRATGKRNQMLPVF 264
DB 241 NPLMRRIIYPRATGKRNQMLPVF 264

DB 241 NPLMRRIIYPRATGKRNQMLPVF 264
RESULT 8
ID AAY25996 standard; Protein: 265 AA.
AC AAY25996;
XX
XX
XX 18-OCT-1999 (first entry)
DT
DE Mistletoe lectin B5 variant protein fragment.
DE
XX Mistletoe; lectin; antitumor; immunostimulant; A-chain; MHA; immunity;
XX ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
XX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
XX cancer; cytotoxicity; antigen; isoform; lectin B5.
XX
XX Viscum album.
XX DE19804210-AL.
XX 12-AUG-1999.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX 03-FEB-1998; 98DE-1004210.
XX
XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
XX Morris P, Stiefel T, Voelter W, Welters P.
XX WPI: 1999-44535/38.
XX N-PSDB; AA209120.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Disclosure; Fig 18b; 78pp; German.
XX
XX This invention describes a novel mistletoe lectin (I) and its fragments
XX which have antitumor and immunostimulatory activity. The A-chain (MHA)
XX of the mistletoe lectin binds to, and inactivates, the 28S subunit of
XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
XX lymphokine-producing macrophages so stimulate immunity. (I) and its
XX fragments are used to treat uncontrolled cell growth (particularly of
XX cancers) and if they lack cytotoxicity, to increase the strength of the
XX immune response, particularly to a co-administered antigen production of
XX (tumour-associated, bacterial or viral). The method allows production of
XX mistletoe lectin, and its individual chains, in many different isoforms
XX and on a large scale, at any time of the year. Recombinant products are
XX free from toxins present in natural mistletoe extracts. This sequence
XX represents a fragment of a variant mistletoe lectin B5 protein.
XX
XX Sequence 265 AA;
SQ
Query Match 98.6%; Score 1397; DB 20; Length 265;
Best Local Similarity 98.5%; Pred. No. 3,66-130;
Matches 260; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 DDTGSASEPTVRIYRNGKRVVDDDFPDGNOIQLPKSNNDPNQMTTKEDGTIRS 60
DB 1 DDTGSASEPTVRIYRNGKRVVDDDFPDGNOIQLPKSNNDPNQMTTKEDGTIRS 60
OY 61 NSGCLTYGTAGVYVMIPDNTAVREATINQINDGIIIPRSNLVLAASGKIGTTLT 120
DB 61 NSGCLTYGTAGVYVMIPDNTAVREATINQINDGIIIPRSNLVLAASGKIGTTLT 120
OY 121 VQTLDTLQGLAGNDTAPREVITIGFRDLCKSSGSGVWVETDSSQKQKALYED 180
DB 121 VQTLDTLQGLAGNDTAPREVITIGFRDLCKSSGSGVWVETDSSQKQKALYED 180
OY 181 GSIRKQNDQCLTSRDSVSIVIVISGASGSGRWFTNMGALINLAKSLANDVAQA 240
DB 181 GSIRKQNDQCLTSRDSVSIVIVISGASGSGRWFTNMGALINLAKSLANDVAQA 240

KM		Lymphokine-producing macrophage; uncontrolled cell growth; treatment;
KW		Cancer; cytotoxicity; antigen; isoform; lectin B4.
XX		Vlaecum album.
OS		
XX	DEI9804210-AL.	
XX		
PD	12-AUG-1999.	
PF	03-FEB-1998;	98DE-1004210.
XX	03-FEB-1998;	98DE-1004210.
PR	(BIOS-) BIOS ARZNEIMITTEL GMBH.	
FA	Morris P, Stiefel T, Voelter W, Welters P,	
XX	MPJ: 1999-445335/38.	
DR	N-PSDB; AA020113.	
XX		
PT	Preparation of mistletoe lectins in heterologous systems,	
XX	particularly for use as anticancer agents and immunostimulants	
XX	Claim 9; Fig 11B; 78BP; German.	
XX	This invention describes a novel mistletoe lectin (I) and its fragments	
CC	which have antitumor and immunostimulatory activity. The A-chain (MA)	
CC	of the mistletoe lectin binds to, and inactivates, the 28S subunit of	
CC	rRNA. The following are preferred forms of (I) activate r-cell and (I) and its	
CC	lymphokine-producing cell fragments are used to treat uncontrolled cell growth	
CC	and cancer and if they lack cytotoxicity, to increase the strength of the	
CC	immune response, particularly to a co-administered antigen	
CC	(tumour-associated, bacterial or viral). The method allows production of	
CC	mistletoe-lectin, and its individual chains, in many different isoforms	
CC	and on a large scale, at any time of the year. Recombinant products are	
CC	free from toxins present in natural mistletoe extracts. This sequence	
XX	represents a fragment of a mistletoe lectin B4 protein.	
XX	Sequence 264 AA:	
Query Match	99.1%; Score 1404; DB 20; Length 264;	
Best Local Similarity	99.2%; Pred. No. 7.2e-111;	
Matches 262; Conservative 0; Mismatches 2; Indels 0; Gaps 0		
DQ	1 DDTYCSAEPTFRIVRGNKAVVDDDPDNDNQLMPSSKNNDPNQMLTKDKDGTRIS 60	
YY	1 DDVTGASSEPTFRIVRGNKSKSVVDPPDNDNQLMPSSKNNDPNQMLTKDKDGTRIS 60	
OY	61 NSGCTTGTGTGGTYGVVFDONZYARENTIKINDNTIPNSKYVAASGCKITLT 120	
DB	61 NGSCTTGTGTGGTYGVVFDONZYARENTIKINDNTIPNSKYVAASGCKITLT 120	
OY	121 VQTLTYTTSGGMVLANDPAPREVTITYGFRLLCMSNGSWWATDSQSDQNGKMALYGD 180	
DB	121 VQTLTYTTLGGMVLAPEEYTIYGFRLCMSNGSWWATDSQSDQNGKMALYGD 180	
OY	181 GSIRPKNQDGLTSRBSVSYSVINIVSCGSSGSGNWTFINCAILNLKGPRADDAQA 240	
DB	181 GSIRPKNQDGLTSRBSVSYSVINIVSCGSSGSGNWTFINCAILNLKGPRADDAQA 240	
OY	241 NPPLRRRIITYPAKTCKPMQMTLPVF 264	
DB	241 NPPLRRRIITYPAKTCKPMQMTLPVF 264	
RESULT 6		
ID	AA025995	
AC	AA025995 standard, Protein, 265 AA.	
XX	AA025995;	
OT	18-OCT-1999 (first entry)	

XX	XX	Mistletoe lectin B4 variant protein fragment.
KM	XX	Mistletoe lectin; antitumour; immunostimulant; A-chain; NLA; immunity?
KM	XX	lysozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KM	XX	lysozyme-producing macrophage; uncontrolled cell growth; treatment;
KM	XX	cancer; cytotoxicity; antigen; isoform; lectin B4.
XX	XX	Viscum album.
XX	XX	DE19804210-N1.
PD	PD	12-AUG-1999.
PF	PF	03-FEB-1998; 98DE-1004210.
PR	PR	03-FEB-1998; 98DE-1004210.
XX	XX	(BIOS-) BIOSYN ARZENMITTEL GMBH.
PI	PI	Morris P, Stiefel T, Voelker W, Welters P.
DR	DR	WPI: 1999-44533/38.
XX	XX	N-FSDB: AA029119.
PT	PT	Preparation of mistletoe lectins in heterologous systems,
XX	XX	particularly for use as anticancer agents and immunostimulants
FS	FS	Disclosure; Fig 17B; 78pp; German.
CC	CC	This invention describes a novel mistletoe lectin (I) and its fragments
CC	CC	which have been shown to be cytotoxic to tumour cells (T-cells) and
CC	CC	cells of the mistletoe lectin binds to and inactivates. The 28S subunit of
CC	CC	ribosomes. Non-cytotoxic forms of (I) activate T-cell and
CC	CC	lymphokine-producing macrophages, so stimulate immunity. (I) and its
CC	CC	fragments are used to treat uncontrolled cell growth (particularly
CC	CC	cancers) and if they lack cytotoxicity, to increase the strength of the
CC	CC	immune response, particularly to a co-administered antigen
CC	CC	(tumour-associated, bacterial or viral). The method allows production of
CC	CC	mistletoe lectin, and its individual chains, in many different isoforms
CC	CC	and in different glycosylation states. Mistletoe lectin products are
CC	CC	free from toxins present in natural mistletoe extracts. This sequence
CC	CC	represents a fragment of a variant mistletoe lectin B4 protein.
SQ	SQ	Sequence 265 AA:
Query Match	99.1%; Score 1404; DB 20; Length 265;	
Best Local Similarity	99.2%; Pred. No. 7.2e-131;	
Matches 262;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1 DVTGSASEPVRIVRGNRGARDVRDDPDHNGCQLMPSKANDPDMQITIKROGTTIS 60	
DB	1 DVTGSASEPVRIVRGNRGARDVRDDPDHNGCQLMPSKANDPDMQITIKROGTTIS 60	
QY	61 NSGCLTYGYAGVGYMFPQCTAREATITQGLMDNGIINFRNSVLAASSGIGKGTLL 120	
DB	61 NSGCLTYGYAGVGYMFPQCTAREATITQGLMDNGIINFRNSVLAASSGIGKGTLL 120	
QY	121 VQGLDPTLGGMLAGNDTAREVITVGFEDLCMESNGSVYVEFCSSQNNQGNALYGD 180	
DB	121 VQGLDPTLGGMLAGNDTAREVITVGFEDLCMESNGSVYVEFCSSQNNQGNALYGD 180	
QY	181 GSIRKRONDDCLTSRDSYSTVINIVSCASASGRVETWEGALINLKTGLANDVQA 240	
DB	181 GSIRKRONDDCLTSRDSYSTVINIVSCASASGRVETWEGALINLKTGLANDVQA 240	
QY	241 NPGLRRITIVPRGKNDMLPTF 264	
DB	241 NPGLRRITIVPRGKNDMLPTF 264	
RESULT 7		
AA125990		

XX 03-FEB-1998; 98DE-1004210.
 XX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
 XX Morris P, Stiefel T, Voelter W, Welters P;
 XX WPI; 1999-44535/38.
 XX N-PSDB; AA209110.
 XX Preparation of mistletoe lectins in heterologous systems,
 XX particularly for use as anticancer agents and immunostimulants
 XX Claim 9; Fig 8b; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (MA)
 XX of the mistletoe lectin binds to, and activates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX also produced. The invention also provides a method for the production of
 XX recombinant proteins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a mistletoe lectin B1 protein.
 SQ Sequence 264 AA;
 Query Match 99.6%; Score 1412; DB 20; Length 264;
 Best Local Similarity 99.6%; Pred. No. 1, 2e-131;
 Matches 265; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DVTGCSAEPPTVAVRGRKRVVDVDDPHDGNQQLMPKSKNDPRLQWIRKDTIR 60
 DB 1 DVTGCSAEPPTVAVRGRKRVVDVDDPHDGNQQLMPKSKNDPRLQWIRKDTIR 60
 QY 61 NSCLTGYGTRAGVYVMIPECTAVREAVTIWQINNGTIIINRSNTVLAASGIGTIT 120
 DB 61 NSCLTGYGTRAGVYVMIPECTAVREAVTIWQINNGTIIINRSNTVLAASGIGTIT 120
 QY 121 VQTDVTLGGMLAGNDAPREVTIVGPDICMESNGSWWETCSQKQKXALYGD 180
 DB 121 VQTDVTLGGMLAGNDAPREVTIVGPDICMESNGSWWETCSQKQKXALYGD 180
 QY 181 GSIRPKNODCLTSGRDSVSTVINIVSGASGQWFTBGAIIINLKGALADVAQA 240
 DB 181 GSIRPKNODCLTSGRDSVSTVINIVSGASGQWFTBGAIIINLKGALADVAQA 240
 QY 241 NPKLRRIIIVPATKRNQWMLPVF 264
 DB 241 NPKLRRIIIVPATKRNQWMLPVF 264
 RESULT 4
 AA25992
 ID AA25992 standard; Protein; 265 AA.
 AC AA25992;
 DT 18-OCT-1999 (first entry)
 DX Mistletoe lectin B1 variant protein fragment.
 KY Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 FX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KV cancer; cytotoxicity; antigen; isoform; lectin B1.
 XX Viscum album.

PN DB19804210-AL.
 PD 12-AUG-1999.
 PF 03-FEB-1998; 98DE-1004210.
 PR 03-FEB-1998; 98DE-1004210.
 PX (BIO-) BIOSYN ARZNEIMITTEL GMBH.
 PY Morris P, Stiefel T, Voelter W, Welters P;
 PZ WPI; 1999-44535/38.
 DR N-PSDB; AA209116.
 DR Preparation of mistletoe lectins in heterologous systems,
 DR particularly for use as anticancer agents and immunostimulants
 DR Disclosure; Fig 14b; 78pp; German.
 XX This invention describes a novel mistletoe lectin (I) and its fragments
 XX which have antitumour and immunostimulatory activity. The A-chain (MA)
 XX of the mistletoe lectin binds to, and activates, the 28S subunit of
 XX ribosomes. Non-cytotoxic forms of (I) activate T-cell and
 XX lymphokine-producing macrophages, so stimulate immunity. (I) and its
 XX fragments are used to treat uncontrolled cell growth (particularly
 XX cancers) and if they lack cytotoxicity, to increase the strength of the
 XX immune response, particularly to a co-administered antigen
 XX (tumour-associated, bacterial or viral). The method allows production of
 XX mistletoe lectin, and its individual chains, in many different isoforms
 XX and on a large scale, at any time of the year. Recombinant products are
 XX also produced. The invention also provides a method for the production of
 XX recombinant proteins present in natural mistletoe extracts. This sequence
 XX represents a fragment of a variant mistletoe lectin B1 protein.
 SQ Sequence 265 AA;
 Query Match 99.6%; Score 1412; DB 20; Length 265;
 Best Local Similarity 99.6%; Pred. No. 1, 2e-131;
 Matches 265; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DVTGCSAEPPTVAVRGRKRVVDVDDPHDGNQQLMPKSKNDPRLQWIRKDTIR 60
 DB 1 DVTGCSAEPPTVAVRGRKRVVDVDDPHDGNQQLMPKSKNDPRLQWIRKDTIR 60
 QY 61 NSCLTGYGTRAGVYVMIPECTAVREAVTIWQINNGTIIINRSNTVLAASGIGTIT 120
 DB 61 NSCLTGYGTRAGVYVMIPECTAVREAVTIWQINNGTIIINRSNTVLAASGIGTIT 120
 QY 121 VQTDVTLGGMLAGNDAPREVTIVGPDICMESNGSWWETCSQKQKXALYGD 180
 DB 121 VQTDVTLGGMLAGNDAPREVTIVGPDICMESNGSWWETCSQKQKXALYGD 180
 QY 181 GSIRPKNODCLTSGRDSVSTVINIVSGASGQWFTBGAIIINLKGALADVAQA 240
 DB 181 GSIRPKNODCLTSGRDSVSTVINIVSGASGQWFTBGAIIINLKGALADVAQA 240
 QY 241 NPKLRRIIIVPATKRNQWMLPVF 264
 DB 241 NPKLRRIIIVPATKRNQWMLPVF 264
 RESULT 5
 AA25989
 ID AA25989 standard; Protein; 264 AA.
 AC AA25989;
 DT 18-OCT-1999 (first entry)
 DX Mistletoe lectin B4 protein fragment.
 KY Mistletoe lectin; antitumour; immunostimulant; A-chain; MA; immunity;
 KW ribosome 28S subunit; non-cytotoxic; T-cell activation; immune response;
 FX lymphokine-producing macrophages; uncontrolled cell growth; treatment;
 KV cancer; cytotoxicity; antigen; isoform; lectin B1.

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us-09-601-667c-9.rta

Page 2

PT Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Claim 9; Fig 10B; 78pp; German.
XX
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MA)
CC of the mistletoe lectin binds to (i) activate T-cells, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (i) activate T-cells and its
CC lymphokine-producing macrophages, so stimulate immunity. (i) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC represents a fragment of a mistletoe lectin B3 protein.
XX
SQ Sequence 264 AA;
Query Match 100.0%; Score 1417; DB 20; Length 264;
Best Local Similarity 100.0%; Pred. No. 3.7e-132;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDTGCSASEPTVRIYVGNKGVVDVDDDFDQNOIQLPKSKNDPQQLMTIKRDTGRS 60
DB 1 DDTGCSASEPTVRIYVGNKGVVDVDDDFDQNOIQLPKSKNDPQQLMTIKRDTGRS 60
QY 61 NSGCLTYGTAGVYVAFPCQNTANREATTQIQNDGTTINPNSNVLAASSGIKETTLT 120
DB 61 NSGCLTYGTAGVYVAFPCQNTANREATTQIQNDGTTINPNSNVLAASSGIKETTLT 120
QY 121 VQTLDTLGGQMLAGNDTAPREVTIYGFPRDLCESSNGSVWETCDSSQKQKALYGD 180
DB 121 VQTLDTLGGQMLAGNDTAPREVTIYGFPRDLCESSNGSVWETCDSSQKQKALYGD 180
QY 181 GSIRKONODQLTSGSDSVSTVINIVSCGASGSGQVWFTNBSALINLKTGLANDVAQA 240
DB 181 GSIRKONODQLTSGSDSVSTVINIVSCGASGSGQVWFTNBSALINLKTGLANDVAQA 240
QY 241 NPKLRRIITYPATGRKQWMLPWF 264
DB 241 NPKLRRIITYPATGRKQWMLPWF 264

RESULT 2

AAZ5994
ID AAZ5994 standard; Protein; 265 AA.

AAZ5994;
XX

DT 18-OCT-1999 (first entry)
XX

DE Mistletoe lectin B3 variant protein fragment.
XX

KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;
KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform; lectin B3.
XX

XX Viscum album.
XX

PN DE19804210-A1.
XX

PD 12-AUG-1999.
XX

PF 03-FEB-1998; 98DE-1004210.
XX

PR 03-FEB-1998; 98DE-1004210.
XX

PA (BIOG-) BIOSTN ARZNEIMITTEL GMBH.
XX

PI Morris P, Stiefel T, Voelker W, Walters P,
XX WPI; 1999-44535/38.
DR N-PDB; AA209118.
XX
XX Preparation of mistletoe lectins in heterologous systems,
XX particularly for use as anticancer agents and immunostimulants
XX
XX Disclosure; Fig 16B; 78pp; German.
XX
CC This invention describes a novel mistletoe lectin (I) and its fragments
CC which have antitumour and immunostimulatory activity. The A-chain (MA)
CC of the mistletoe lectin binds to (i) activate T-cells, the 28S subunit of
CC ribosomes. Non-cytotoxic forms of (i) activate T-cells and its
CC lymphokine-producing macrophages, so stimulate immunity. (i) and its
CC fragments are used to treat uncontrolled cell growth (particularly
CC cancers) and if they lack cytotoxicity, to increase the strength of the
CC immune response, particularly to a co-administered antigen
CC (tumour-associated, bacterial or viral). The method allows production of
CC mistletoe lectin, and its individual chains, in many different isoforms
CC and on a large scale, at any time of the year. Recombinant products are
CC represents a fragment of a variant mistletoe lectin B3 protein.
XX
SQ Sequence 265 AA;
Query Match 100.0%; Score 1417; DB 20; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.7e-132;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDTGCSASEPTVRIYVGNKGVVDVDDDFDQNOIQLPKSKNDPQQLMTIKRDTGRS 60
DB 1 DDTGCSASEPTVRIYVGNKGVVDVDDDFDQNOIQLPKSKNDPQQLMTIKRDTGRS 60
QY 61 NSGCLTYGTAGVYVAFPCQNTANREATTQIQNDGTTINPNSNVLAASSGIKETTLT 120
DB 61 NSGCLTYGTAGVYVAFPCQNTANREATTQIQNDGTTINPNSNVLAASSGIKETTLT 120
QY 121 VQTLDTLGGQMLAGNDTAPREVTIYGFPRDLCESSNGSVWETCDSSQKQKALYGD 180
DB 121 VQTLDTLGGQMLAGNDTAPREVTIYGFPRDLCESSNGSVWETCDSSQKQKALYGD 180
QY 181 GSIRKONODQLTSGSDSVSTVINIVSCGASGSGQVWFTNBSALINLKTGLANDVAQA 240
DB 181 GSIRKONODQLTSGSDSVSTVINIVSCGASGSGQVWFTNBSALINLKTGLANDVAQA 240
QY 241 NPKLRRIITYPATGRKQWMLPWF 264
DB 241 NPKLRRIITYPATGRKQWMLPWF 264

RESULT 3

AAZ5996
ID AAZ5996 standard; Protein; 264 AA.

AAZ5996;
XX

DT 18-OCT-1999 (first entry)
XX

DE Mistletoe lectin B1 protein fragment.
XX

KW Mistletoe; lectin; antitumour; immunostimulant; A-chain; MA; immunity;
KW ribozyme 28S subunit; non-cytotoxic; T-cell activation; immune response;
KW lymphokine-producing macrophages; uncontrolled cell growth; treatment;
KW cancer; cytotoxicity; antigen; isoform; lectin B1.
XX

XX Viscum album.
XX

PN DE19804210-A1.
XX

PD 12-AUG-1999.
XX

PF 03-FEB-1998; 98DE-1004210.
XX

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us-09-601-667c-9.reg

Page 1

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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18; Search time 26.0864 Seconds
(without alignments)
166.345 Million cell updates/sec

Title: US-09-601-667c-9

Perfect score: 1417

Sequence: 1 DDTCSASEPTVRIAGNNK.....RRITIPATKQNDMLPVP 264

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 159726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

A: Geneseq_19Jun03:*

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2: /SIDSI/gcgdata/geneseq/genesep-emb1/AA1981.DAT:*

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7: /SIDSI/gcgdata/geneseq/genesep-emb1/AA1986.DAT:*

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23: /SIDSI/gcgdata/geneseq/genesep-emb1/AA2002.DAT:*

24: /SIDSI/gcgdata/geneseq/genesep-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match length	DB	ID	Description
1	1417	100.0	264	20	AAV25988	Mistletoe lectin B
2	1417	100.0	264	20	AAV25989	Mistletoe lectin B
3	1417	100.0	264	20	AAV25990	Mistletoe lectin B
4	1412	99.6	264	20	AAV25992	Mistletoe lectin B
5	1404	99.1	264	20	AAV25993	Mistletoe lectin B
6	1404	99.1	264	20	AAV25995	Mistletoe lectin B
7	1397	98.6	264	20	AAV25990	Mistletoe lectin B
8	1397	98.6	264	20	AAV25996	Mistletoe lectin B
9	1379	97.3	264	20	AAV25997	Mistletoe lectin B

10	1379	97.3	265	20	AAV25993	Mistletoe lectin B
11	1333.5	94.1	264	20	AAV25995	Mistletoe lectin B
12	1333.5	94.1	264	20	AAV25991	Mistletoe lectin B
13	1333.5	94.1	531	20	AAV25979	Mistletoe lectin I
14	1333.5	94.1	533	20	AAV25982	Mistletoe lectin I
15	1327.5	93.7	264	18	AAV64662	Mistletoe lectin B
16	1327.5	93.7	264	18	AAV10023	Mistletoe lectin B
17	1327.5	93.7	264	18	AAV25973	Mistletoe lectin B
18	1327.5	93.7	264	18	AAV25976	Mistletoe lectin B
19	1327.5	93.7	564	18	AAV10021	Mistletoe lectin B
20	1327.5	93.7	564	18	AAV25977	Mistletoe lectin B
21	1291	91.1	264	20	AAV25978	Mistletoe lectin B
22	1291	91.1	264	20	AAV25972	Mistletoe lectin B
23	1291	91.1	264	20	AAV25970	Mistletoe lectin B
24	1291	91.1	533	20	AAV25973	Mistletoe lectin B
25	1291	91.1	533	20	AAV25976	Mistletoe lectin B
26	1253.4	88.4	267	19	AAV64667	Mistletoe lectin B
27	1253.4	88.4	267	19	AAV64667	Mistletoe lectin B
28	1113.5	76.6	264	22	AAV47094	B-chain isoforn fo
29	1085.5	74.3	264	22	AAV47095	B-chain isoforn fo
30	1052.5	70.5	266	22	AAV47093	B-chain isoforn fo
31	999	64.2	565	22	AAV50166	Sequence of prepro
32	909.5	64.2	565	22	AAV78300	Sequence of prepro
33	909.5	64.0	576	8	AAV78304	Sequence of prepro
34	907.5	64.0	576	8	AAV78302	Sequence of prepro
35	907.5	64.0	576	8	AAV78301	Sequence of prepro
36	907.5	64.0	576	8	AAV78301	Sequence of prepro
37	907.5	64.0	576	8	AAV78301	Sequence of prepro
38	907.5	64.0	576	8	AAV78301	Sequence of prepro
39	907.5	64.0	576	8	AAV78301	Sequence of prepro
40	907.5	64.0	576	8	AAV78301	Sequence of prepro
41	907.5	63.7	567	22	AAV60240	Prepro-ricin. Ricin
42	907.5	63.7	567	22	AAV60240	Prepro-ricin. Ricin
43	891.5	63.6	267	10	AAV29006	B chain B lectin w/c
44	891.5	63.6	267	10	AAV29006	B chain B lectin w/c
45	887.5	62.6	251	9	AAV81125	The ricin B chain

ALIGNMENTS

RESULT 1

ID AAV25988 standard; Protein, 264 AA.

AAV25988;

18-OCT-1999 (first entry)

Mistletoe lectin B3 protein fragment.

Mistletoe lectin B3 protein fragment.

Mistletoe lectin B3 protein fragment.

Mistletoe lectin B3 protein fragment.

Mistletoe lectin B3 protein fragment.

Mistletoe lectin B3 protein fragment.

Mistletoe lectin B3 protein fragment.

Mistletoe lectin B3 protein fragment.

Mistletoe lectin B3 protein fragment.

Mistletoe lectin B3 protein fragment.

Mistletoe lectin B3 protein fragment.

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us-09-601-667c-1.rpr

Page 1

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CM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 / Search time 16.5679 Seconds

(without alignments)
3093.817 Million cell updates/sec

Title: US-09-601-667C-1

Sequence: 1 VERLRLRFLVHTQITGKXKXFP.....RILIIYPAKGNKQWMLPV 533

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR_76:*

1: PIR:*

2: PIR:*

3: PIR:*

4: PIR:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1290	49.3	264	2	PD0019
2	1279.5	48.9	265	2	PD0030
3	1231	47.1	576	1	RLCSP
4	1183.5	45.2	528	1	TL2SA
5	1165.5	44.6	254	2	PD0018
6	1138.5	43.5	562	2	S16022
7	1137.5	43.5	528	2	S23431
8	1137.5	43.5	564	1	RLC49C
9	1109.5	42.4	570	2	S62677
10	849.5	32.5	570	2	S62677
11	822	31.4	263	2	S06330
12	443.5	17.0	251	2	C39761
13	309.5	11.8	247	2	JC0532
14	308.5	11.8	289	1	RLWT
15	307.5	11.8	247	2	UT0393
16	307.5	11.8	289	2	UC5606
17	307.5	11.8	289	2	UC5606
18	291	11.1	245	2	UC5606
19	284	10.9	316	2	TC4253
20	270	10.3	286	2	UT0393
21	261	10.0	286	1	RLPUCG
22	256.5	9.8	278	2	S23519
23	247	9.4	277	2	S22494
24	241	9.2	250	2	UN0108
25	229	8.8	278	2	A39817
26	196	7.5	261	2	UC0401
27	189.5	7.2	313	2	S17957
28	170.5	6.3	394	2	S24421
29	170.5	6.3	394	2	S24421
30	172.5	6.6	106	2	B9761

30	161.5	6.2	272	2	UC4811	betavulgin - bect
31	159.5	6.1	253	2	S28539	RNA N-glycosidase
32	157.5	6.0	253	2	S28542	RNA N-glycosidase
33	157.5	6.0	253	2	S28542	RNA N-glycosidase
34	153.5	5.9	283	2	S05202	RNA N-glycosidase
35	150.5	5.8	253	2	S28541	RNA N-glycosidase
36	148.5	5.7	292	1	RL0H2	RNA N-glycosidase
37	138.5	5.3	253	2	A58923	RNA N-glycosidase
38	136	5.2	310	2	S46239	RNA N-glycosidase
39	128.5	4.9	293	2	S17535	ribosome-inactivat
40	125.5	4.8	277	2	UC7935	chitinase (EC 3.2.
41	123.5	4.7	336	2	S12392	RNA N-glycosidase
42	123.5	4.7	336	2	S12392	endo-1,4-beta-xyla
43	118.5	4.5	477	1	J80589	30K ribosome inact
44	116.5	4.5	281	2	S8664	
45	115.5	4.4	383	2	T34603	xylinase A - Strept

ALIGNMENTS

RESULT 1

PD0019: mistletoe lectin I B chain - Viscum album (fragment)

C:Species: Viscum album

C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #ext_change 07-May-1999

C:Accession: PD0019

R:Bechthold, S.; Krauspehn, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, B.; Blohm, B.; Blohm, S.; Res. Commun. 247, 367-372, 1998

A>Title: Primary structure and molecular modelling of mistletoe lectin I from Viscum

A:Reference number: PD0019, WUID:96308123, PMID:9642133

A:Accession: PD0019

A:Protein type: protein

A:Protein family: 1204

C:Superfamily: lectin; RNA N-glycosidase homology

Query Match 49.3%; Score 1290; DB 2; Length 264;

Best Local Similarity 92.4%; Pred. No. 1.3e-116;

Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY	270	DDVTGASEPTVAVIGKXKXWVDRDDPDGNOIQLPSSNNDDNQLTAKDXTIR	329
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QY	330	NSGCTVGTAGVYVWIPDQNVRENTWQIMNGTINPSNKLVAASGCKKGTIT	389
DB	61	NSGCTVGTAGVYVWIPDQNVRENTWQIMNGTINPSNKLVAASGCKKGTIT	120
QY	390	VGLTADTIGQSMACQNTAEPETIIGRDLCSNKGSSVWETCKSSQKQXKXWALYD	449
DB	121	VGLTADTIGQSMACQNTAEPETIIGRDLCSNKGSSVWETCKSSQKQXKXWALYD	180
QY	450	GSIRPQKQCCITGSDSVTVNVCSSXKXKXWVFNKXKXKXKXKXKXKXKXKXKXKX	509
DB	181	GSIRPQKQCCITGSDSVTVNVCSSXKXKXWVFNKXKXKXKXKXKXKXKXKXKXKX	240
QY	510	NPKIRLIIYPAKGNKQWMLPV	532
DB	241	NPKIRLIIYPAKGNKQWMLPV	263

PD0018
 mistletoe lectin I A chain - Viscum album (fragment)
 C/Species: Viscum album
 C/Accession: PD0018 #sequence_revision 10-Oct-1998 #ext_change 26-Aug-1999
 R/Schubert, J. PD0018
 R/Schubert, J.; Krausepfeiffer, R.; Mikhailov, A.; Stoeve, S.; Betzel, C.; Voelter, W.
 Biochem. Biophys. Res. Commun. 247: 167-172, 1998
 A>Title: Primary structure and molecular modelling of mistletoe lectin I from Viscum album
 A/Reference number: PD0018; PMID:9808123; PMID:9642133
 A/Accession: PD0018
 A/Molecule type: Protein
 A/Residues: 1-254 <ES>
 A/Chemically modified: RNA N-glycosidase homology
 F:1-246/Domain: RNA N-glycosidase homology <RNG>
 Query Match 44.6% Score 1165.5 DB ? Length 254;
 Best Local Similarity 92.2% P-Val. No. 1.3e-104;
 Matches 23; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1 YKRLKLRVTHQTGGKPEKPRITLLDLRYVSGSGSFNEIPLLRQSTITVSDAKORVYVELIN 60
Db 1 KRLAKLRVTHQTGGKPEKPRITLLDLRYVSGSGSFNEIPLLRQSTITVSDAKORVYVELIN 60
QY 61 QGKXSTALINMYVYVAAKQKQKQSYFLAPRQATKTLFGTKXKSLPKYSXLYL 120
Db 61 QGQSTYTAIDIVNMYVAAKQKQKQSYFLAPRQATKTLFGTKRSLPKNSYDLYL 119
QY 121 RVAGHRDQIPVGIKXDLIQSYALXLPKPGSGSTKQASITLLIQMSIAPARFNPILMKRQX 180
Db 120 RVAGHRDQIPVGIKXDLIQSYALXLPKPGSGSTKQASITLLIQMSIAPARFNPILMKRQY 179
QY 181 TNSGKRPFDKMYALETSNMGQSTQVHSGTIDGKPNPKALIXKNTVLLANPKYLAS 240
Db 180 TNSGASRPFDVYVLETSNMGQSTQVHSGTIDGKPNPKALIKPNSVYLLANRQYLAS 239
QY 241 LAIQLPFCQGEKPESS 255
Db 240 LAIQLPFCQGEKPESS 254

```

RESULT 6
S16022
N:contains: abrin-c precursor - Indian licorice
C:Species: RNA N-glycosidase (EC 3.2.22)
C:Update: 19-Mar-1997 #sequence_revision 19-Mar-1997 #extl_change 20-Aug-1999
R:Accession: S16022
R:Author: Bloembergen, J. M.; Newmyczek, E. J.; Ptacek, M.
R:Date: 1988-07-23
A:Title: Preproabrin: genomic cloning, characterization and the expression of the A-chain
A:Accession number: S16022
A:Reference number: S16022
A:Status: preliminary
A:Molecule type: DNA
A:Cross-references: EMBL:X5567; NID:G16084; PTD:CA93202.1; PTD:G16085
A:Cross-references: RNA N-glycosidase in A chain, which inhibits protein synthesis by inactivating
the A and B chains and is linked
C:Superfamily: ricin; RNA N-glycosidase; glycosylase
C:Keywords: duplication; glycoprotein; homology; hydroxylase; lectin; pyroglyutamic acid
P:35-285/Product: abrin-c chain A #status predicted <RCH>
P:41-280/Domain: RNA N-glycosidase homology <RNG>
P:595-359/Product: abrin-c chain B #status predicted <BCH>
P:511-359/Product: 403-441, 448-481, 526-562/Region: 40-residue repeats
P:360/Motif: motif site: PYRROLIDONE CARBOXYLIC ACID (Gln) (in mature form) #status predicted
P:199-201/Active site: substrate (tyr, tyr, gln, asn) #status predicted
P:383-387,390-339,363-380,451-464,480-507/Distal:dis bonds: #status predicted
P:322,345/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
P:534,556/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

```

Best Local Similarity 46.1%; Pred.No.146-101;	
Matches 242;	Conservative 82; Mismatches 190; Indels 11; Gaps 9;
QY	9 THQYGVKFRFILLADIVYSGSSVEEILLQSTIVSDAQRFLVLEWYVQKDGSDXA 68
Dh	43 TEQAQSQSGKQFIALRKEQLTGGIHIDFVLPDPTTVEENRNRVITVEISNSEEIEV 100
QY	69 AIDVNTXVYVAKQKQSDVFYFLADPGAFPHLFGTETXSSLSPPKSYXDLSEPVAGH-RD 127
Dh	101 GIDVNTVYVAPRAGSGSSTFELKRPASASVYFPGTQRI-SLEFDSQGLSEMAHGTSE 159
QY	128 QTFIDFQKQLQSYALNAPGSGSTRQKARSLILLQMSAPAEFNPILMRKQXINSKXEP 187
Dh	160 EISLDQALTHLPIFLRSGANBESKATLIVYLQMSAPKPKRTINRNGISITGTAP 219
QY	220 QGPAPMSELENNMNLGSGVQGVODTFPNNVILSINRQPVVDSLSHPYVALNLMF 279
Dh	188 LRPXYMLFETSGNQSGQVQVHSDTGVPNNPXYLAXKXNPYTLKXV-RVLSIALIMLF 246
QY	247 VCGEPPSSDVPNVPYLFIRPIADVTCGS-EPYRIYKGSXKAVDVRDDDFHGNQIQ 305
Dh	280 VCMR-PNANQ---PILIRSTVSESKICSSRSEYETVRIQGDGMCVDVDDYGHNGRIIL 335
QY	306 LMPKSNKNNPQNLTKEDXITIKSGSGCLTGYTGAGVYVIMEDCKTAEATINQIKXN 365
Dh	336 AKMKCDRLSENLQTLAKSKTILINSKGLITGYPAPNPVIMVDCISVMEATVWELWON 395
QY	366 GIIINPSKULVLAASGKIRGTLTVQGLIDYLGQSGLAQNDJAPREVTIYGGPDIOMESN 425
Dh	396 GIIINPSKALVYVLESSESSGKGLITVQNLNLSLQDMKMTNDSLPVSTISGYSIDCQMQQ 455
QY	426 XGSMVDTCKSQKQKQKGLVQSDGSTRPQKQDGLTGMDSVSTVNTVSGSXXKQ 485
Dh	456 GSNVLDLADNNKKEG-QMHLVDSSTIRSYQVNLNGISKDHQGSFVLMACSGMAQSD 514
QY	486 RWFVETKALINLXXXXXXDVQAPAPKRLARIITVPAKGPQMWL 530
Dh	515 RMLFENDGSIYVLDIMDVQKSSPSKSLITLTFPHNGENQVIML 559

SEQUENCE 7
S32431
Abiridin precursor - Indian licorice (fragment)
N:Contains: rRNA N-glycosidases (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C:Date: 30-Sep-1997 #sequence_revision 01-AUG-1997 #text_change 01-AUG-1997
A:Accession: S32431; S34408
R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
U: Mole. Biol. 229, 263-267, 1993
I:Title: Primary structure of three distinct isoenzymes determined by cDNA sequencing
A:Accession: S32431; S32425; X01D:9512796; F01D:842315
A:Molecule type: mRNA
A:Residues: 1-528 <HUN>
A:Cross-references: GB:M96346
R:Hung, C.; Lee, M.; Lee, T.; Lin, J.
submitted to the EMBL Data Library, March 1993
A:Reference number: S34408
A:Accession: S34408
A:Molecule type: mRNA
A:Residues: 1-1697 C, 171-1930 T, 322-528 <HUN>
A:Cross-references: GB:M96346
C:Comment: A chain consists of an A chain, which inhibits protein synthesis by inacti-
vating the A and B chains are linked by a single disulfide bond, which is essential for
C:Specificity: ricin, rRNA N-glycosidase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; leu-
tine; 251/Product: abiridin chain A status predicted <RNO>
R:246/Domian: rRNA N-glycosidase homology <RNO>
R:282-323/Product: abiridin chain B status predicted <RCH>
R:383-528/Product: abiridin chain C status predicted <RCH>
P:102/Modified sites: 569701,144-149,453-492,493-528/Region: 40-residue repeats
P:102/Modified sites: 569701,144-149,453-492,493-528/Region: 40-residue repeats
P:74,113,195/Binding site: substrate rRNA, rRNA status predicted
P:64,147/Active site: Glu, Arg, Asn status predicted

F/200 253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/247-269,286-305,329-346,417-430,456-473/Diulfide bonds: #status predicted
 F/286,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F/500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 43.5% Score 1137.5; DB 2; Length 528;
 Best Local Similarity 46.1%; Pred. No. 1.6e-101;
 Matches 242; Conservative 83; Mismatches 189; Indels 11; Gaps 9;

9 TQCTGKXEFRTLLRDYVSGSFSNRPILRQSTFVSDAQFVLELTMQGXDXK 68
 9 TQCTGKXEFRTLLRDYVSGSFSNRPILRQSTFVSDAQFVLELTMQGXDXK 68
 69 AIDVTKXVYVAVKQSGYFLADAPRGATLPTGTAKSLPFGKSYDLERYAGH-ND 127
 69 AIDVTKXVYVAVKQSGYFLADAPRGATLPTGTAKSLPFGKSYDLERYAGH-ND 127
 67 GIDVYVAVKQSGYFLADAPRGATLPTGTAKSLPFGKSYDLERYAGH-ND 125
 67 GIDVYVAVKQSGYFLADAPRGATLPTGTAKSLPFGKSYDLERYAGH-ND 125

128 QIFLGIXQILOSVALKPKGSTRKXKRSILILQWISBAAPFPLMKXKXGKXSF 187
 128 QIFLGIXQILOSVALKPKGSTRKXKRSILILQWISBAAPFPLMKXKXGKXSF 187
 126 EISDGLQALHAIISPLKSGKNDKRTLVILQWISBAAPFPLMKXKXGKXSF 185
 126 EISDGLQALHAIISPLKSGKNDKRTLVILQWISBAAPFPLMKXKXGKXSF 185

186 QDPKMLSLNNMNTLSGQVQSGVDTFNNVTLISINRQPVYDLSHPVAVLALMF 245
 186 QDPKMLSLNNMNTLSGQVQSGVDTFNNVTLISINRQPVYDLSHPVAVLALMF 245

247 VCGEPSSDVKRWVPLRVPLADVTCAS-EPYRIVRGKXKXVDVDDDPHQQIO 305
 247 VCGEPSSDVKRWVPLRVPLADVTCAS-EPYRIVRGKXKXVDVDDDPHQQIO 305

246 VCP-PRANOS--PLIRISIVRSKICSGSYEPYRIVRGKXKXVDVDDDPHQQIO 301
 246 VCP-PRANOS--PLIRISIVRSKICSGSYEPYRIVRGKXKXVDVDDDPHQQIO 301

306 LPPXMLETSWQSGSTOVQSHSTGVNNKXRLAIXGNFVTLKXN-EXVILSLALMF 246
 306 LPPXMLETSWQSGSTOVQSHSTGVNNKXRLAIXGNFVTLKXN-EXVILSLALMF 246

302 AMKCDRLKEMQWLTLSKDKTIRNSGCLTYGTAGVYVMIPOCATREAIQWIKN 365
 302 AMKCDRLKEMQWLTLSKDKTIRNSGCLTYGTAGVYVMIPOCATREAIQWIKN 365

366 GTIIMPNSVLVAASGKGTITVOTLDYTLQCGMLAGNDPAREVITVPGPDCKESN 425
 366 GTIIMPNSVLVAASGKGTITVOTLDYTLQCGMLAGNDPAREVITVPGPDCKESN 425

362 GTIIMPNSVLVAASGKGTITVOTLDYTLQCGMLAGNDPAREVITVPGPDCKESN 421
 362 GTIIMPNSVLVAASGKGTITVOTLDYTLQCGMLAGNDPAREVITVPGPDCKESN 421

426 XGSWVETCKSSQXKXMAVYGDSTRKXKXVDVDDDPHQQIO 485
 426 XGSWVETCKSSQXKXMAVYGDSTRKXKXVDVDDDPHQQIO 485

422 GSNVWLVADCKNKEQ-QMLVYDSTRKXKXVDVDDDPHQQIO 480
 422 GSNVWLVADCKNKEQ-QMLVYDSTRKXKXVDVDDDPHQQIO 480

486 RWFTNEXALINLKKKXKXMAVYGDSTRKXKXVDVDDDPHQQIO 530
 486 RWFTNEXALINLKKKXKXMAVYGDSTRKXKXVDVDDDPHQQIO 530

481 RWFTNEXALINLKKKXKXMAVYGDSTRKXKXVDVDDDPHQQIO 525
 481 RWFTNEXALINLKKKXKXMAVYGDSTRKXKXVDVDDDPHQQIO 525

RESULT 8

S32430
 Abirin-b precursor - Indian licorice (fragment)
 N/Contains: RNA N-glycosidase (EC 3.2.2.22)
 C/Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
 C/Accession: S32430; UCI399

R/Kimura, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
 J. Mol. Biol. 229, 263-267, 1993

A/Title: Primary structure of three distinct isozymes determined by cDNA sequencing.
 A/Reference number: S32430; PMID:9312798; PMID:842313

A/Accession: S32430

A/Molecule type: mRNA

A/Cross-references: GB:W93145; NID:G166266; PTDN:AAA32625.1; PID:G166297

A/Keywords: Biotechnol. Biochem. 57, 166-169, 1993

A/Title: The complete amino acid sequence of the B-chains of Abirin-a and Abirin-b, toxic

A/Accession: UCI399

A/Molecule type: protein

A/Residues: 250-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'W', 427, 'D', 429-430

A/Experimental source: seed

A/Keywords: diulfide bond, disulfide isomerase, glycosidase, hydrolase, lectin, F

F/1-250/Product: abirin-b chain A #status predicted <ACH>

F/7-245/Domain: RNA N-glycosidase homology <RNG>

F/360-527/Product: abirin-b chain B #status experimental <ACH>
 F/282-324,325-365,366-406,413-448,452-473/Region: 40-residue repeats
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
 F/74,113,194,195/Binding site: substrate (Tyr, Tyr, Gln, Asn) #status predicted
 F/110,360,400/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/163,166/Active site: Gln, Arg #status predicted
 F/246-268,285-304,328-345,416-429,455-472/Diulfide bonds: #status predicted
 F/287,311/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
 F/499,520/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 42.5% Score 1113; DB 2; Length 527;
 Best Local Similarity 45.5%; Pred. No. 3.8e-99;
 Matches 239; Conservative 83; Mismatches 191; Indels 12; Gaps 10;

9 TQCTGKXEFRTLLRDYVSGSFSNRPILRQSTFVSDAQFVLELTMQGXDXK 68
 9 TQCTGKXEFRTLLRDYVSGSFSNRPILRQSTFVSDAQFVLELTMQGXDXK 68
 9 TQCTGKXEFRTLLRDYVSGSFSNRPILRQSTFVSDAQFVLELTMQGXDXK 66
 9 TQCTGKXEFRTLLRDYVSGSFSNRPILRQSTFVSDAQFVLELTMQGXDXK 66

69 AIDVTKXVYVAVKQSGYFLADAPRGATLPTGTAKSLPFGKSYDLERYAGH-ND 127
 69 AIDVTKXVYVAVKQSGYFLADAPRGATLPTGTAKSLPFGKSYDLERYAGH-ND 127
 67 GIDVYVAVKQSGYFLADAPRGATLPTGTAKSLPFGKSYDLERYAGH-ND 125
 67 GIDVYVAVKQSGYFLADAPRGATLPTGTAKSLPFGKSYDLERYAGH-ND 125

128 QIFLGIXQILOSVALKPKGSTRKXKRSILILQWISBAAPFPLMKXKXGKXSF 187
 128 QIFLGIXQILOSVALKPKGSTRKXKRSILILQWISBAAPFPLMKXKXGKXSF 187
 126 EISDGLQALHAIISPLKSGKNDKRTLVILQWISBAAPFPLMKXKXGKXSF 185
 126 EISDGLQALHAIISPLKSGKNDKRTLVILQWISBAAPFPLMKXKXGKXSF 185

186 QDPKMLSLNNMNTLSGQVQSGVDTFNNVTLISINRQPVYDLSHPVAVLALMF 245
 186 QDPKMLSLNNMNTLSGQVQSGVDTFNNVTLISINRQPVYDLSHPVAVLALMF 245

247 VCGEPSSDVKRWVPLRVPLADVTCAS-EPYRIVRGKXKXVDVDDDPHQQIO 305
 247 VCGEPSSDVKRWVPLRVPLADVTCAS-EPYRIVRGKXKXVDVDDDPHQQIO 305

246 VCP-PRANOS--PLIRISIVRSKICSGSYEPYRIVRGKXKXVDVDDDPHQQIO 301
 246 VCP-PRANOS--PLIRISIVRSKICSGSYEPYRIVRGKXKXVDVDDDPHQQIO 301

306 LPPXMLETSWQSGSTOVQSHSTGVNNKXRLAIXGNFVTLKXN-EXVILSLALMF 246
 306 LPPXMLETSWQSGSTOVQSHSTGVNNKXRLAIXGNFVTLKXN-EXVILSLALMF 246

302 AMKCDRLKEMQWLTLSKDKTIRNSGCLTYGTAGVYVMIPOCATREAIQWIKN 365
 302 AMKCDRLKEMQWLTLSKDKTIRNSGCLTYGTAGVYVMIPOCATREAIQWIKN 365

366 GTIIMPNSVLVAASGKGTITVOTLDYTLQCGMLAGNDPAREVITVPGPDCKESN 425
 366 GTIIMPNSVLVAASGKGTITVOTLDYTLQCGMLAGNDPAREVITVPGPDCKESN 425

362 GTIIMPNSVLVAASGKGTITVOTLDYTLQCGMLAGNDPAREVITVPGPDCKESN 421
 362 GTIIMPNSVLVAASGKGTITVOTLDYTLQCGMLAGNDPAREVITVPGPDCKESN 421

426 XGSWVETCKSSQXKXMAVYGDSTRKXKXVDVDDDPHQQIO 485
 426 XGSWVETCKSSQXKXMAVYGDSTRKXKXVDVDDDPHQQIO 485

422 GSNVWLVADCKNKEQ-QMLVYDSTRKXKXVDVDDDPHQQIO 480
 422 GSNVWLVADCKNKEQ-QMLVYDSTRKXKXVDVDDDPHQQIO 480

486 RWFTNEXALINLKKKXKXMAVYGDSTRKXKXVDVDDDPHQQIO 530
 486 RWFTNEXALINLKKKXKXMAVYGDSTRKXKXVDVDDDPHQQIO 530

481 RWFTNEXALINLKKKXKXMAVYGDSTRKXKXVDVDDDPHQQIO 524
 481 RWFTNEXALINLKKKXKXMAVYGDSTRKXKXVDVDDDPHQQIO 524

RESULT 9

RCSNG
 agglutinin precursor - castor bean
 N/Contains: RNA N-glycosidase (EC 3.2.2.22)
 C/Species: Ricinus communis (castor bean)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C/Accession: A24261; A24210

R/Roberts, L.W.; Lamb, D.J.C.; Lord, J.M.
 J. Biol. Chem. 268, 16683-16685, 1993

A/Title: The primary structure of Ricinus communis agglutinin. Comparison with ricin

A/Reference number: A24261; PMID:8605949; PMID:2899130

A/Accession: A24261

A/Molecule type: mRNA

A/Cross-references: GB:M12089; NID:G169700; PTDN:AAA3369.1; PID:G169701

A/Keywords: Biophys. Acta 872, 277-285, 1986

A/Title: The complete amino acid sequence of the B-chain of the Ricinus communis ag

A/Accession: A24210

A/Molecule type: protein

A/Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V'

A:Residues: 1-69, '86, '72-209, 'N, 211-241, 243-250, 'V, 252-263 <RBA>
 A:Residues: 1-69, '86, '72-209, 'N, 211-241, 243-250, 'V, 252-263 <RBA>
 C:Superfamily: rRNA N-glycosylase homology
 C:Keywords: duplication; glycoprotein; glycosidase; hydrolase
 F:1-263/Product: rRNA N-glycosylase; hydrolase
 F:11-59, 60-100, 103-141, 148-183, 187-226, 229-263/Region: 40-residue repeats
 F:20-39, 63-80, 151-164, 190-207/Distillate bonds: #status predicted
 F:35, 135/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 31.4%; Score 822; DB 2; Length 263;
 Best Local Similarity 35.2%; Pred. No. 1.8e-71;

Matches 154; Conservative 32; Mismatches 72; Indels 2; Gaps 2;

DB 4 CNDPEYIVRIVGRNG/CVVDGRFHNGNAIQLPCKNDIDANQWLKRENTIRNKC 63
 QY 274 CSASEPTVIRVGRNGKXVVDVDDPHQNOIQLPCKNDIDANQWLKRENTIRNKC 333
 DB 334 LTTVGTAGVYVIFPCMTAERATIQVWKGITINFRSNVYLAASGIGKTTITVQL 393
 DB 64 LTTVGTAGVYVIFPCMTAERATIQVWKGITINFRSNVYLAASGIGKTTITVQL 123

QY 394 DYTLCQGLAGNDPARETTITVGRFDCNESKSTVETVCSQKXKXALKQSGIT 453
 DB 124 IVAGQGLPMTNQTPTTIVGLKGCANSGKXVLEDCSEKADQ-QMLKADSGIR 182

QY 454 PRONOCITKGRDVSIVIVSCKSXKXQRFVPEKXILNKXXXXXDVQAKNP-K 512
 DB 183 PQQRNDCLTDANIKATVAILSCGVSSQGRWFXDPTILVINGLADVRSDPS 242

QY 513 LRRIITVATGRNQWMLPV 532
 DB 243 LKQILVFRHGNLQMLDP 262

RESULT 12
 C39761
 abrin (clone 7.2) precursor - Indian licorice (fragment)
 N:Contains: rRNA N-glycosylase (EC 3.2.2.22)
 C:Species: Abrus precatorius (Indian licorice)
 C:Date: 21-Feb-1992 #sequence revision 31-Dec-1993 #text_change 20-Aug-1999
 C:Accession: C39761; S14471
 R:Bjerskov, G.; Mathiesen, A.; Sundan, A.
 A:Title: Direct molecular cloning and expression of two distinct abrin A-chains.
 A:Reference number: A39761; MUID:91201329; PMID:2016500
 A:Accession: C39761
 A:Molecule type: DNA
 A:Residues: 1-251 <EV>
 R:Bjerskov, G.; Mathiesen, A.; Sundan, A.
 A:Title: Direct molecular cloning and expression of two distinct abrin A-chains.
 A:Reference number: S14471
 A:Accession: S14471
 A:Molecule type: DNA
 A:Residues: 1-251 <EV>

A:Cross-references: EMBL:X54872; NID:G16088; PDB:CAA3654.1; PID:G16088
 C:Superfamily: rRNA N-glycosylase homology
 C:Keywords: duplication; glycosidase; hydrolase; lectin; toxin
 F:1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
 F:7-246/Domains: rRNA N-glycosylase homology <RNS>
 F:74, 113, 195, 196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F:104, 167/Active site: Glu, Arg #status predicted

Query Match 17.0%; Score 443.5; DB 2; Length 251;
 Best Local Similarity 43.8%; Pred. No. 5.6e-35;
 Matches 106; Conservative 34; Mismatches 97; Indels 5; Gaps 5;

QY 9 TQOTGXEFREFTLADVYSSGPNFIPLDQSTPVSDQGVVAVELVHQXSKSTA 68
 DB 9 TQOTGXEFREFTLADVYSSGPNFIPLDQSTPVSDQGVVAVELVHQXSKSTA 66
 QY 63 AIVTXXVYVAGGDSYFLANPQGHFHTFTGTXSLPFGSGYKILERRACH RD 127

DB 67 GIVTNAVYVAVRAGSOSYFLRADAASVTFPTGQRY-SLRFDSGIDLERNAQRE 125
 QY 128 QIEGIXLOLVYAAKRGSGSTRKQSRITLLOVISEARPNILMKRXQNSGSP 187
 DB 126 QIEGIXLOLVYAAKRGSGSTRKQSRITLLOVISEARPNILMKRXQNSGSP 185
 QY 188 LPTXVMELETSNQOSQDQVGHSTQGVNPNPRLAKXGNFVTLXNV-KVYASLAIMLF 246
 DB 186 QDPNALSLENNWNLISRGVSDCTFPNAVLERVNNQPVIVDSILQSVAVLIMLF 245
 QY 247 VC 248
 DB 246 VC 247

RESULT 13
 J05032
 Karasurin-B - Trichosanthes kirilowii var. japonica
 C:Species: Trichosanthes kirilowii var. japonica
 C:Date: 27-Feb-1997 #sequence revision 27-Feb-1997 #text_change 23-May-1997
 C:Accession: J05032
 R:Kombo, I.; Kikuchi, H.; Takagi, T.; Ogihara, Y.
 A:Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B
 A:Reference number: J05032; MUID:97108848; PMID:8951155
 A:Accession: J05032
 A:Comment: This protein belongs to type I ribosomal-inactivating proteins which can
 A:Superfamily: rRNA N-glycosylase homology <RNS>
 F:14-243/Domains: rRNA N-glycosylase homology <RNS>

Query Match 11.8%; Score 109.5; DB 2; Length 247;
 Best Local Similarity 35.6%; Pred. No. 4.6e-22;
 Matches 85; Conservative 45; Mismatches 96; Indels 13; Gaps 8;

QY 11 TQYEFREFTLADVYSSGPNFIPLDQSTPVSDQGVVAVELVHQXSKSTA 72
 DB 10 TQYEFREFTLADVYSSGPNFIPLDQSTPVSDQGVVAVELVHQXSKSTA 70
 QY 73 TQYEFREFTLADVYSSGPNFIPLDQSTPVSDQGVVAVELVHQXSKSTA 130
 DB 67 TQYEFREFTLADVYSSGPNFIPLDQSTPVSDQGVVAVELVHQXSKSTA 126
 QY 131 GIXIOLVYVAGGDSYFLANPQGHFHTFTGTXSLPFGSGYKILERRACH RD 190
 DB 127 LQPLDADATTLTPYVANS-AASALMVLVIGSTSEKARYFEQIGKVDK-TFLPS 182
 QY 191 XYMELETSNQOSQDQVGHSTQGVNPNPRLAKXGNFVTLXNV-KVYASLAIMLF 245
 DB 183 LPTXVMELETSNQOSQDQVGHSTQGVNPNPRLAKXGNFVTLXNV-KVYASLAIMLF 245

RESULT 14
 R1472
 rRNA N-glycosylase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - (Mongol)
 N:Alternate names: alpha-TCS; type I ribosome-inactivating protein
 C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)
 C:Date: 30-Sep-1988 #sequence revision 26-Jan-1996 #text_change 23-Mar-2001
 C:Accession: J05056; A36274; J01093; A36273; J05003
 R:Shaw, P.C.; Chung, W.H.; Zhu, R.H.; Ho, W.K.; Ng, T.B.; Yeung, H.W.
 A:Title: Cloning of Trichosanthin cDNA and its expression in Escherichia coli.
 A:Reference number: J05056; MUID:9153657; PMID:1992921
 A:Accession: J05056
 A:Molecule type: rRNA
 A:Residues: 1-289 <SHA>
 A:Cross-references: GB:M34858; NID:G170536; PDB:AAA4207.1; PID:G170537
 A:Experimental source: tuber
 U:Shaw, P.C.; Chung, W.H.; Zhu, R.H.; Ho, W.K.; Ng, T.B.; Yeung, H.W.
 A:Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type

Tue Dec 11 16:03:44 2003

US-09-601-667C-1.exp

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 11, 2003, 13:53:18 ; Search time 9.15946 Seconds
(without alignments)

2736.539 Million cell updates/sec

Title: US-09-601-667C-1

Sequence: 1 YERLRARYHTQTEKXEPF.....RRIITPAKPKMKWMLPFV 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database: SwissProt_41.*

Prod No. is the number of results predicted by chance to have a
score greater than or equal to the score of the candidate being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1230	49/5	1 MUB_VISAL	P03130 Viscum album
2	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
3	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
4	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
5	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
6	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
7	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
8	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
9	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
10	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
11	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
12	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
13	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
14	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
15	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
16	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
17	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
18	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
19	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
20	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
21	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
22	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
23	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
24	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
25	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
26	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
27	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
28	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
29	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
30	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
31	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
32	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
33	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album

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6	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
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11	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
12	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
13	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
14	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
15	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
16	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
17	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
18	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
19	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
20	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
21	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
22	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
23	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
24	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
25	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
26	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
27	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
28	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
29	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
30	1183.5	45/2	1 ABRP_ABRP	P03130 Viscum album
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